

(2) INFORMATION FOR SEQ ID NO: 20:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTTGAAGAG TGTACAGTAC AGGATTATTA TAATGAAAGT TTATATCAAC AGGGTTTCGT 60
15 TGGCTCTGCA TATATTATAA GCAAAAGAGA TTGGTAAAGT GCCACAGTAT TCCAGATAAC 120
TTTTCAGTTG CGGCCTTTCT TCTCGTTCTT TAATTTGAAA CCTAGATACA TGCAGTAAAA 180
20 ACTAGGAGAA TGACTTTTAC CCTTGGGGAC AGCCAAGTTT TGTGATAAAA CCTATTTCCT 240
AGCATGCCTT CAGGAAGTTG TGCCAGACCC TAGATTGTGA AGGACCCACT GTTCTTCTGT 300
TGTACGAGCT CCCTGAACCA TTGTTTCAGAG GACCAATGTC ACATCGCTTC ATGGGCATGG 360
25 NCCATGGGAG CATCTGGGTG ATAYCTGTCT ACAGTATTGG CTCTTCTGCG AGGCTGATAC 420
ACAAGGCCTC TCTTCCACAT GATCATTTGC AAACCTCCCC CAGCCCCTAC CATCCAATGT 480
30 GGAAGGAAAA CAAGAACTGC CTGAAGAAGA GTCCAAGCTA CAGATACACA GCGTGTGCAT 540
TGCGGCTGTC ACCTTCCTCC TCCCACTTCT GTATCCTCAG AGATGCTGCG TGGATGTTTC 600
CTTAACCTCA GCTGACTTCC CTGTGAATGT CTAATGCTAG TTCAGGGCCT CCAGGCATTG 660
35 ATTTGTACAG TGGTAACTCC CAATGAGGCT TCTGTTATCA TTTGGTGTGC TTTTCTGTG 720
ATTAAAGAA ATGATTTTCC C 741

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(2) INFORMATION FOR SEQ ID NO: 21:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACCAGTC TCCCCTGGGG AAGTTTTTCT TTTTCAGGAG GGAGGAGGGC TTTCCAGGT 60
AATGTGTCTA GAGTGTGGG CAGAAAATCT GGGACCACAC CACACCAGTT CTCTCCTTAA 120
55 TCCACGTCAT TTGCCTTCTA TCCCAGCTAT GTTCCAGTG TCCTCTGGGT GTTCCAAGA 180
GCAACAAGAA ATGAATAAAT CTCTGGTGAG TTGTTTATTT GTTCTTCACT TTGTTTTACA 240
60 CTGTATTTTC TGAGTTTATG GGTGTCTGTG AATTAAAAAG GAAAAGTAGA AATAAGTAAA 300

ACTCAGGTTG AAGGAAATAT ACATAAATAA GATAAAGCTG ACCTGTAGAT ATAGCAGGTT 360
 5 ATAAAGCTTA GAGTTGTCTA AGTTGAGTGC AAATTTTCCT CTGATCTTTC TGATGCCGAA 420
 CAAAAAGCA GTCATGTTTG TTATGTGATT GGAATGGAAC CCGAGAAGAG AGCATGCTGT 480
 GTTCTTGTTGG GACAGGAAAG CTTGCGTGCA CCAAGTCTGA ACCACCACCT TCATGGTGAC 540
 10 ATAGATTATG TGCTGGAACA TATTTACACAC CGGCCTGGCA GTAAACACTT GTAGTGTGTG 600
 GCAGTGAAA CGGTCATCTT CCGCTAAAGC ACGGCGTGTT GTGCAGCGGA AATGGTCATC 660
 15 TGCTGCTAAA ACACAGCTTC CATCGTAATG TATGCTCCTT ACTCAAAGAG TGTGGTCCCA 720
 AACAGCCTTT GGGAGGTCCT CCTTGATTCA TGGATGAAAC CTGGAACATC TTGAGGACTG 780
 AGTTAACCAT AGGTCCTTAA ATAACCTCTCC ACACGTTTTT CTTAGTTTAT CTCTACATGC 840
 20 AGGGTGTGCA GCAGCCTGTT CAAAGTCATA TTTTCTGGGA AATATTCCA GTGTTTATTT 900
 GCACTTAGC CCACTCTGTG TAGCCTTATT TCTTCTAAAC TCACCATTAA TCTGAATAAT 960
 25 AGTCAAATTT AGGGGGACTG TATTTGCCTT A 991

30 (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

40 CCACGCGTCC GGAATTCCTT TGAGGATCTT GGGCTATCTT TGACAGGGGA TTCTTGCAAG 60
 TTGATGCTTT CTACAAGTGA ATATAGTCAG TCCCCAAGA TGGAGAGCTT GAGTTCTCAC 120
 AGAATTGATG AAGATGGAGA AAACACACAG ATTGAGGATA CGGAACCCAT GTCTCCAGTT 180
 45 CTCAATTCTA AATTGTTTCC TGCTGAAAAT GATAGTATCC TGATGAATCC AGCACAGGAT 240
 GGTGAAGTAC AACTGAGTCA GAATGATGAC AAAACAAAGG GAGATGATAC AGACACCAGG 300
 50 GATGACATTA GTATTTTAGC CACTGGTTGC AAGGGCAGAG AAGAAACGGT AGCAGAAGAA 360
 GTTGTATTG ATCTCACTTG TGATTCGGGG AGTCAGGCAG TTCCGTCACC AGCTACTCGA 420
 TCTGAGGCAC TTTCTAGTGT GTTAGATCAG GAGGAAGCTA TGGAAATTAA AGAACACCAT 480
 55 CCAGAGGAGG GGTCTTCAGG GTCTGAGGTG GAAGAAATCC CTGAGACACC TTGTGAAAGT 540
 CAAGGAGAGG AACTCAAAGA AGAAAATATG GAGAGTGTTC CGTTGCACCT TTCTCTGACT 600
 60 GAAACTCAGT CCCAAGGGTT GTGTCTCGG AGGCATCCAA AAAAAAAAAA AAA 653

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

5	GGCAGGCTGA CGACCTGCAA GCCACAGTGG CTGCCCTGTG CGTGCTGCGA GGTGGGGGAC	60
10	CCTGGGCAGG AAGCTGGCTG AGCCCCAAGA CCCCAGGGGC CATGGGCGGG GATCTGGTGC	120
15	TTGGCCTGGG GGCCTTGAGA CGCCGAAAGC GCTTGCTGGA GCAGGAGAAG TCTCTRGCCG	180
20	GCTGGGCACT GGTGCTGGCA SGARCTGGCA TTGGAATCAT GGTGCTGCAT GCAGAGATGC	240
25	TGTGGTTTCGG GGGGTGCTCG GCTGTCAATG CCACTGGGCA CCTTTCAGAC AACTTTGGC	300
30	TGATCCCAT CACATTCTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC ACCATGTGGG	360
35	GCAAGATCGT YTGCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC CTGCTGGTGG	420
40	CCGTGGTGGC CCGGAAGCTG GAGTTTAACA AGGCAGAGAA GCACGTGCAC AACTTCATGA	480
45	TGGATATCCA GTATACCAA GAGATGAAG AGTCCGCTGC CCGAGTGCTA CAAGAAGCCT	540
50	GGATGTTCTA CAAACATACT CGCAGGAAG AGTCTCATGC TGCCCGCANG CATCAGCGCA	600
55	ANCTGCTGGC CGCCATCAAC GCGTTCGCGC AGGTGCGGCT GAAACACCGG AAGCTCCGGG	660
60	AACAAGTGAA TTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT GACCTGCAGC	720
65	AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG GCGGGGAAGC	780
70	TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT CCAGAACCCA	840
75	GCCAGCAGTC CAAGTAGCTG GACCCACGAG GAGGAACCAG GCTACTTTCC CCAGTACTGA	900
80	GGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCCAGCCCTG AACAAAGCAC CTCAAGTGCA	960
85	AGGACCAAAG GGGGCCCTGG CTTGGAGTGG GTTGGCTTGC TGATGGCTGC TGGAGGGGAC	1020
90	GCTGGCTAAA GTGGGKAGGC CTTGGCCAC CTGAGGCCCC AGGTGGGAAC ATGGTCACCC	1080
95	CCACTCTGCA TACCTTCATC AAAAACAATC TCACTATGCT GCTATGGACG ACCTCCAGCT	1140
100	CTCAGTTACA AGTGCAGGCG ACTGGAGGCA GGAATCCTGG GTCCCTGGGA AAGAGGGTAC	1200
105	TAGGGGCCCC GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAACT	1260
110	GGGTATGAGG CTGGGGCGGG GCTGGAGGTG GCGCCCCCTG GTGGGACAAC AAAGAGGACA	1320
115	CCATTTTTC CAGAGCTGCAG AGAGCACCTG GTGGGGAGGA AGAAGTGTA CTCACCAGCC	1380
120	TCTGCTCTTA TCTTTGTAAT AAATGTTAAA GCCAGAAAAA AATAAAAAAA AAAAAAAAAA	1440

AACTCGAGGG GGGCCCRKAC CCAATCWCCC TATAGTAKAC GTANNN

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(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

	CTTCGCCGTT TCTCCTGCCA GGGGAGGTCC CGGCTTCCCG TGGAGGCTCC GGACCAAGCC	60
	CCTTCAGCTT CTCCTCCGG ATCGATGTGC TGCCGCGGCC GCCGCCCGCC TCCCGCGTCC	120
20	TTCCGTCTCT GCTCCCGGA CCCGGCTCCG CGCAGCCAGC CAGCATGTCG GGGATCAAGA	180
	AGCAAAAGAC GGAGAACCAG CAGAAATCCA CCAATGTAGT CTATCAGGCC CACCATGTGA	240
25	GCAGGAATAA GAGAGGGCAA GTGGTTGGAA CAAGGGGTGG GTTCCGAGGA TGTACCGTGT	300
	GGCTAACAGG TCTCTCTGGT GCTGGGAAAA ACAACGATAA GTTTTGCCCT GGAGGAGTAC	360
	TTGTCTCCCA TGCCATCCCT GTTAATTCCT GGATGGGGAC AATGTCCGTC ATGGCCTTAA	420
30	CAGAATCCCC CAGATGGCTT CATGGCCCC AAAGCATGGA AGGTCTGAC AGATTATTAC	480
	AGGTCCCTGC AGAAGAACTA AGCCTTTGGT CCAGAGTTTC TTTCTGAAGT GCTCTTTGAT	540
35	TACCTTTTCT ATTTTATGA TTAGATGCTT TGTATTAAAT TGCTTCTCAA TGATGCATTT	600
	TAATCTTTTA TAATGAAGTA AAAGTTGTGT CTATAATTAA AAAAATATAT ATATATATAC	660
	ACACACACAT ATACATACAA AGTCAAACG AAGACCAAAT CTTAGCAGGT AAAAGCAATA	720
40	TTCTTATACA TTTCATAATA AAATTAGCTC TATGTATTTT CTAAGTACC TGAGCAGGCA	780
	GGTCCCAGAT TTCTTAAGGC TTGTTTGAC CATGTGTCTA GTTACTTGCT GAAAAGTGAA	840
45	TATATTTTCC AGCATGTCTT GACAACCTGT ACTCTTCCAA TGTCATTTAT CAGTTGTAAA	900
	ATATATCAGA TGTGTCTCT TCTGTACAAT TGACAAAAA AAAAATTTT TTTTCTCACT	960
	CTAAAAGAGG TGTGGCTCAC ATCAAGATTC TTCCTGATAT TTTACCTCAT GCTGTACAAA	1020
50	GCCTTAATGT TGTAATCATA TCTTACGTGT TGAAGACCTG ACTGGAGAAA CAAAATGTGC	1080
	AATAACGTGA ATTTTATCTT AGAGATCTGT GCAGCCTATT TCTGTCACAA AAGTTATATT	1140
55	GTCTAATAAG AGAAGTCTTA ATGGCCTCTG TGAATAATGT AACTCCAGTT ACACGGTGAC	1200
	TTTTAATAGC ATACAGTGAT TTGATGAAAG GACGTCAAAC AATGTGGCGA TGTGCTGGAA	1260
60	AGTTATCTTT CCCGCTCTTT GCTGTGGTCA TTGTGTCTTG CAGAAAGGAT GGCCCTGATG	1320

	CAGCAGCAGC GCCAGCTGTA ATAAAAAATA ATTCACTA TCAGACTAGC AAGGCACTAG	1380
	AACTGGAAAA GACCACAGAA AACAAAGAAT CCAACCCTTT CATCTTACAG GTGAACAAAC	1440
5	TGTGATGATG CACATGTATG TGTTTTGTA GCTGTGAGCA CCGTAACAAA ATGTAAATTT	1500
	GCCATTATTA GGAAGTGCTG GTGGCAGTGA AGAAGCACCC AGGCCACTTG ACTCCCAGTC	1560
10	TGGTGCCCTG TCTACACCAG ACAACACAGG AGCTGGGTCA GATTCCTTC AGCTGCTTAA	1620
	CAAAGTTCCT CGAACAGAAA GTGCTTACAA AGCTGCCTTC TCGGATACTG AAAGGTCGAG	1680
	TTTCTGAAC TGCCTGATT TTATTGCAGT TGAAAAAAA AAAAAGCTAT TCCAAAGATT	1740
15	TCAAGCTGTT CTGAGACATC TTCTGATGGC TTTACTTCCT GAGAGGCAAT GTTTTTACTT	1800
	TATGCATAAT TCATTGTTGC CAAGGAATAA AGTGAAGAAA CAGCACCTTT TAATATATAG	1860
20	GTCTCTCTGG AAGAGACCTA AATTAGAAAG AGAAACTGT GACAATTTTC ATATTCTCAT	1920
	TCTTAAAAAA CACTAATCTT AACTAACAAA AGTCTTTTG AGAATAAGTT ACACACAATG	1980
	GCCACAGCAG TTTGTCTTTA ATAGTATAGT GCCTATACTC ATGTAATCGG TTAICTACTA	2040
25	CTGCCTTTAA AAAAAAAAC CAGCATATTT ATTGAAAACA TGAGACAGGA TTATAGTGCC	2100
	TTAACCGATA TATTTTGTGA CTAAAAAAT ACATTTAAAA CTGCTCTTCT GCTCTAGTAC	2160
30	CATGCTTAGT GCAAATGATT ATTTCTATGT ACAACTGATG CTGTCTCTTA TTTTAATAAA	2220
	TTTATCAGAG TGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	2323
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(2) INFORMATION FOR SEQ ID NO: 25:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

	GGCAGAGCC TGTGTGGTCA GTTCTCTCGT GGTGCAGTAC CTGACATGAG CCAGCCACGC	60
50	TCAGTGGCTG AACAGCATTC CCACAGCCTG CAAGTGTGTG TGTGTGTGAA AGAGAGAGGG	120
	GGGCCAGAG CCGCCTTTTG AAATGTTTGC CTGTCTGAAC TGTGAAGACA CTTGGGAGTG	180
55	ATTGTGGTCT AATTCCAAC CTGCTCTGTT TTCTGTGACA TCTTGGAGGG GAGCTAGTGC	240
	CACACCATGC GCGGTGCTTA GAAATGAAAA AGTCCCGGGT CTGTCTCTCT CACTCTCGCT	300
	CTCATGGGGG AGGGAAAGAA TGGCTTTGGT GGCTTTGTTC ACACAGCTGA TGCCTGCTGG	360
60	GAAGGTGTCC ACAGTGAGCC TGTGTGCAGG ACTGTCCACA CGGTTACAC TTGTCACCAT	420

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25	CTGAGAAAAGG AAAGCATTTCG GATCTGCTGC AAAAACACAT ATATCCATAA AGACTCATGT	60
	TATTCAGAAA ACAGATTGTG AACACAATCA CATTGCGATG AATCCTTTAA AAGGAAGAAG	120
	ACCTTAAAGT ATCTGCAAAT CTGAATTTCT ATTTATTCCT TCACTGAATA TAGAAACAAT	180
30	GGTTATCTGA TTATTAGAGA TATTATTTTG GATATGTTAC TTATTAACIT GCTATGGCTG	240
	GTAACCATGA TAAAGTCTGT TATTAATAAC AACATAATTC TTTTTTTTAA GAAGAAAAGC	300
35	TTATTTTTTCA TTGACAGTGT ATAGATTTAT CTACTTAGTT GTGTTTGTCT ATTAGTGTTT	360
	TAATTTTTTTT TTTAAGTTGA GTGTTTGATA AATTTTAA GAAGTCTCCC ACCTTGTTTTT	420
	GAGTCCTGTG TTGACTACAG GTATATAGCY CAWTTTAAAA ATCCTAAAGC AAAAGAATTT	480
40	TATTTATAAA AGAATCMAMC MGTGTCATGC ATGAGGCTGT GAAGTCAGAT ATTTAGTAAT	540
	AAAAGCAGCA GTGCCTTTTT TTGTATTTAC CCATTGACCC CCACCAAATG CAACTGTTTTT	600
45	ATATTAAGAA AATAGTAACA ATTTTAAAAT CTCAGAGTAA AATCTATTTT ACTACATGCT	660
	TTTCCCCCCT TGTTCCTGATT TAAGCAGTGT GTACTTGGCA TCTCTACATT GTCCTAGGGA	720
	CAGTGGTGTT CTACAATATT ATCATGTATG ATGTTTTATT GGTGCTTTTT ATTCATAGTG	780
50	GCTTCTTACC AGAAACAGTA GGAAGAAACA CATGAACTGT GTACAAGACA TGAAACATTG	840
	CTGCTGATAT GTTGTTTTTT CACATGCTTT TGAGTTTTCA CTTTTTAAAC GAGAGCCAGC	900
55	AAGCAAAATA GATGTGGCTG GGTCTGCCTG TCCGGGCGGC TYTTTGCACC GAGCTCTCAA	960
	ATCCTGTGTA TTGAGGGTTC CTTTTTGGTA CTCAGGATTG GAGCTACAGC TGGGCCCCCC	1020
60	TCTCTCCCAT TCGTTTGAAG AGACACTGAG GGAAACAAGG GTTCTTTTTG AGGTGTCCTT	1080

GGCTGCCTTT TACGGGATGG GAGCCTTCTC CGGATCTTTT GTTCTTCTGC ACCTCTTGTA 1140
 GCTACTGCCG GTGCAAGGTT GTAGATGTTA TTCCCCAGGA GCCTGGGCTK GGGGGCTGAG 1200
 5 CTGGGCTGAA TGCAAAAGCA TGCAACCAGA AGGCGGGCAA GGGGAGGAAA AGCAGGCCTG 1260
 GCCTCATTGG TCCCCTGGAG ATGTCTGTAG CAGTCAGCTC CAGCTTGGGC CTGGGGAAGC 1320
 10 AGCCTGACCA AGGCGCTCAG GTGTGCCTGT TACAAGAAGA ACCTGCAGAA GGATAATTTG 1380
 CACATGGAGC TGTGATAACA CTAATGTTGA TTTTTTTTTT TTTTACAAGT CATCAGRAT 1440
 GTTTGCAAAG TGAGTTTTAT TTTTTTGTAA TTCCTTTATC TTTACTTAAA GGTGAATGTG 1500
 15 TATTCCTCTG GGAGGAATAG GAAGAAAACA GGAATGTTAA TAATGTCGAA CAGAAAACCTT 1560
 CCTCCCTTAT TAATATATAA TCYTCAATGA TTTATGCCNT AATGTAAGCT GACTTTTAAA 1620
 AAGCTTTCTT TTGTTGCATG CCCTGTGCAG GCATCTGTAT TGTACATGCA TGCCTTTCTG 1680
 20 CCTGTTTTCC TGTATAAAGT TAGTGAACAA AGAAATATTT TTGCCCTAGT TCATGTTGCC 1740
 AAGCAATGCA TATTTTTTAA ATTTGTCATA TATGGAAAGA GCATGTTTGT TACATGTAAA 1800
 25 AGCTTTACTG ATATACAGAT ATACTAATGT TTGAAGATGC TGTCTTTTGC AAGTGTACAG 1860
 TTTTCAAATG TTGTTACCAG TGAAACACCC TTGTGGTTTA AACTTGCTAC AATGTATTTA 1920
 TTATTCAATT CCTCCCATGT AACTAAGAAT CATGGCTATA TTTCATATCA ACGTTATATT 1980
 30 GAAAGTGAAG GGAAATGATT AATACAAGGT TTTGTAACAA AAAAAANAA ANNAAA 2036

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(2) INFORMATION FOR SEQ ID NO: 27:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

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GGCACGAGAT AACATAGGCA CAATAATACT GTATGTCTAC TTCTAGGATT ATAAGGAATT 60
 AACATTGAGA TGACATTTCC ATTTGAGAAG AAAATAGTTG CTTTCAGTGC CTTTATTTG 120
 ATTCCTGGAG AGAGCAGACT CGCACCAACA TTCAACCCCA GCGCTGATAT GACAGTAATC 180
 CTCAGAGGCA GAGCCCAGCA CAAAACAGCA ATGCTAGAAA GTTACAATTG GAAAGTTTCC 240
 TGCCAGCTTC GGGAAATGACA CTGCAAAGCT GATGCCAGAA ACTGCCAGAG TAATTCTCCT 300
 CATTACTGCT CTACCCACCC ACTTTTCAGCT CCCCAAATTA ACTAGTGCAG TTGACTAATC 360
 CTCTTTACCT TTATCATTTA GGTGAGGCAT TGCACAAAAA CTCTCGACTT TGCCATATAA 420
 GGGCTGTGGT TCTCTGTGGT CCTGGATAAG AGGCATCACC ATTATCTGGA AACATGCAGT 480

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AAATGCAGAT TCTTCATCTT CTCCCCAGAC CTCCTGAGTT AGAAATTCAC AAGTTCTCCA 540
GGTGATCTCA TACATGCTAA AGTTTGAGAA CCATTGAGTA AAGTTAATGC ATTAAGAAGA 600
GATTAGATAG GGATGGTGGC GTATCTTCCT ACAGTTTCCC TGTTAACAAG AAAGTCAGAG 660
GTCAGTTGAT CAGACATTAG ATTATTTATT GCTAAACTA AAAAAAATTA AAAAAA 717

(2) INFORMATION FOR SEQ ID NO: 28:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

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GAATTCGGCA CGAGCAGCAT CCTAATTTTA GTTTGGAGAT GCATTCTAAA GGATCTTCTC 60
TATTGCTTTT TCTCCACAA TTAATCTTGA TTCTGCCTGT CTGTGCACAT TTGCATGAGG 120
AACTGAACTG TTGTTTTCAT AGGTAAATGA GAGACTGAGT TTTTTCATTT CTGAAGAGAA 180
AGGGCATTTG CTCCTACAAG CTGAAAGGCA CCCCTGGGTG GCTGGGGCCC TCGTGGGAGT 240
TTCTGGGGGA TTGACCCCTA CAACATGCAG TGGCCCTACA GAAAAACCTG CAACTAAAAA 300
TTATTTTITA AAAAGGCTCC TCCAGGAAAT GCATATAAGG GCTAATCACC CAGTATTTTG 360
ARGCTTCGAA GARGTAATAR AMCCCTGGAG AGAGAACTG AGACATGTAA GAGGGTGGGA 420
ATGACTCAGT GGTGGCACAC TATGGAGTCC TGCCCAACAAG TAGCACACAT CAACCCACTA 480
CACAGAAATC CTAGG 495

(2) INFORMATION FOR SEQ ID NO: 29:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

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AGCTTAACGT CATGATTCAT TAGGGGAATG CAAGGCAAAA CCATGATGAG AATGCCCTTA 60
GACACCTCTT AGAAGAGCTG CTAGAAAGGC AGACAGCACC AAGCGCTTAA ATGAGATGGG 120
GGCACTGGTG CTTCTTCTGT GCCTACTGGT AGGGGTGCAG CAGAGTGGTT CAGTCTGGGA 180
CAGTTAGCTG GACATCACGT GGACCCAACA CACGCATTTT CTGGGTACT TACCAAGGAG 240

AATAGAAAGC AGGCAGATCT TTACAGCAGC TCTTACCTGW TTGCAAAACA ATGGAAATGC 300
 CCACATGTCC ACAAACAAGT KTGTGGTCTG CCTGTGCCAT GAAGCACAGT GTGGCTGAGC 360
 GTCAAGAGTC CCCACACTCA AAGGAGGCAG CAGATACAGG GCTGCACACT GTGTGATTCC 420
 ACACATGTGA CATTCTGGAC ACGGACATGC TGGATGGCAA AACGAGCATC GGGCTGAGAG 480
 GACTGCTGAG AAGGGGAACG GGGCTGCTGG GATGTGGGTT GATTGTAGCA GTAGCTCATG 540
 GAGATGTGAC CTCAAA 556

15

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTAAATGGTG ACTGTGGCTT TGTCGAGACA GGCCCCAAAT GGTAGGTGTG AACACAACAT 60
 GCACAGAATG AGGAGACATG CAGAGTGCTG AAATACTGTC CTGGACAGAT GTGTTACATG 120
 ACTTTCTTTT CAGCTTATTT CTGTGGCCTG CCTTTGAAGA TAGAGCTTTG TTGATATTTA 180
 CATTAAACCA AATTGTATAA YTATGTTCCA TTCTGACATG TTATTTAGCA AARGAAAAAR 240
 GAGTAATTCT ACATCAGCAT CTTTAGTGCA TGCTAAAAGA TTAAAAATGT CTTTGGGGA 300
 ACATGTTTTG TATACATAAA TGTTTAGATA-GAAATATTTA TAGAATNETC TATGTGAGTA 360
 TTNATCTCCC TATGTATATT TATATCTAGA TGTGTCAATC TTTGTATTGA TATGAAATGC 420
 TATGAATAGT GAGA 434

45

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCACGCGTCC GATCTCACAG CTCCGACACT ATTGCGAGCC ATACACAACC TGGTGTGAGG 60
 AACGTAATC CCAAATAAG CCCAAGATGC AAAGTTTGGT TCAATGGGGG TTAGACAGCT 120
 ATGACTATCT CCAAATGCA CTCCTGGAT TTTTCCGAG ACTTGGTGTG ATTGGTTTTG 180

CTGGCCTTAT TGGACTCCTT TTGGCTAGAG GTTCAAAAAT AAAGAAGCTA GTGTATCCGC 240
 CTGGTTTCAT GGGATTAGCT GCCTCCCTCT ATTATCCACA ACAAGCCATC GTGTTTGCCC 300
 5 AGGTCAGTGG GGAGAGATTA TATGACTGGG GTTTACGAGG ATATATAGTC ATAGAAGATT 360
 TGTGGAAGGA GAACTTTCAA AAGCCAGGAA ATGTGAAGAA TTCACCTGGA ACTAAGTAGA 420
 10 AAACCTCATG CTCTGCCATC TTAATCAGTT ATAGGTAAAC ATTGGAACCTC CATAGAATAA 480
 ATCAGTATTT CTACAGAAAA ATGGCATAGA AGTCAGTATT GAATGTATTA AATTGGCTTT 540
 CTTCTTCAGG AAAAAGTAGA CCAGACCTCT GTTATCTTCT GTGAAATCAT CCTACAAGCA 600
 15 AACTAACCTG GAATCCCTTC ACCTAGAGAT AATGTACAAG CCTTAGAACT CCTCATTCTC 660
 ATGTTGCTAT TTATGTACCT AATTAATAACC CAAGTTAAAA AAAAAAAAAA AAAAA 715
 20

(2) INFORMATION FOR SEQ ID NO: 32:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 486 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGCCAGTGC CGGCGAAAGG GGACCTTCCT CTACTTCCTG CCACAGACCC TGTCCCCACA 60
 35 CACTTCCTGC CCCTGCTCTG CTGGGAGGCC ACTTCCTCCC CCAGTGCTGG ATTCCACCCC 120
 CAGCTCACCC TCAAACATGG CCCCCTCTCT CCTCTGCTT GCCCCTCTCT GCTCCCTGGA 180
 GGCTGTTCTG TCCTCCCCTC TTGAAAAGCA ATGCCAGCTT CCTGGGATCT TCTGCCAACT 240
 40 CCAGCTACCA TGCCCTTTGC TCCTGTCTAGC TCAGCTCCTC AAGGGAATTG TCTAMCCTCG 300
 GTGTCCTGCT TCCCTCCCTC AACCTCCTCA CCCTGCTCCA AGCTGGCATC TGCCCCCTCA 360
 45 CTGCACAGAA CGGNTCCCCC ACCACCTGCC TTTACAGGGA GGAAGCAGCA ACATGGAAGA 420
 ANCGAACTAT AGGGGCTACA ANGATGCTCA GCTCTGATCC CGAAGGCAAA AAGNATCTTT 480
 GGGCAC 486
 50

(2) INFORMATION FOR SEQ ID NO: 33:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5 GTTCCTCTGG TAATAATTAG GTTATMCCCA GAAGCACAGT GTCATTCTTT AAATAAAAGC 60
 TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA AGATTCCCCC TAGGGTTGAT 120
 ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTCA TTTTAAAGCT TTGGCTATAT 180
 10 AGTCAGAAAT GTCCTAAATA ACAAATATT TTGTATTTAA TTTAGGGAAG ACTAAAGGGA 240
 AGAAAAATGA AAATCAGTC TTTATGTAAG CTCCAAGGAT ATTAGGGCTT AAAGGGCTTT 300
 TCTAGTTTTA TGAGAATTG TACTACTGAT TTTTATATAT TCCTGTTTTT GATGAACAGA 360
 15 TCTCTGGGGA AATTGTTGAG TTACAATGGC ATTTCACTGT GATCCCTCTC AAGCTCAGAT 420
 CAGTTCTATA ACCCAATGAC AACCTGTCTC TTTGGTTTAC TGTCCTGTGA AATGTCAGCT 480
 20 CAAGTTTCCC AGAAGTCGTG TGTATTATGAT GAGTCAGAGT GCTTTTCCTC GGTGGGACAG 540
 TTGCTGGCCC TCTTAATTTT GGTGTATGTG CTCCAAGTA TCTAAACCTC CAGTCTGATC 600
 TGTATATGCT ATCCTAACTG TTAATTGTAT TATTGATTAT GTTGATTATC TTGCTTGAAG 660
 25 GTTCATACTT TTCAATTTGA TAGAAATAAA GTTTTTTTCT GCTTATAAAA AAAAAAAAAA 720
 AAAAA 725
 30

(2) INFORMATION FOR SEQ ID NO: 34:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CACACAGCAT GCTGCCCTCA GACGTGTCCA TCCTGTACCA CATGAAAACG CTGCTGCTCC 60
 45 TGCAAGATAC TGAGAGATTG AAGCATGCTC TGGAAATGTT CCCAGAACAT TGCAAGATGC 120
 CTCCTGCTTT TATTGGCTCT TGTGAAATC AAATTGGAAG ATCTTCAGTC CCAGCTGCAC 180
 CCAACGTGGA AAAGTATTCC AGGTCCATCC CCAAGGAACC AACACCGATG ACATGGACTC 240
 50 AGGAATCTTA TAACCTACGT GGACTCTTTC CATCCGTACA TTGTGCTGCA CATGCCACTC 300
 ATCACCTGGC GTGCCCAGAT CCTCGCARGG CAACACCCTG TGATAATTCC AGGTGATTCT 360
 55 CTACATCTGC AGCTTGAGGT TAGCCTCATA TCACATTACA TTCTCACTAN AAACNAAAAA 420
 AAAAAAAAAA AACTCNA 437

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- (A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

	GGCACGAGCT	GGAACAGAGA	CTAAATCCCA	CGAAACTGAC	ATTGTTAAAC	ACACTAAAAC	60
15	AGAAGTACTT	ACCTCTTGAA	GATTTAATAT	ATAATGGTTG	ACATGATACA	TGTACATGAT	120
	GAATGACCAG	ATGCTTATGG	TCTACATTTT	CCTTTATCCT	GTTAGTATTA	CCTTCCTTAA	180
	TCTTTGTTCA	TTAACATGCT	AATTCCTCTT	CAGTGTTTAT	TTTCTAGTGA	CAGAATGCTA	240
20	ACATTTCTTA	CACCCTGGCA	GAAGGGAGAG	AAATGTGTTT	TGGGGTGGGT	AACTAAATTT	300
	TTGAGTGAAA	TATCATAAGA	TGANAATGGA	AANAAGGAGA	CACAAANAGT	TATNACAAAA	360
	AAACAATGGT	TTTTTTAGCC	ATTTGACTGG	CTCTTTAAAT	AGTCTACAAG	ACATTACAGT	420
25	TTAACATCAC	TTTTTAGTGAA	ATAAAATGTG	CCATACTAGT	ATGTGCTTCA	AAAGGGCAAA	480
	TGTGCTTTAG	TGCCCTAAGG	CTAAATTTTG	GTCATTTGAC	ATCAGAGATG	TTGTAAGTAT	540
30	TGCACTTAAT	ACGCACCTAT	TTNICAATAG	TGTTATTTTT	TGGNTAGCAT	TTTTTTTACC	600
	ACTATNTTGT	TGATAGCTTT	TTGTTCTNTN	AGGTTGNAAN	ATGACAGTGC	TNATNTCAAA	660
	CAGATTACCC	ATNTGCAGAA	CTAAGGGAAG	CNATTTATGT	ATGAAAGNAA	TTNTTGAATT	720
35	NGTCATTNTC	AACCNPTGNA	TTAAAGCTTA	GACTAAATAG	TAATATATNG	TGGGNAGGAT	780
	TTTGGTTTTG	TGATAATTNT	GTGNATTAAG	GNATAGATGT	TAACCNTTAT	TTTGTAGNAA	840
40	AGTGANTTGT	ATGTGGTTAA	TTATAAATAA	AACTGGTACC	AGGNAAAAAA	AAAAAAAAAN	900
	NAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA		943

(2) INFORMATION FOR SEQ ID NO: 36:

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- (A) LENGTH: 604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCACGAGAA ATCTTCATGC TGTAGTCACT CCAGACCATG GAGTGGCTTT CCAGCTGAAT 60
GAATCCTATG TCTCGCGTGC AGGTGGTTGG TTTTCAATGT TCTTGCTAAT TTTTTTCTA 120

TTGGATCTTG GGAGTTTCTT TGTTTGCTC CTGTGTTTGC CCAGCTTTAA TAAAACCAGG 180
 CGCAAACAAA AACCATAGCA TTCTGAACAA TAGGGGGCCC ACATTGGACC CAGTATGTCA 240
 5 CTTTAATGGA CTTCAAGAAA AAATCTGAAT GGGAAAAATG ACACTAGGAA TGTATACTCC 300
 ACACATTTTA TGCCATATAA TGGTGTGTTT TCTTAATTTT GTTCTTGTG GCGAAATGTG 360
 10 GCTTTCAAAT TAAATGACC TTTTCTTCTT TGAAACTTTT TGTTTTGACT TGTATAATTA 420
 AGGGTTTGA AAGATTGATA ATTCTGAGAG AGGTTTGCAA CCAGGAGATA CAAAGAAGTC 480
 TCAGTAGTAA TCTGTTCAT GTGCTTTTAC AGCCAGCTAC ATTTAAGGAT GTATTAGTTA 540
 15 CAGAAATTAT ATGTCTGTGT ATGTGTCTCT ACTCAATAAA GTACATGCCT CCACAAAAAA 600
 AAAA 604

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(2) INFORMATION FOR SEQ ID NO: 37:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGAGTGCCC GGGAGCCCCG AGGCCCTGCC CCTAAGAAGG ATATCTYTRA CCGCTCCCTT 60
 35 GTCCACACCC TAACCCCCCA GCTGCTCAGG CAGTGGGCAC ATGGCAGGGG CCTCACTGGG 120
 GGCACATAGA GCATTTGGGG GACTGCGAGT GCTCACCTTT GACTTCCTGC AGGTCGGGGG 180
 AAAACCAGAT CATGATGACC AAAGTYTACA TATCTTGAT CTTATGGTG CTGATCCTGC 240
 40 CCTCCCTGGG TCTACCAGG TATATGCCAC CACTTCTGY TCTAAATCA GAATAAGAGT 300
 CACATCAGGA GAGCACTGTC CCCAGGANAA TGCAAACGGG TTGGCAGCA 349

45

(2) INFORMATION FOR SEQ ID NO: 38:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTAGTCGTTG CGGTTGCCGG GATGGCGAAG ATCTCGCCGT TTGAAGTCGT AAAACGCACC 60
 60 TCGGTACCGG TGCTTGTTGG TTTGGTGATT GTWATCGTTG CTACAGAGCT GATGGTGCCA 120

	TCTCTGTAGA TTTGCTTATT CTGGTCATTT CATATAAATG GAATTCCTACA ATATTCGGTC	900
-5	TTTTGGGACT GGCTTCCCAA ATATGATTTT CTATATGGAG TGAGAAAATT CTTCTCATCT	960
	TGAGAACTCT TATTGCTGTG AAAGGGAGTG GTTGGTAAAA TCAATAGATT TCAGGCAAGA	1020
	GGGCCAGATA CCTAACAGGT TTTTCTCCGT GAATCTTATG CTGAGTAGTT TTTCTCATA	1080
10	ACCAAGCATT TATGATATAT TACTACTTAT AATACTGTGG CTAGTCTCTA GAATGGATGT	1140
	TGAAATCTTT GCCTCCTCAG TCGGGAAGAG TCCTGCTAAA AATCAGGCTA AAAATCAGGC	1200
15	CAAAAATCAG GCCAAATGAC TTGGCAAATA ATTGACAAAG TGGTTTTCAC GTGTGTCTAT	1260
	CTTTGCTAGC AGCTTGTATA CCTCAGGCCA GGTGAGCTCC CCAAATTTCT TTTTTCATTT	1320
	ACTCCAGTGA GTTCTGCTG TCTTTTTCAA GTATGTACCA TAGGACTTAA AGGTGATTTG	1380
20	GATGCGTTGT AACACTGCTA AATATGCTAA GTACAGAATT TTATCTACAG TACTGTGAGA	1440
	CAGTCAATTA TTGCCTAGGG TAGTCAAAA ATATGATGTG AGCTAGTTAA GCCTTTGCTT	1500
25	GACTGATTTT AGTGATATTC AGAAGTGTGT ACCAATCAAG GCTCTTTAAA ATACGGAACG	1560
	ACTCACTTAA TAACCAGGGA ACCAGCCAAA TACTGTGCAG CCGCAGAATA TGCATATCAA	1620
	TGAGTTGGAG GTGATTATTC TCTGTAATC CTAATGATT GTTTTCTAAG CATTGTGGCT	1680
30	TCTCAGTGGC TTGACAGCAT CTTCTGGTT GTATGTGGCC TGTTTACATG ATGTATTGAA	1740
	TAATGTTGTT TGTGTGAGC ATCAATGCCT GTAACACCAA ACTAAACACG TGTMTTGGG	1800
35	ATATGTTTCC AATCTTTAAA TGACCTTGCC CTGTCCAATA AATAAATGAT TGTCTCACCC	1860
	TGTTAAAAAA AAAAAAATT AAAAAAATG GNGGGGGGC CCGGTACN	1908

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(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

55

	CCTCAAAAAA AAAAANGAAA GGAAAGAGGT CTCTACACAA GCCCGTGATT CTTTCATGGCA	60
	AGGGATAACA TCAGAAATGT TTCAITTYCK GCTATTAGTT TCCAATTCCTT TCCCCATCCA	120
	GGCATAAAGA GAAACAAAAG ACAATGATGG TATTCTCTGT GTCCTCAGCT TTGGCACTTT	180
	TGTTGATGTT GCTAAGGAGC AGTGACCTTG CTAAAAAGAC TGAATAATCC ACCCACTGAA	240
60	TAGCTAACCT GGGGAGGAAA TGAAAATTC CTTTGTGGAT CTCCCCAAAT CCATTGTTGT	300

CACCAGGCCC TCCCAGAACC TCCTCAGTTC CTTCACAGTG CAACCCTGTG TACTTGGCCC 360
 GCAACCCAAT AGTATTGTGC CTCACCTTAC CTTCATGGG CAACTGCCCT CCCTTCTGGA 420
 -5 CATAAAACCT CATATTTTAA ATNAAGTTGA AATTTGAA 458

10 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

20 GGCACAGAGC CTCCGACCCA GGTGGTCTGG AGCCTGCCGG GAGAGTGGTG GCATCTGAGA 60
 GGCTGGTCGT GGA CTGTGGT TGGGGGAGGT GGGAGCTGTT TTAACCGTGT GCCCCCTCTC 120
 CTGTGCCCGC GTGGGCATCC CCCGGGGCAG TGGAACCCGG GCGCTCCTCC AGCTTCCGAG 180
 25 TCCAGCCAGC CTGGGCGCGG GCGCGCCCC GAGACACCCG AGGAGTCCGT TCCTCCCTGG 240
 TTACGTGGAC TGTGGAGCTG GTCTCTTGTG GCTCAGCGCC GTGCGGAGGT TGAAGCGTAC 300
 30 CTGCGGAGGT CGCACCAGGG CGTGAGGAGG AGGAGGAAGG GCATGAGCCG AGCTTGAGGA 360
 ATCCGTGCTC CAAACTCTAC ACTCAAGGAT GCACTGCGCA ACTCTGGTGG CGATGGGCTG 420
 GGGCAGATGT CCTTGGAGTT CTACCAGAAG AAGAAGTCTC GCTGGCCATT CTCAGACGAG 480
 35 TGCATCCCAT GGAAGTGTG GACGGTCAAG GTGCATGTGG TAGCCCTGGC CACGGAGCAG 540
 GAGCGGCAGA TCTGCCGGA GAAGGTGGGT GAGAACTCT GCGAGAAGAT CATCAACATC 600
 40 GTGGAGGTGA TGAATCGCA TGAGTACTTG CCCAAGATGC CCACACAGTC GGAGGTGGAT 660
 AACGTGTTTG ACACAGGCTT GCGGGACGTG CAGCCCTACC TGTACAAGAT CTCCTTCCAG 720
 ATCACTGATG CCCTGGGCAC CTCAGTCACC ACCACCATGC GCAGGCTCAT CAAAGACACC 780
 45 CTGCCCTCTG AGCGTCGCTG GATCTCTGGG AGCTCCTTGA TGGCTCCCAG ACCTTGGCTT 840
 TTGGGAATTG CACTTTTGGG CCTTGGGCT CTGGAACCTG CTCTGGGTCA TTGGTGAGAC 900
 50 TTGGAAGGGG CAGCCCCCGC TGGCTTCTTG GTTTTGTGGT TGCCAGCCTC AGGTATCTCT 960
 TTTAATCTTT GCTGACGGTT CAGTCCTGCC TCTACTGTCT CTCCATAGCC CTGGTGGGGT 1020
 CCCCCTCTT TCTCCACTGT ACAGAAGAGC CACCACTGGG ATGGGGAATA AAGTTGAGAA 1080
 55 CATGAGTTTG GGCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
 AAAAAAAAAA AAA 1153

(2) INFORMATION FOR SEQ ID NO: 42:

-5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1983 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GGCACGAGAG GGGCCGAGCC GACAAGATGT TCTTGCTGCC TCTTCCGGCT GCGGGGCGAG 60
15 TAGTCGTCCG ACGTCTGGCC GTGAGACGTT TCGGGAGCCG GAGTCTCTCC ACCGCAGACA 120
TGACGAAGGG CCTTGTTTGA GGAATCTATT CCAAAGAAAA AGAAGATGAT GTGCCACAGT 180
20 TCACAAGTGC AGGAGAGAAT TTTGATAAAT TGTTAGCTGG AAAGCTGAGA GAGACTTTGA 240
ACATATCTGG ACCACCTCTG AAGGCAGGGA AGACTCGAAC CTTTATGTTT CTGCATCAGG 300
ACTTCCCCAG CGTGGTGCTA GTTGGCCTCG GCAAAAAGGC AGCTGGAATC GACGAACAGG 360
25 AAAACTGGCA TGAAGGCAAA GAAAACATCA GAGCTGCTGT TGCAGCGGGG TGCAGGCAGA 420
TTCAAGACCT GGAGCTCTCG TCTGTGGARG TGGATCCCTG TGGAGACGCT CAGGCTGCTG 480
CGGAGGGAGC GGTGCTTGGT CTCTATGAAT ACGATGACCT AAAGCAAAAA AAGAAGATGG 540
30 CTGTGTCGGC AAAGCTCTAT GGAAGTGGGG ATCAGGAGGC CTGGCAGAAA GGAGTCCTGT 600
TTGCTTCTGG GCAGAACTTG GCACGCCAAT TGATGGAGAC GCCAGCCAAT GAGATGACGC 660
35 CAACCAGATT TGCCGAAATT ATTGAGAAGA ATCTCAAAAG TGCTAGTAGT AAAACCGAGG 720
TCCATATCAG ACCCAAGTCT TGGATTGAGG AACAGGCAAT GGGATCATTC CTCAGTGTGG 780
CCAAAGGATC TGACGAGCCC CCAGTCTTCT TGGAAATTC A CTACAAAGGC AGCCCCAATG 840
40 CAAACGAACC ACCCCTGGTG TTTGTGTTGA AAGGAATTAC CTTTGACAGT GGTGGTATCT 900
CCATCAAGGC TTCTGCAAAT ATGGACCTCA TGAGGGCTGA CATGGGAGGA GCTGCAACTA 960
45 TATGCTCAGC CATCGTGTCT GCTGCAAAGC TTAATTTGCC CATTAATATT ATAGGTCTGG 1020
CCCCCTCTTG TGAAAATATG CCCAGCGGCA AGGCCAACAA GCCGGGGGAT GTTGTTAGAG 1080
CCAAAAACGG GAAGACCATC CAGGTTGATA AACTGATGC TGAGGGGAGG CTCATACTGG 1140
50 CTGATGCGCT CTGTTACGCA CACACGTTTA ACCCGAAGNT CATCCTCAAT GCCGCCACCT 1200
TAACAGGTGC CATGGATGTA GCTTTGGGAT CAGGTGCCAC TGGGGTCTTT ACCAATTCAT 1260
55 CCTGGCTCTG GAACAACTC TTCGAGGCCA GCATTGAAAC AGGGGACCGT GTCTGGAGGA 1320
TGCCTCTCTT CGAACATTAT ACAAGACAGG TTGTAGATTG CCAGCTTGCT GATGTTAACA 1380
60 ACATTGGAAA ATACAGATCT GCAGGAGCAT GTACAGCTGC AGCATTCCCTG AAAGAATTCG 1440

	TAATCATCC TAAGTGGGCA CATTTAGACA TAGCAGGCGT GATGACCAAC AAAGATGAAG	1500
	TTCCCTATCT ACGGAAAGGC ATGACTGGGA GGCCCAAG GACTCTCATT GAGTCTTAC	1560
-5	TTCGTTTCAG TCAAGACAAT GCTTAGTTCA GATACTCAA AATGTCTTCA CTCTGTCTTA	1620
	AATTGGACAG TTGAACTTAA AAGGTTTTTG AATAAATGGA TGAAAATCTT TTAACGGAGA	1680
10	CAAAGGATGG TATTTAAAAA TGTAGAACAC AATGAAATTT GTATGCCCTG ATTTTTTTTT	1740
	CATTTACAC AAAGATTTAT AAAGGTAAAG TTAATATCTT ACTTGATAAG GATTTTAAAG	1800
	ATACTCTATA AATGATTAAA ATTTTATAGAA CTTCTAATC ACTTTTCAGA GTATATGTTT	1860
15	TTCAATGAGA AGCAAAATTG TAACTCAGAT TTGTGATGCT AGGAACATGA GCAAACTGAA	1920
	AATTACTATG CACTTGTCAG AAACAATAAA TGCAACTTGT TGTGCAAAAA AAAAAAAAAA	1980
20	AAA	1983

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

35	ATGATGATGA CTTTGAAGAC GATTTTATTC CTCTTCCTCC AGCTAAGCGC CTTGAGGTTA	60
	ATAGTTGGAA AAGACTCTAT AGATATTGAC ATTTCTTCAA GGAGAAGAGA AGATCAGTCT	120
	TTAAGGCTTA ATGCCTAAGC NCTTGGTCTT AACTTGACCT GGGATAACTA CTTTAAAGAA	180
40	ATAAAAAATT CCAGTCAATT ATTCCTCAAC TGAAAGTTTA GTGGCAGCAC TTCTATTGTC	240
	CCTTCACTTA TCAGCATACT ATTGTAGAAA GTGTACAGCA TACTGACTCA ATTCTTAAGT	300
45	CTGATTTGTG CAAATTTTTA TCGTACTTTT TAAATAGCCT TCTTACGTGC AATTCTGAGT	360
	TAGAGGTAAA GCCCTGTTGT AAAATAAAGG CTCAAGCAAA ATTGTACAGT GATAGCAACT	420
	TTCCACACAG GACGTTGAAA ACAGTAATGT GGCTACACAG TTTTPTTAAC TGTAAGAGCA	480
50	TCAGCTGGCT CTTTAATATA TGAATAAACA ATAATTTAAA ACAAATCATA GTAGCAGCAT	540
	ATTAAGGGTT TCTAGTATGC TAATATCACC AGCAATGATC TTTGGCTTTT TGATTTATTT	600
55	GCTAGATGTT TCCCCCTTGG AGTTTGTGTA GTTTCACACT GTTTGCTGGC CCAGGTGTAC	660
	TGTTTGTGGC CTTTGTTAAT ATCGCAAACC ATTGGTTGGG AGTCAGATTG GTTCTTAA	720
	AAAAAAAAA AAAACGACAT ACGTGACAGC TCACTTTTCATTATTATA TGTACCGAGG	780
60	GTAGCAGTGT GTGGGATGAG GTTCGATACA GNCGTATTTA TTGCTTGTCA TGTAAATTAA	840

AAACCTTGTA TTAACTCTT TTCAATCCTT TTAGATAAAA TTGTTCTTTG CAAGAATGAT 900
 TGGTGCTTAT TTTTTCAAAA ATTTGCTGTG AACAACTGA TGACAACAAG CAACATTTAT 960
 -5 CTAATGAACT ACAGCTATCT TAATTGGTT CTCAAGTTT TCTGKTGCAC TTGTAAAATG 1020
 CTACAAGGAA TATTAAAAAA ATCTATTCAC TTAACTTAT AATAGTTTAT GAAATAAAAA 1080
 10 CATGAGTCAC AGCTTTTGTG CTGTGGTAAC CTATAAAAAA AGTTTGTCTT TGAGATTCAA 1140
 TGTAAGAAG TGAAAACAAT GTATATGTTG TAAATATTTG TGTGTTGTGA GAAATTTTGT 1200
 TCATAAGAAA TAAAAGAAG TTACCAGGAA GGTTTTAAAG TTAGAAATAT TCCATGCCAA 1260
 15 TAAATAGGA AATTATAAAT ATATAGTTTT AAGCCTGCAT CAGTGGGAGT CTTGGCTATG 1320
 TAGTTATGTA GTTATTATGN AACCACCAAG ATTTTTTTGG CTATTTACCG TAACCAAAGG 1380
 20 GGCCGATTAA NTGGTTTGAA GNCTTG 1406

25 (2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1391 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

35 GGGCTGAAG GCGGCRGCC AGTCCCGAGC AGTGCTCGCT CCTGCTCGGG GCGCTGCGGC 60
 - CCGGGGCGTC GCCATGACCA GTGAGCTGGA CATCTTEGTG GGGAACACGA ECCTTATCGA - 120 -
 CGAGGACGTG TATCGCCTCT GGCTCGATGG TTA CTGCGTG ACCGACGCGG TGGCCCTGCG 180
 40 GGTGCGCTCG GGAATCCTGG AGCAGACTGG CGCCACGGCA GCGGTGCTGC AGAGCGACAC 240
 CATGGACCAT TACCGCACCT TCCACATGCT CGAGCGGCTG CTGCATGCGC CGCCCAAGCT 300
 45 ACTGCACCAG CTCATCTTCC AGATTCCGCC CTCCCGGCAG GCACTACTCA TCGAGAGGTA 360
 CTATGCCTTT GATGAGGCCT TTGTTGCGGA GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC 420
 CAAGAAAGAC CTGGATGACA TCAGACCAA AACAGGCATC ACCCTCAAGA GCTGCCGGAG 480
 50 ACAGTTTGAC AACTTTAAAC GGGTCTTCAA GGTGGTAGAG GAAATGCGGG GCTCCCTGGT 540
 GGACAATATT CAGCAACACT TCCTCCTCTC TGACCGGTTG GCCAGGGACT ATGCAGCCAT 600
 55 CGTCTTCTTT GCTAACAACC GCTTTGAGAC AGGGAAGAAA AACTGCAGT ATCTGAGCTT 660
 CCGTGACTTT GCCTTCTGCG CTGAGCTCAT GATCCAAAAC TGGACCCTTG GACCCGTCGA 720
 60 CTCACAGATG GATGACATGG ACATGGACTT AGACAGGAAT TTCTCCAGGA CTTGAAGGAG 780

CTCAAGGTGC TAGTGGCTGA CAAGGACCTT CTGGACCTGC ACAAGAGCCT GGTGTGCACT 840
 GCTCTCCGGG AAAGCTGGGC GTCTTCTCTG AGATGGAAGC CAACTTCAAG AACCTGTCCC 900
 5 GGGGGCTGGT GAACGTGCCG CCAAGCTGAC CCACAATAAA GATGTCAGAG ACCTGTTTGT 960
 GGACCTCGTG GAGAAGTTTG TGGAAACCTG CCGCTCCGAC CACTGGCCAC TCAGCGACGT 1020
 10 GCGGTTCTTC CTGAATCAGT ATTCAGCGTC TGTCCAATCC CTCGATGGCT TCCGACACCA 1080
 GGCCCTCTGG GACCGCTACA TGGGCACCCT CCGCGGCTGC CTCCTGCGCC TGTATCATGA 1140
 CTGAGGTGCC TCCCAACGTC CGCCACGCT GACAATAAAG TTGCTCTGAG TTTGGAGACT 1200
 15 GGTCTCTGCT CCGGGGAGCA AGTGGGGGGC GTGCAGATGT GCCTGTGTCT GTCTCTGAGC 1260
 ACCTGGTGTC CGTGACAAG GATGGATGTG TNCNGTGGCT CCTTGGGAAC TGAGACATAT 1320
 CTCAGGGAAT GGTGTCTGTG CTCAGCCCAT CCACCAGAAG AGTCTGCTCA CAAAAAAAAA 1380
 20 AAAAAAAAAA A 1391

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(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35

GGCACGAGTG GAGATGGCTG CGGCCGTGGC GGGGATGCTG CGAGGGGGTC TCCTGCCCCA 60
 GGCGGGCCGG CTGCCTACCC TCCAGACTGT CCGCTATGGC TCCAAGGCTG TTACCCGCCA 120
 40 CCGTCGTGTG ATGCACCTTC AGCGGCAGAA GCTGATGGCT GTGACTGAAT ATATCCCCC 180
 GAAACCAGCC ATCCACCCAT CATGCCTGCC ATCTCCTCCC AGCCCCCAGC AGGAGGAGAT 240
 45 AGGCCTCATC AGGCTTCTCC GCCGGGAGAT AGCAGCAGTT TTCCAGGACA ACCGAATGAT 300
 AGCCGTCTGC CAGAATGTGG CTCTGAGTGC AGAGGACAAG CTTCTTATTG CGACACCAGC 360
 TGCGGAAACA CAAGATCCTG ATGAAGGTCT TCCCCAACCA GGTCTTGAAA GCCCTTCCTG 420
 50 GAGGATTCCA AGTACCAAAA TCTGCTGCCC CTMTTGTGG GGCACAACAT GCTGCTGGTC 480
 AGTGAAGAGC CCAAGGTCAA GGAGATGGTA CGGATCTTAA GGGACTGTGC CATTCCTGCC 540
 55 GCTGCTAGGT GGCTGCATTG ATGACACCAT CCTCAGCAGG CAGGGCTTTA TCAACTACTC 600
 CAAGCTCCCC AGCCTGCCCC TGGTGCAGGG GGAGCTTGTA GGAGGCCTCA CCTGCCTCAC 660
 AGCCAGACC CACTCCCTGC TCCAGCACCA GCCCCTCCAG CTGACCACCC TGTGAGACCA 720
 60 GTACATCAGA GAGCAACGCG AGRAAGGATT CTGTCATGTC GGCCAATGGG AAGCCAGATC 780

	CTGACACTGT TCCGGACTCG TAGCCAGCCT GTTTAGCCAG CCCTGCGCAT AAATACACTC	840
5	TGCGTTATTG GCTGTGCTCT CCTCAATGGG ACATGTGGAA GAACTTGGGG TCGGGGAGTG	900
	TGTTTGTCAC TTGGTTTTCA CTAGTAATGA TATTGTCAGG TATAGGGCCA CTGGGAGATG	960
	CAGAGGATTC CATTTTCAGAT GTCAGTCACC GGCTTCGTCC TTAGTTTTCC CAACTTGGGA	1020
10	CGTGATAGGA GCAAAGTCTC TCCATTCTCC AGGTCCAAGG CAGAGATCCT GAAAAGATAG	1080
	GGCTATTGTC CCCTGCCTCC TTGGTCACTG CCTCTTGCTG CACGGGCTCC TGAGCCCACC	1140
15	CCCTTGGGGC ACAACCTGCC ACTGCCACAG TAGCTCAACC AAGCAGTTGT GCTGAGAATG	1200
	GCACCTGGTG AGAGCCTGCT GTGTGCCAGG CTTTGTGCTG AGTGCTGTTA CATGTATTAG	1260
	TTCTTTTACT GCTGACCACA TTGTACCCAT TTCACAGAGA AGGAGCAGAG AAATTAAGTG	1320
20	GCTTGCTCAA GGTCAATGAG TTAGTAAGTG GCAGAACAGG GACTTGAACC AAGCCCTCTG	1380
	CTCTGAAGAC CGCGTCCTGA ATTTCTTCAC TAGAGCTTCC TCATCAGGTT ACCCAGAAGT	1440
25	GGGTCCCATC CACCATCCAG GTGTGCTTGG ATGTTAGTTC TCCACCCTCG AGGTGTACGC	1500
	TGTGAAAAGT TTGGGAGCAC TGCTTTATAA TAAAATGAAA TATATTCTAA AAAAAAAAAA	1560
	AAAAAAAAA	1569

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(2) INFORMATION FOR SEQ ID NO: 46:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1924 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	GGGCCCCCCC WCGWKTTTTT TTTTTTTTTT TTTAATTAGG ATAATGCCTT TATTAACGAG	60
45	AATGAAACGT TCATTCCTCC TTCCACTCCT TCTCGTTGGT TTTCTGGACA CAGCTCACCT	120
	GATCCTGCTA GAAACGTTGT CAGTCTGCTT GTGGCTTCCC TCCTTGATTG ACTCACGCTG	180
50	TGTGATGTCT TGAGAAGTAT CTATCCACTT CATGTGAATG AGCACTCCAA TATCAGCCAA	240
	CATCAATCAT TCTTACCTAA AGAATAATAA GAAAAAGTTA ATATAAAGA CAAGGGTATA	300
	AAATAAAGGT TTGAAAATGC TAGTCAACTT CAAAATTTAA AGAGTAAAAA TCCAGAGATA	360
55	AAGATTGGGG GTAAGTTACA GCATAAAAAA ATAGGAAGAA ACTTCATGGT GGGGGGGAAA	420
	TCTAAATTA TTCTTACATA AAATAAGTAG ACACCTGAAT TAGAATGAAA ACTGTATTTT	480
60	CTTTAAAATG TAAAAGCCTG ACTCTCAGTT TCACCAGTCT GAGCACAAGT TTGACTGCAA	540

CCCAAAATAT ACTATCCCTT ATGTGAAGGT ATGTGACAAC GTTGACCTCA CCAAATGAGT 600
 TTAAACATCA GCTCTTTTTT CATATGAAAG CACATACCCT GCTCCCCATT CAAGTATGTC 660
 5 TTCCATTGTC AGGCAGGCTG ACCACCTTCA GCAGGAGTCC TCCAAGAGTG CCCAACTCCC 720
 CTTCACACAG TACACAACGC TGTAGTTGTT GTCTGCAAT CCTTTGTATT TACCTCATTG 780
 10 TTTCCTCATCT AAGTCCTCAC TGAGTTTTAA AGTTAGGGCT GGAAAAGCTA TGCCTTACTG 840
 GGACAGCAAG GAACCAATTT TTTCTGAGG GAGAAGACAT TCACCTTCAC TATATGCCTG 900
 GCAGGGCCAC AGTGCACAAA ACAAGATCA GCCTTCATTG AAGTCCAGG TTTTCTTCC 960
 15 TCCCTGAATG ATTACTGCAA AGGGTATATG AAGTAAGAGT TCCCTGTTGC ACATGTACCA 1020
 TCCATAAGGG ATACTATATC GTTTGTCATT CTTCCTCCCA TTCTCCACAT TGTCTTATCT 1080
 TAAGTCCAAG CCCTTTTCAC TCTCAAAAAA AAAAAAAAAA TATTTTTC AGCACTGGTG 1140
 20 TTCAAAAGCA ACGTTTTTAT GGTAAATGGT TTACCAGCAA CTGTTGAGAT TTCCAGTTGA 1200
 GTCTTAAAAA TTGCCAATCA TTATCTAGCA GCAATGACAG ATGATTAGGA GCAGTCAAAT 1260
 25 CCTCTGAATT CTTTCCCTAA TAGGCAGCCA TTTGAGAACT GCACTAGCTG ACATCACTAA 1320
 AACATTATCA GCTAAAGCCA AAACCAAATA AAGGCCCAGA CCAACATCCT GGCTCTCTAA 1380
 AACCTGTCCA AAATCATTAA GTGAAAGGCA GTAAATGCAG GACTGTGGAT CATGTCACTG 1440
 30 CAGCTGACAA TGATTAACAA TAGGAGACAT GCAACCCCA TTAAGGTTAA AAGTCCAAAA 1500
 CTAGTCACAC GCATCTCTTT ATTGGGAAA AGTGAGACTA TTATGCATTG TTGGTAGGTT 1560
 35 TGCAACCTTG CATGAAGAGC ACCCATGCA TTTCTTTTAT CTTTCAGAAA GCACCGGTAT 1620
 CTGTTCCAAG GGCCTAACAG TACGAAAATA CATTCTGGCA TCACACCTCT GAACCCAAGA 1680
 CTGTTCTCAT TAAAAATAAT TTTGGTTTGT AACAAAATTA TGAAATACAA TGCAAGCACC 1740
 40 TCGGTATAGC ATTATTACTG AAACCACTTA ATTCCCAGCT TTTTGAGTTT TTTAAAAAAA 1800
 CCCACTGCAC TAAGATTAC AATTCATTGC TACATACAAA TTAAAGCTAG TAAGAACACA 1860
 45 CTAACGTCAC AAGTTTCTCA TTCTAAAGTG CAAAAGCCTA ATCATCTGAA AGTGAACAGG 1920
 GTAA 1924

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(2) INFORMATION FOR SEQ ID NO: 47:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TGGTGTGGGG CCCAGAAAMC AAGGGACCAG TGAAAACAMC CCCAGAGACT TGTATCCGCC 60
 AGGAAAGCCA TTGCCAMTYC TGAGCCCTTG AAGGGCAAGG AGGGAAACAG TGTTACCAGA 120
 5 GCCCAGTAAG AACTGCTGTC ATGAAGGAGG GGCCACCTTG TAAGAGACAT CATTACTACC 180
 AGAACTGTGG TGCCAAATTG CTGGTGTCTC TCTTTGGAGA AACCAACCAG ATACATCTGC 240
 10 TGGAGACCCA GGTGGGCACA GAGAAGGGTG GAGAGAGAAT CTGGGAAGAG AAATGGAGAA 300
 TAAGCAGCAC AGTGTATTTC ATTTCTGTAA ATTCTATGT AGAAGGCTCA GTGTTAGAAA 360
 TAAAGTTATT CTACTAGTTG CAAGTTAAGT GTTCTGTTT GTTCTGCTTT CCTGTTAGCA 420
 15 TAAGTAAACT CCCTTTGGAA CTACACAGGT ATGTCTCTCC TTCAACATGT GTGAA 475

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(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 346 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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AAGGGACAGA GACCTGGATT CAGATCTCAT TTTACAATGA AGACCCCAAT GCAGAAAGTC 60
 ATGTCTGAAA TTCTGAGCTT ACTCTTCTGC CTGCTGGGAC CTGCTCTGGA TGAGAGAAGG 120
 35 GAGGAAAAGG ACTAATCAGA GGAGCCAATG AAGTCACTCC ATGAGTTTCC TGAACCCTGC 180
 CCAGCTAGAG ATTAACGTYT GACCWTCAAC GTAGGACACT GTGCAGATGG CTAETTGCTG 240
 GCGCATGA AGACCAAAGC CAGGACCAAG CCCCMASCCT GCTWAACACG GCAGARTCTT 300
 40 GCCCAGCCMA CYTCTGTGAR AATCTGCTTC CCTCCACAGC TGACCC 346

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(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1366 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

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TAGGTGTCAG CCGCCACCCC CCCCCATAT GCAGATTTAC TSGGCATGGT AGTGGCCAGC 60
 TTCTAACACA GCTGGTATTT CAAGTCTCCT GGGACCTCAC TCAGGAATGA TACCCCTCA 120
 60 GTAGAAGCAG CAGGTGATCT TAACTCCTTT CAAAGAGCAG GCCTGTCTGG GAAGCCATGT 180

	CCTCAGCAGG CACAGCAACC CCTCTGGAAA TGGATCACAA ACTCACTTCT CAGCCAGGCA	240
5	GGCCAAGCTT CTATTGTAAC AGTAGGCACA GTATAGTCGG ATCATCACAT CAGCTGGGTT	300
	TTTGGTTTAG TCATCTAGAG TCGTCTGGAC TAAAGGTCTT TCAGGTCTCC TTGCCCTGTG	360
	AGTGCGTGAA CCTCCCCACC CGAATTGCCT CAGTGTCTCT GAGCCTCATG TCTCTCCTGG	420
10	TGGTGGGCCA GGCCCCTGCA TGGGAAGGGA GCCTGCTGCG GGCAGGCCA GCTGGGGGTG	480
	CTCACCTATG CGCAATGANA GTTATTGAAG GACTGGTTGT TGATGTTGGT GAGCGTATCC	540
15	TTCATGGCCA GCGCGAAGTC GGCCAGGTCA GCCAGGTGCT GCCAGCGCTC TCTCTCGGAC	600
	TTGTCTTCCT GTGCCAGGGG ACCGTGGAGA AAGTGTCAAG GCCCGCTCAC TGCAGCAGCC	660
	TGCTCTGCTG CCTTCCCTGG CAGTGTCTCT GGGGTGGATT CCCTACAMCT AGATGTTCAA	720
20	GGCCTTACTT TTCCTCCAC AAAGGAGTCG CAGCCACGCT AGCTCTGACT TGCCACTGTG	780
	ACAAAGTTCA CGTAGCAGGT CTAGGCAAAG ACTGGGCAAT TGAGCAGAGG AGACGGACCT	840
25	GTGAGTCTGA CCRYGAGSCG GRCCCCTTCA CCTTGGCTGG GCTGGTCTCT GTCTTAGGT	900
	TTTGTCAAGT TGTCCTTGTG TGGATCCCTC AACTAGGTGA TAAGCACTGG AGGGGGATGA	960
	CCCCCCTTGG ACGTGTTTCT TTAACCTCAT CCATATAATA GGGCCGTGGG ATGGTTGTAG	1020
30	AGGTAAAGCA GGATGATGGT GTTTTAAGAC CAGAGCTTGG GACCAGGGCT CCTACACCTA	1080
	ATTTTCTCTC CTGGTAGCTG AACAAAGGTC TAAATTAGCT TAACAAAAGA ACAGGCTGCC	1140
35	GTCAGCCAGA GTTCTGAAGG CCATGCTTTC AGTTTCCCTT GTTGACAATT GCTCTCCAGT	1200
	TCCTATGAAA GCACAGAGCC TTAGGGGGCC TGGCCACAGA ACACAACCAT CTTAGGCCTG	1260
	AGCTGTGAAC AGCAGGGGGT TGTGTGTCTG TTCTGTTTCT CTGCTTGCCG AACTTTCTCA	1320
40	ATAAACCCCTA TTTCTTATTT ATAAAAA AAAA AAAA	1366

45 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

55	GCAGTAATTC CTGTTAGCCA CTGCATCCAC CAAACTAGT TTATTTTCC CCTCAAATTC	60
	ATGATTTTFA CGTCTGTTAC AAAGGGAATT TTGCTGATAG CTCTTTGGGT CCCACTGTTC	120
60	CATTTTATGC TAATAGATTC CATTTAGGG CCCAGCCGTC TCTTGACTGA TGGTGTTC	180

	TTTAACCCCTT GGCATGTATA ATAGAATTTT GGTGAATGAA AGAACCCAAA TAGGCCAGAT	240
	AGTCCCCCCA GGCCCTGATA TCCATAAAAG GCTTGGGAAT GCATTATGTA ATTGTCCTTA	300
5	GTCTTTTGTG TGTTTTAGAA AAAAAAACA AGATGGGCTC AGATGGATGC CTACGTAAAA	360
	ATGGTTCCCTA GCTGTGTACT CATAACTTTT CTTTGAATTG AGTAGTGAAA GGAAGGAGGA	420
10	GGAAAGGAAA TTAAATGTCC TTCTAGTATT CTCTGGACTC AAGTCTGACA TATGAGATAA	480
	TAACCTATAT TGAAATGCCA AGAATTGTAT CTGAAACAAG AGAACAGTTT GACACATTTA	540
	TCATGCCTTC ATATTACATA TTAAGTGAAA CCAATTAATA AACATATGAA ATATCCATTG	600
15	CACAAGGCAA AGGCACCTAA ACCTTTTGTT TCTTTTCTA CATAGCAGAA ATTGATTTTT	660
	TTTTTATTTT TTTAGGGGAA CCTATATAAT TATGACCCAG TGATGTCCTT TGGTGACTTA	720
20	AGCTTATGAA TTCAGGTTAC AATGAGTTG ATTCTAGATG GTTACTACCT TGAAAAGGAT	780
	GTTGGTGCCT TATGTGACAC GAGCCAGAGC CTGCTGGGGA ATAAACAAAG CAGGTTTCAT	840
	GCCAACACCA ACTCGTAGCT TTAGTGGGCA GATGGGGAGT GGTTCACAGA CTTCCCAAAA	900
25	TGTGGGGGCT TTGGGATTTT CCACACCATC CCACGTGTGT TGTTCATTCT TCCTCTTTTC	960
	ACACTCTTGG ATGGATWATT TGRAAATGGT GRAAWYMMCY YYKRAATTTG CCCAATAGCC	1020
30	WIGRGCCACC ATTCTTWATG ACACCATAAC CAAATAGTTC CWTAAATGTTG AAATATTAGA	1080
	AACCTGTTAC CAGCCYKSMA KIWACCCWWA WTTTTCCCAT GTTTGTGGAA TTGATATTGA	1140
	AATAGCAGGG CTAAGGAATT ACTGGCAAGT TTTAGCCTGT GGGTAATACC TTAGGGTTAT	1200
35	TTAAATATTT GTAATTTTAT TTAAATGTTT ATGAATGTTT GAAAGGAACA AAATTATCAG	1260
	GGATGGCTCT TIGCCATGGG TCPTATTTTC ACCCTCTTTT CTGTAAGAAA AAAGAACAAT	1320
40	GTCTTAATGT ATTTTAAAG TTTTGGTAT AGTTTCTAAT TCCAATTTTA ATAAAAGTTT	1380
	TWTRTAAAAA AAAAAAAAAA AAAAA	1405

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(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 504 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

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CGGATTTTCT AGGACCCCAA AAAAAAAAAA AGGGNAAAAA AAACCCNCAA AACCANCCAA 60 |AACCCCAAAA AAAAAAAAAA TCCACAAAAA CAAAAAACT ATAAAAAGA AAGAATTAAA 120 |AACTTTCAGA GAATTACTAT TTACTTTATT AACTTACGGA TTTATTATAT AAATATATAT 180 |

TCACCTAGCA ACATATCTCT GCCGTCTCTC CTGCTCTCAT AATGAAGACA TAGCCGATTC 240
 TCTGCCCGGG CCCCTTGCTG ATGCTCCTCC GGGTCTGCGT CGGGCGTGGG TCTCTGGGGA 300
 5 CCCTCCAGAG GTGGAGGTGG GCTGATGGCC TGGCTGCCTG GTGGTTGATG GTTTTGCTCC 360
 CCCTACCTTT TTTTMTGAG TTTATTCTGA TTGATTTTTT TTCTTGTTTT CTGGATAAAC 420
 10 CACCCTCTGG GGACAGGATA ATAAAACATG TAATATTTTT AAGAAGGAAA AAAAAAAAAA 480
 AAAAACTNG GGGGGGGCCC CGAA 504

15

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

NAAGTATCTT GGCCAGTTTA TTACAGAGGA CGATAAATGA TTCCATGTGG ATAGGGCATA 60
 ACATACAGAG AATGAGACTA TGCCAGAAAT GGGAGGAGGC ATTTGAAACA ACATGAGTAT 120
 30 CTCAGGACA GATGGATTGA TTCTGCTATT GGTAGCCTG GAAGCAANGG TCAGAAGTAG 180
 CAAAAAATGG ATACCAAAG CACTATTWGT CACCCAAGCT AAGTGAATA GCTGGCCAG 240
 35 TAGGAGAAAT GCAGGTTTTG CTCTACACTA AGTTCTCCAA CTCTTGATAA GCCTCCAAAA 300
 ACAAATGTTA GGGGAAAAAA ACGCAGCTGG TTATGAAAAG ATATATCTCA TTTCATTAAA 360
 AAATCAATGT CAATGCTGTT AATAGAATCC TTTTATCTTC AGGACAGAGG CAATGCCCTA 420
 40 AACAAACACC AGCTCAAGAG CCTCTGATGC CAACCTAGAG GGTACCCAAA CACAACTTA 480
 GCATAGAGGT AAGAATCTCT ATGTCTTTTG GTGGAGGCAA AGCCATTTGG TTGGTACTTC 540
 45 ACAGGAACAT CTTCTACCA AGTCTTCATC ATATGGTATG TGCCACGAGT CTCCAGTTGT 600
 TTGCACCACT GTGTCATAGC TGAGAATACG CTGAAAGGTT AGTTTTGATC CTGGAAACCT 660
 ATTTACAATT GCCAGCTGAT GTCCCTGCTG CCACTTAAAA AAGGCTTGGG TCTGGCATAG 720
 50 GCAGAMAGGC CTGTGGTCCC CTCGTGCCGA TTCTNGGCTC GAGGCCAATT NCCTTAT 777

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(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

5 ATGACTACAG TGTATACCC TCCAATCTTT GCAGGTGGGC ATGGAACACT GCTTGTATCA 60
CTCTGTGCAC GGTATAAATC CATATATCCA CAAAAACACA CATCCATCCA TCAACATATA 120
10 CATGGTTTGG GATGAGCAGG TCAATAGTTT TGAGAGGGAG TTGTTCCTT TTTTTCCTT 180
CATTATACTC TTAAATTGTT GTCAGTTATC AAACAAACAA ACAGAAAAAT TGTTCGGAAA 240
AACCTTGCAT ACGCCTTTTC TATCAAGTGC TTTAAATAT AGACTAAATA CACACATCCT 300
15 GCCAGTTTTT TCTTACAGTG ACAGTATCCT TACCTGCCAT TTAATATTAG CCTCGTATTT 360
TTCTCAGTA TATTTACCTG TGACTTGTAT TTGTTATTTA AACAGGAAAA AAAACATTCA 420
20 AAAAAAGAAA AATTAAGTGT AGCGCTTCAT TATACTATTA TATTATTATT ATTATTGTGA 480
CATTTTGGAA TACTGTGGAA GTTTTATCTC TTGCATATAC TTTATACGGA AGTATTACGC 540
25 CTTAAAAATA CGAAAATAAA TTTTACAAGG TTCCGGTTTT GGTGGTGGAA AGAGTAAATT 600
GA 602

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(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

40 AGTCACTGAC TTGGAGCCGC TCGGGGAAG TCCGCCCAG ACAGGCGGTG GGTGGGAATG 60
CCTCACTTCA GTTTGAAGAG GGTCCGGATC CAAAGGGGTT AAAACGAGCG AACCCCGATC 120
45 CCCGACCACA CTTCCTCGCT CCTTAAACG CACACCCGC TAGCCATGGG CAGCCGCGAC 180
CACCTGTTCA AAGTGCTGGT GGTGGGGGAC GCCGCAGTGG GCAAGACGTC GCTGGTGCAG 240
50 GATTATTCCT AGGACAGCTT CAGCAAACAC TACAAGTCCA CGGTGGGAGT GGATTTTGCT 300
CTGAAGGTTT TCCAGTGGTC TGACTACGAG ATAGTGCGGC TTCAGCTGTG GGATATTGCA 360
GGCAGGAGC GCTTCACCTC TATGACACGA TTGTATTATC GGGATGCCTC TGCCTGTGTT 420
55 ATTATGTTTG ACGTTACCAA TGCCACTACC TTCAGCAACA GCCAGAGGTG GAAACAGGAC 480
CTAGACAGCA AGCTCACACT ACCCAATGGA GAGCCGGTGC CCTGCCTGCT CTTGGCCAAC 540
AAGTGTGATC TGTCCCCTTG GGCAGTGAGC CGGGACCAGA TTGACCGGTT CAGTAAAGAG 600
60

	AACGGTTTCA CAGGTTGGAC AGAAACATCA GTCAAGGAGA AAAAAAATAT TAATGAGGCT	660
	ATGAGAGTCC TCATTGAAAA GATGATGAGA AATTCCACAG AAGATATCAT GTCTTTGTCC	720
5	ACCCAAGGGG ACTACATCAA TCTACAAACC AAGTCCTCCA GCTGGTCCTG CTGCTAGTAG	780
	TGTTTGGCTT ATTTTCCATC CCAGTTCTGG GAGGTCMTT AAGTCTCTTC CCTTTGGTTG	840
10	CCCACCTGAC CATTTTATTA AGTACATTG AATTGTCTCC TGACTACTGT CCAGTAAGGA	900
	GGGCCCATTG TCACTTAGAA AAGACACCTG GAACCCATGT GCATTTCTGC ATCTCCTGGA	960
	TTAGCCTTTC ACATGTTGCT GRCTCACATT AGTGCCAGTT AGTGCCTTCG GTGTAAGATC	1020
15	TTTCATCAG CCTCAATTT GTGATCCGA ATTTTGTGAG AAGGATTAGA AATCAGCACC	1080
	TGCGTTTTAG AGATCATAAT TCTCACCTAC TTCTGAGCTT ATTTTCCAT TTGATATTCA	1140
20	TTGATATCAT GACTTCCAAT TGAGAGGAAA ATGAGATCAA ATGTCATTTT CCAAATTTCT	1200
	TGTAGGCCGT TGTTTCAGAT TCTTCTGTC TTGGAATGTA AACATCTGAT TCTGGAATGC	1260
	AGAAGGAGGG GTCTGGGCAT CTGTGGATTT TTGGCTACTA GAAGTGTCCT AGAAGTCACT	1320
25	GTATTTTGA AACTTCTAAC GTCATAATTA AGTTTCTCTT GTCTTGGCAT CAAGAATAGT	1380
	CAAGTTTTTT GGCCGGGCAT GGTGGCTCAT GCCKGTAATC CCAGCACTTG GGGAGGCCAA	1440
30	GGCAGGCGGA TCACATGAGG CCAGGAATTC GAGACCAACC TGGTCAGCAT GGCAAAACCC	1500
	CGTCTCTACT AAAAGTACAA AAATTAGCCA GGCCTGATGG CACGTGTCTG TAATCCCAGC	1560
	TACTCTGGAG ACTGAGGTGG GAGAATCGCT TGAGACTGGG AGGCAGAGGT TGCAGTGAAC	1620
35	CGAGATCATG CCACCGCACT TCAGCCTGGG TGACAGAGAA GGACTCCGTC TCAAAAAAAA	1680
	AAAAAAAAAA AAAACTCGAG GGGGGGCCCG GTACCCAAAT CGCCSTGATA GTGATCGTAW	1740
40	ACAATCNAA	1749

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

55	AAAGAGATGG GCTCTTTATT TTCTCGAAAA ACCAATTGG AGTTACTCAT TTTCCATAA	60
	CATTAAATTT CTTACAGTGA ACTACATATT GTCCATAAGT GCTTCATCAG GACTCATCGC	120
	CCTCCTGTCT ACTGGCTCCA AATAGACCAT GTCAGCTTCA CCCCCTGGCT TTGTGTCTAT	180
60	GGGTGGCCTG TGGTATATGG AAAAGTAGCA GGGTGGTCAG GGTGGGAGAC ACAAGATGTT	240

	TTTATAGTCT AGAGCCTTTA AAAAACCAG CAGAATGTAA TTCAGTATTT GTTTATGGC	300
5	TGTTTTTTGA CAGATTGTTG AAATTAATG AATTGAAAGG GAAACTCAGA GTACTAGGAC	360
	GTATATATAA AGGAAAAAAA TGTCTTGCAA TGTGCTGTAA TCACAAGAGG AGAAAAATAAC	420
	TTGTTTCCTT GATCTGTCAG AGGTCACAGT AACCTGGGCC GAGCTGTTAT TATTTATTAT	480
10	ATAATAGTAG TAGGAAGTTA ATAACGGTT CTCTGTGTTT CAAGCACAAT ATTACAACCT	540
	CTTTTGAACC GTAAATATCA GAATGAATCC TCTTCCCAGG GGATTGAACA GAAGCTTAAT	600
15	GTATACAAGT GTTTGAATTT GTGATCTGAA ATAACACAAA ATTAAAAACA TGATTCTCT	660
	AATTTTCCAA CTAGAGGAAG AGAACTTGT GGAAAGTTC TTTTTTTTTC TTTTTTTTTT	720
	CTTAAAGAAG GGCAGCCAAG GTAGTAACCT AAAAATAGTG CCCAGGCATA TGAGAGTTGT	780
20	CCTACGAGGT TAAAGAACAC ACTGTTCCAC TGTATGGCTT TGGCCCTGAG TGGCCAGGGA	840
	GGTCAACTTG ACCCTGCCAT GTTGGTTTGA CTTACTAAGA CACAGGAATC ATTGTTTTCC	900
25	TTGACCAGGG TCTCACACCC TGGAGGAATG TTAAGTAAGA GAAAGAACCT CTTTCCTGAA	960
	TATTGACATG TAAAAGACCA AAGTAATTTT TCTGAACTTC TGCAATTCTG AGAACTCTCC	1020
	AAGGAATTTA CAGTGATTTT AGTGCTTGTC AGCATTTTTT CATGAGGACT TTCATACATT	1080
30	TGACTCTTTA GTTCACAGGT TCCCATGAT TGTGAGCAAG ATATTTATCT CTTTAGCCCT	1140
	TGGGGATCCA GCTGAGAGCA ATCTCTTGCA TTTTMTTACC CGTGATGTA CAGATATCAT	1200
35	TTCTGTGTA TGCCATGACT TGAAAAAGTT TGGGAAGCTC TTTAGCAATA TCAGCTAAAA	1260
	GGATATGAAA TCACAGGTGA TAGCAGTTGT CATTCAGTAA TTTCTTACAA GCAGCACCCC	1320
	AAAGGAAATA TAGTCCTAAT CTTTACTATC CACTTCTAAA TTAAATGTGA ATTCATACA	1380
40	TGTTATTAGT TGTTTTCTTT ATAATTTTAT AAAAATTATT CATCGGGAGT TTAACCTCCA	1440
	CTTCCATGCT ATCGGATGTG TTGGGCTCCA TGCAAGAACT TGAAGAAAA ACAGGCAGGA	1500
45	ATGCATTTGC ATAATGACCC AGATCATCAT TTTCTGCAAC TGAGAATTAT ATTCATCAT	1560
	TGCTTCTAGA AGTCTGCAAT TCTTTACTTT TCTTTGGTGC ATTATTATCT AGGTGCCATC	1620
	ACTGGATAAT GTGGAGTGAC TAGAGAAGTC AYATATCACT GTAAGGTACA GTTAGGGGTA	1680
50	ACACTTTAGA GGTATTATTAT TTTTAAAAAA CTTTCTTGA ACTCCTGGGC CAACATGGGT	1740
	GAAACCCCGT CTTCTTACTT AAAAATACCC AAAATTAGGC CAGGGGCGTG GATGGGTGGG	1800
55	GTGCCTGTTA ATCTTCAGCT ACTTNGGGGA GGGCTTGAAG CCAGGGAGGA ACTGCCCTGG	1860
	ANCCCCGGGG NGGGCCAGNA GGTTTGCCAG TTGAGT	1896

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

10 TCTTTTAAAA ATAGACATTT GTGGGGCTCA CACAATATAT GAAATAGTAC CCTCTAAAAA 60
AGAGAAAAAA AAAATCAGGC GGTCAAACCT AGAGCAACAT TGTCTTATTA AAGCATAGTT 120
15 TATTTCACTA GAAAAAATTT AATATCAAGG ACTATTACAT ACTTCATTAC TAGGAAGTTC 180
TTTTTAAAT GACACTTAAA ACAATCACTG AAAACTTGAT CCACATCACA CCCTGTTTAT 240
TTTCCTTAAA CATCTTGGAA GCCTAAGCTT CTGAGAATCA TGTGGCAAGT GTGATGGGCA 300
20 GTAAATACC AGAGAAGATG TTTAGTAGCA ATTAAAGGCT GTTTGCACCT TTAAGGACCA 360
GCTGGGCTGT AGTGATTCTT GGGGCCAGAG TGGCATATG TTTTACAAA ATAATGACAT 420
25 ATGTCACATG TTTGCATGTT TGTTCGCTTG TTGAATTTTT GAACAGCCAG TTGACCAATC 480
ATAGAAAGTA TTACTTTCTT TCATATGGTT TTTGGTTCAC TGGCTAAGA GGTTCCTCAG 540
AATATCTATG GCCACAGCAG CATACCAGTT TCCATCCTAA TAGGAATGAA ATTAATTTTG 600
30 TATCTACTGA TAACAGAATC TGGGTCACAT GAAAAAAAT CATTTTATCC GTCTTTTAAG 660
TATATGTTTA AAATAATAAT TTATGTGTCT GCATATTGCA GAACAGCTCT GAGAGCAACA 720
35 GTTTCCTATT AACTCTTTCT GACCAATAGT GCTGGCACCG TTGCTTCCTC TTTGGGAAGA 780
GGAAAGGGTG TGTGAACATG GCTAACAATC TTCAAATACC CAAATTGTGA TAGCATAAAT 840
AAAGTATTTA TTTTATGCCT CAGTATATTA TTATTTAATT TTTTAGGTAA TGCCTATCTC 900
40 TTGGTCTATT AAGGAAAGAA GCAATCAGTA GAGAATTCAG GATAGTTTIG TTAAATTTCT 960
TGCAGATTAC ATGTTTTTAC AGTGGCCTGC TATTGAGGAA AGGTATTCTT CYATACAACT 1020
45 TGTMTTAACC TTTGAGAACA TTGACAGAAA TTATGCAATG GTTTGTTGAG ATACGGACTT 1080
GATGGTGCTG TTTAATCAGT TTGCTTCCAA AGTGGCCTAC TCAAGAGGCC CTAAGACTGG 1140
TAGAAATTAA AAGGATTTCA AAAACTTTCT ATTCTTTCT TAAACCTACC AGCAAACCTAG 1200
50 GATTGTGATA GCAATGAATG GTATGATGAA GAAAGTTTGA CCAAAATTGT TTTTTGTGTT 1260
TTGTGTGTGT TTTGAATTTG AAATCATTCT TATTCCTTTT AAGAAATGTT ATGTATGAGT 1320
55 GTGAAGATGC TAGCGAACCT ATGCTCAGAT ATTCATCGTA AGTCTCCCTT CACCTGTTAC 1380
AGAGTTTCAG ATCGGTCACG GATAGTATGT ATTCTTTAG TAAGAATGTG TTAATAATTAC 1440
AATGATCTTT TAAAAGATG ATGCAGTTCT GTATTTATTG TGCTGTGTCT GGTCTAAGT 1500
60

GGAGCCAATT AAACAAGTTT CATATGTATT TTTCCAGTGT TGAATCTCAC AACTGTACT 1560
 TTGAAAATTT CCTTCCATCC TGAATAACGA ATAGAAGAGG CCATATATAT TGCCTCCTTA 1620
 5 TCCTTGAGAT TTCACTACCT TTATGTTAAA AGTTGTGTAT AATTGTTAAA ATCTGTGAAA 1680
 GAATAAAAAG TGGATTTAAA TTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1740
 10 AAAAAAAGG GGG 1753

(2) INFORMATION FOR SEQ ID NO: 57:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

25 GCGGAAGTGA CTGCAGCCGC GGTGTTGTGC TGTGGGGAAG GGAGAAGGAT TTGTAAACCC 60
 CGGAGCGAGG TTCTGCTTAC CCGAGGCCGC TGCTGTGCGG AGACCCCGG GTGAAGCCAC 120
 CGTCATCATG TCTGACCAGG AGGCAAAACC TTCAACTGAG GACTTGGGGG ATAAGAAGGA 180
 30 AGGTGAATAT ATTAACTCA AAGTCATTGG ACAGGATAGC AGTGAGATTC ACTTCAAAGT 240
 GAAAATGACA ACACATCTCA AGAACTCAA AGAATCATAC TGTCAAAGAC AGGGTGTTC 300
 AATGAATTCA CTCAGGTTTC TCTTTGAGGG TCAGAGAATT GCTGATAATC ATACTCCAAA 360
 35 AGAACTGGGA ATGGAGGAAG AAGATGTGAT TGAAGTTTAT CAGGAACAAA CGGGGGGTCA 420
 TTCAACAGTT TAGATATTCT TTTTATTTT TTTCTTTTCC CTCAATCCTT TTTTATTTTT 480
 40 AAAAAAGTAT CTTTTGTAAT GTGGTGTTC AAACGGAATT GAAAAGTGGC ACCCATCTC 540
 TTTGAAACAT CTGGTAATTT GAATTCTAGT GCTCATTATT CATTATTGTT TGTTTTCATT 600
 45 GTGCTGATTT TTGGTGATCA AGCCTCAGTC CCCTTCATAT TACCTCTCC TTTTAAAAA 660
 TTACGTGTGC ACAGAGAGGT CACCTTTTTT AGGACATTGC ATTTTCAGGC TTGTGGTGAT 720
 AAATAAGATC GACCAATGCA AGTGTTCATA ATGACTTTCC AATTGGCCCT GATGTTCTAG 780
 50 CATGTGATTA CTTCACTCCT GGACTGTGAC TTTCACTGGG AGATGGAAGT TTTTCAGAGA 840
 ACTGAACTGT GGAAAAATGA CTTTCTCTTA ACTTGAAGCT ACTTTTAAAA TTTGAGGGTC 900
 TGGACCAAAA GAAGAGGAAT ATCAGGTTGA AGTCAAGATG ACAGATAAGG TGAGAGTAAT 960
 55 GACTAACTCC AAAGATGGCT TCACTGAAGA AAAGGCATTT TAAGATTTTT TAAAAATCTT 1020
 GTCAGAAGAT CCCAGAAAAG TTCTAATTTT CATTAGCAAT TAATAAGCT ATACATGCAG 1080
 60 AAATGAATAC AACAGAACAC TGCTCTTTTT GATTTTATTT GTACTTTTTG GCCTGGGATA 1140

TGGGTTTTTAA ATGGACATTG TCTGTACCAG CTTCATTAAA ATAAACAATA TTTGTAAAAA 1200
 TCAWAAAAAA AAAAAAAAAA 1220

5

(2) INFORMATION FOR SEQ ID NO: 58:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

20

TCGCGCCTGC AGACACAGCA TCTACTCAGC GTGGGTCACC TCTGTGAACA TCACTGACTG 60

CAAGCCTCCC TCAATTTCTG GTGCAGCCCA TCAGGGACCC ACAGCGCCTG GGAGGATGGT 120

GCGGATCTTG GCCAATGGGG AAATCGTGCA GGACGACGAC CCCCAGTGA GGACCACTAC 180

25

CCAGCCACCA AGAGGTAGCA TTCCTCGACA GAGCTTCTTC AATAGGGGCC ATGGTGCTCC 240

CCCAGGGGGT CCTGGCCCCC GCCAGCAGCA GGCAGGTGCC AGGCTGGGTG CTGCTCAGTC 300

30

CCCCTTCAAT GACCTCAACC GGCAGCTGGT GAACATGGGC TTTCCGCAGT GGCATCTCGG 360

CAACCATGCT GTGGAGCCGG TGACCTCCAT CCTGCTCCTC TTCCTGCTCA TGATGCTTGG 420

TGTCGTGGC CTCCTCCTGG TTGGCCTTGT CTACCTGGTG TCCACCTGA GTCAGCGGTG 480

35

ACCTCTGAGG GCTGATAGGG GTGGGTTTGT TGAGAGGGAC TTGCTGGGCC TTGGTGTGAG 540

AGCAGGCATA TTTGGAGGGG ATCTGGTGGT GCCTTGAAGG TATGATCAGA GAGGGGACCA 600

40

CAGGTGTGTG TTTCCCCTTT GTGTTAAGCG TGAGGCAGAG GGAGACGTTA GTCCCAGCAT 660

TTCCCAAAGT GTGGGTGGGT CCGTGGTTC CCGAGATACT TTTAGGTGGT ATGGGGCCTG 720

CATTAAGTGG CACAAAATCA GAGCAAGAAA GCGATGCCCT TCCCAATTCT CTCAATCCTT 780

45

TTATGCCGAG AAGATCTCAG CTGGATGCCA ACATGTTCCG ATGCCTGTGG AAGACATGCC 840

GACGTCTCCT CTGCCTAGGG AGCAGGACTT GGGCTTAGGG CAGGTGGAAA AAATTCCAGA 900

50

CTTTTITAGC ACTGTTTTTG TTTTAATGGT ATATTTTAT TGGCTACTTT ATTGTTTAGG 960

ACAAGTGGTA GTGGCATTCT ATTTATTTGTG ACCTTTTCAA TAAATAGATT TAAGTAAAAA 1020

AAAAAAAAA AAAACTCGAG GGGGGGCC 1049

55

(2) INFORMATION FOR SEQ ID NO: 59:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

	AAAGAGGATG TGMAGCTAGA GGTCCCCGAT GGCTGGTCCG ATGGGAAGCA CAAGGCTGAG	60
10	GGACTGGATT GTAAAGGCAC TAAGTCGTTC TCGGTGAGA ATCAGACATG GGGGACCTCT	120
	AGCTTCACAT CCTCTTTCCT TGCAGSTCTG GACATCCTGA GCCCAAGTCC CCCACACTCA	180
15	GTGCAGTGAT GAGTGCAGAA GTGAAGGTGA CAGGGCAGAA CCAGGAGCAA TTTCTGCTCC	240
	TAGCCAAGTC GGCCAAGGGG GCAGCGCTGG CCACACTCAT CCATCAGGTG CTGGAGGCC	300
	CTGGTGTCTA CGTGTPTTGA GAACTGCTGG ACATGCCCAA TGTAGAGAG CTGGCTGAGA	360
20	GTGACTTTGC CTCTACCTTC CGGCTGCTCA CAGTGTTCG TATATGGACA TACGCTGACT	420
	ACTTAGCTGA AGCCCGGAAT CTTCCTCCAC TAACAGAGGC TCAGAAGAAT AAGCTTCGAC	480
25	ACCTCTCAGT TGTACCCCTG GCTGCTAAAG TAAAGTGAT CCCATATGCA GTGTTGCTGG	540
	AGGCTCTTGC CTGCGTAAT GTGCGGCAGC TGGAAGACCT TGTGATTGAG GCTGTGTATG	600
	CTGACGTGCT TCGTGGCTCC CTGGACCAGC GCAACCAGCG GCTCGAGGTT GACTACAGCA	660
30	TCGGGCGGGA CATCCAGCGC CAGGACCTCA GTGCCATGCG CCGAACCCTK AANAAAAACC	720
	ATTAAAGTTA CGACGGCAGC AGCAGCCGCA GCCACATCTC AGGACCCTGA GCAACACCTG	780
35	ACTGAGCTGA GGGAAACCAGC TCCTGGCACC AACCAGCGCC ASCCAGCAAG AAAGCCTCAA	840
	AGGGCAAGGG GCTCCGAGGG ANCGCCAAGA TTTGGTCCAA GTCGAATTGA AAGRACTGTC	900
	GTTTCCTCCC TGGGGATGTG GGGTCCCAGC TGCCTGCCTG CCTCTTAGGA GTCCTCAGAG	960
40	AGCCTTCTGT GCCCCTGCC AGCTGATAAT CCTAGGTTCA TGACCCTTCA CCTCCCCTAA	1020
	CCCCAAACAT AGATCACACC TTCTCTAGGG AGGAGKCAA TGTAGGTCAT GTTTTGTGTG	1080
45	GTACTTTCTG TTTTPTGTGA CTTCATGTGT TCCATGTCT CCCGCTGCCA TGCTCTCTCC	1140
	CTTGTTTCCT TAAGAGCTCA GCATCTGTCC CTGTTCAATTA CATGTCATTG AGTAGGTGGG	1200
	TAGCCCTGAT GGGGGTCGCT CTGTCTGGAG CATAACCCAC AGGCGTTTTT TCTGCCACCC	1260
50	CATCCCTGCA TGCCTGATCC CCAGTTCCTA TACCCTACCC CTGACCTATT GAGCAGCCTC	1320
	TGAAGAGCCA TAGGGCCCCC ACCTTTACTC ACACCCTGAG AATTCTGGGA GCCAGTCTGC	1380
55	CATGCCAGGA GTCACTGGAC ATGTTTCATCC TAGAATCCTG TCACACTACA GTCATTTCTT	1440
	TTCTCTCTC TGGCCCTTGG GTCCTGGGAA TGCTGCTGCT TCAACCCAG AGCCTAAGAA	1500
	TGGCAGCCGT TTCTTAACAT GTTGAGAGAT GATTCTTTCT TGGCCCTGGC CATCTCGGGA	1560
60	AGCTTGATGG CAATCCTGGA AGGGTTTAAT CTCCTTTTGT GAGTTTGGTG GGGAAGGGAA	1620

GGGTATATAG ATTGTATTAA AAAAAAAAAAG GTATATATGC ATATATCTAT ATATAATATG 1680
ACGCAGAAAT AAATCTATGA GAAATCTATC TACAAAMWAA AAAAAAAAAA AAAAAAAAAA 1740
-5 AGGAATTCGA TNTCAAGCTT ATCGATACCG TCNACC 1776

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(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

20

ACAGATAAAT AAATAAATAA TAAATTAAAT TAAATAAAAA ATCTGAGCTA ATCTGAATAA 60
ATTGAGAGAT TTCACATGAA AGCCAGGATT TCTGGCTTCC CAGGAACAGT CAGAAGAGCT 120
25 AGCTAGCAAC ACTGGTCTGC TTGGCTACCT TCTTTGGAAC AACATGAAAT CTAGCTCCCT 180
TTTTTTTTTT TTTTGGCCCC ACTTCATCCA TTCACATGAC CTGCCTGGCC TCTGCAGGTA 240
AGTGAGTATG CAACAAAAAT GTAGCACAGG TTTTGTGCTG GAACTACGTG GTTTCAGGTC 300
30 CAGCTCTGCC ACTTGCTAGC ATGACCTCGT GCCGAATTCC NGCACGAAGT TTTTTTTTTT 360
TTTTTCAGTG CTCCAGTCCC CCTATTGGAG AATCCTGCCC CCCCTGGGA CAGAATGTTT 420
35 ACCCTGGCCC CGCGANTCCC TGA 443

40

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 2888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

50

TTAATGTTGT CAATAACCAC CAGGCCAAAC AGAATTTATA TGACCTGGAT GAAGATGATG 60
ATGGTATAGC TTCCGTTTCT ACTAAACAGA TGAAGTTTGC AGCCTCAGGC GNCTTTCTCC 120
ACCACATGGC TGGGCTAAGC AGTTCCAAGC TTTCCATGTC CAAGGCCCTC CCTCTCACCA 180
55 AAGTGTTTCA GAATGATGCA TACACAGCTC CTGCTCTCCC TTCCTCTATT CGAACAAAAG 240
CCTTGACCAA CATGTCCCGG AACTGGTGA ACAAGGAAGA ACCCCCCAAA GAGCTGCCAG 300
60 CTGCTGAGCC TGTTCCTCAGC CCATTGGAAG GCACCAAGAT GACTGTGAAT AATCTGCACC 360

	CTCGAGTCAC TGAGGAGGAC ATTGTTGAGC TTTTCTGTGT GTGTGGGGCC CTCAAGCGAG	420
- 5	CTCGACTGGT CCATCCTGGG GTAGCGGAGG TGGTGTGTGT GAAAAAGGAC GATGCCATCA	480
	CCGCATATAA GAAGTACAAC AACCGGTGTC TGGACGGGCA GCCGATGAAG TGCAACCTTC	540
	ACATGAATGG GAATGTTATC ACCTCAGACC AGCCCATCCT GCTGCGGCTG AGTGACAGCC	600
10	CATCAATGAA AAAGGAGAGC GAGCTGCCTC GCAGGGTGAA CTCTGCCTCC TCCTCCAACC	660
	CCCCTGCGA AGTGGACCCT GACACCATCC TGAAGGCACT CTTCAAGTCC TCAGGGGCCT	720
15	CTKTGACCAC GCAGCCCACA GAATTCAAAA TCAAGCTTTG AGCAGGGGAG TGAGGCAGCC	780
	AGAAGTGGGG GCAGAGGAGG GTGGCTCTGT TTCCCCAAGG CAAAGCTTAT GACCAATGGG	840
	CCATCGGACT GGAGACCCCT GATTGTGGGA AGGGTTGCCA GGGATAAAGA GCTTCCTCAC	900
20	TGGATGGGAC CCGCCTTTCT GTGTTGTGTT CTGCCCTGTG CTCTTCTCTC TACGTTAAGC	960
	TTTCCTGTAG TATGTTTCTT CATCTCATCG CCAAGGTAGG CTGTGTGTTT TCAGTGTGTG	1020
25	CCTCCCCGAG CCTCAGCCCC AAGCTGATTT CTTATCTGGA AATGGTACAC TGAATTCTCT	1080
	GGGTGGCTTT CTGTGGCCCC CATGGGATGC AGCGTGGGGG CTGTCTGAAG GACCCTGCTT	1140
	TTTCCAGGGG CCGAGGGGCT GCCTTTCTCT TGTGTGTATT AAGCTTTTCA AACAATGGAG	1200
30	GGGATGGAGA GCCCTGGTGT CCTGACGGGA GCCAGGTCCG CCTGAGAGCT GTGCCGCTCC	1260
	TCTGTCTGT CAGTGGAGGT GCCTGGGTGG GGAGCAGGTC TCAGGCCTCT TGTCTCTCTC	1320
35	CCAGTGGCTC CAGGCCTCAC TAGTGGCAAG GGCAGGATGA GGCTGCACCG CTGGGAAGAG	1380
	TCTATCTAAG YCTTGGCTT GGAGTCCCGT GTCGTCTCCR CCCAGAGGAA GTTCTCCAGA	1440
	GTTACCTTT CCCTTTCTCT TGAGTTGTGC TGAATGCCCC ACCCCAGCTC TCTTTCCCTT	1500
40	CTGGGTGTCT TTGCTGGGAG GGGGCTGTGT TGTGAGCCCT CCCGTTCTC ACCTCGCCTG	1560
	GCACTTAACC ACACCCTGGT TTTGTGTAGC CGCCAGCTCT CTTCTGGTTG GGCCTTTGAA	1620
45	AGGCTCAGCC TCCCATGTG CAGTGCTTGG GTTTGGAGCT TATTTGAATG GAAGAGGTCA	1680
	GTTTGTCTCT GGCTCTCCAT TTCTGGCCTC AGTTGTCTAC AGGACAGTGG TCAGGGATGC	1740
	CTGGAGGCAT ATATCCAGCT GCCACCAAGG GGCAGTGTG GTTCCCACTT ATGTGAGTGA	1800
50	CCCCATCCAT CCATGACCAG AGGATTATTT TCCTGCCTTG GCAGAGGAGG AGGAGTCAAG	1860
	GGAGCAGGGC AGCTCTACCA GGCAAGGTGT TTCCCCAGCA TAGGCGCAGA CAGTTGGGAC	1920
55	GAAACTTCAG AGCCCAGGCA GTCCCTGAAT GACCAGGCCA GTGTTGTAC TGAGTGGTCC	1980
	CCTGCTGGTT GGGAGTGAAG AGAATCCAGG CTGGCAGAGC TGGAGCCAGT TGGGGAGCAC	2040
	GGTTCTGGGA GCTCTGCAA ATCAGTAGCA AGTGCTGGAA AAGGCACATG CCGAAGATAC	2100
60	TCAAGAGCTC CCAAGATTTG CTTGAGGCTA GCCCAGTGAA RAAAACCAGA GACTCATGTT	2160

TCCAGGGGTC AGTCTGTCAG GCAGGAAGGA CCCAGGATTT GAACCCAGCT TCAGTGTGCA 2220
 GGCTCTGAGG CTGCCCAGGA CGGGAAAGTC CAAGGAAGGG GCCTGGTGGT GCTCCACTTG 2280
 CAGTTCCTTA AAGAATGCTG CTTTTTATTC TCCTAACCCCT TTCAAGTGGG TGCAGACTTC 2340
 TCGTTAGCAG CTGGAAGACA TTCTCCAC ACTTTTCCCT TCCTGGCCCA AGAGAGCATC 2400
 CAGAAGGCAG TAGGACCTGG TTTTTCAGGT ACTGGGAGCC GGGGGCTCAC TGCTTGCACT 2460
 GTGCTTAGGG TAGGGATGGT AAATATCCTC CCTGCATGGC TTTATCCTCC CTCTCATCCC 2520
 AAAGCAGGTA TCTTCTGGTT GTCACAGAGT TTCATTGAGT CCAGCTGCAG CCACGTGGCC 2580
 ATCTGGAGCT GGTGCTATAG GTGACCATCT GGTACATTGA GGGGACCTGT TTGCCTCCTC 2640
 CACTCTATAA GCAGTCATCT TGGGAGACCG GGAGGAGAAG GTGGTGGGCT AGTCCTGTGT 2700
 CCTCCTCCAC TTCCCATGCC TCTATGTTAC CCATCTGTGT CTCCTGTGCA GAAGGAGAGG 2760
 AAGGGGCATT AAGAGATGAA GGGTGATTAT GTATTACTTA TCCATTCTG AATAAACATT 2820
 TGTATTTCCT AAAAAAAAAA AAAAAAACT CGAGGGGGG CCCGGWACC AWATCGCCSK 2880
 AAAGTGAG 2888

30

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

40

CACTAGTATA ATTTATAATT ATAACCTATT CTGATTTCTT TTCAAATATT AGGTGTCCTA 60
 GTTGCCTATG AAGGTTTGCC ACTTCATCTT GCACTGTTCC CCAAACCTTG GACTGAGCTA 120
 TGCCAGACTC AGTCTGCTAT GTCAAAAAAC TGCATCAAGC TTTTGTGTGA AGATCCTGTT 180
 TTGCAGAAT ATATTAAATG TATCCTAATG GATGAAAGAA CTTTTTTAAA CAACAACATT 240
 GTCTACACGT TCATGACACA TTTCTTCTA AAGGTTCAAA GTCAAGTGTT TTCTGAAGCA 300
 AACTGTGCCA ATTTGATCAG CACTCTTATT ACAAACCTGA TAAGCCAGTA TCAGAACCTA 360
 CAGTCTGATT TCTCCAACCG AGTTGAAATT TCCAAAGCAA GTGCTTCTTT AAATGGGGAC 420
 CTGAGGGCAC TCGCTTTGCT CCTGTCAGTA CCACTCCCA AACAGTTAAA CCCAGCTCTA 480
 ATTCCAACCTC TGCAAGAGCT TTTAAGCAAA TGCAGGACTT GTCTGCAACA GAGAACTCA 540
 CTCCAAGAGC AAGAAGCCAA AGAAAGAAAA ACTAAAGATG ATGAAGGAGC AACTCCCATT 600

60

	AAAAGGCGGC GTGTTAGCAG TGATGAGGAG CACACTGTAG ACAGCTGCAT CAGTGACATG	660
	AAAACAGAAA CCAGGGAGGT CCTGACCCCA ACGAGCACTT CTGACAATGA GACCAGAGAC	720
5	TCCTCAATTA TTGATCCAGG AACTGAGCAA GATCTTCCTT CCCCTGAAAA TAGTTCTGTT	780
	AAAGAATACC GAATGGAAGT TCCATCTTCG TTTTCAGAAG ACATGTCAAA TATCAGGTCA	840
10	CAGCATGCAG AAGAACAGTC CAACAATGGT AGATATGACG ATTGTAAAGA ATTTAAAGAC	900
	CTCCACTGTT CCAAGGATTC TACCCTAGCC GAGGAAGAAT CTGAGTTCCC TTCTACTTCT	960
	ATCTCTGCAG TTCTGTCTGA CTTAGCTGAC TTGAGAAGCT GTGATGGCCA AGCTTTGCCC	1020
15	TCCCAGGACC CTGAGGTTCG TTTATCTCTC AGTTGTGGCC ATTCCAGAGG ACTCTTTAGT	1080
	CATATGCAGC AACATGACAT TTTAGATACC CTGTGTAGGA CCATTGAATC TACAATCCAT	1140
20	GTCGTCACAA GGATATCTGG CAAAGGAAAC CAAGCTGCTT CTGACATTA GGTGTAGCAT	1200
	GTCTACTTTT AAGTCCCTCA CCCCCAACCC CCATGCTGTT TGTATAAGTT TTGCTTATTT	1260
	GTTTTGTGC TTCAGTTTGT CCAGTGCTCT CTGCTTGAAT GGCAAGATAG ATTTATAGGC	1320
25	TTAATTCTTG GTCAGGCAGA ACTCCAGATG AAAAAAAGCT GCATCTTCAG TATACTTCCT	1380
	AAAGGGCAAT CAGATAATGG ATATGTTTTA TGTAATTAAG AGTTCACTTT AGTGGCTTTC	1440
30	ATTTAATATG GCTGTCTGGG AAGAACAGGG TTGCCTAGCC CTGTACAATG TAATTTAAAC	1500
	TTACAGCATT TTTACTGTGT ATGATATGGT GTCCTCTGTG CCAGTTTTGT ACCTTATAGA	1560
	GGCAGATTGC CTCGATCGC TGTGGTTCTT ATTATCAAAA TTAAGTTTAC TTGTATACGG	1620
35	AACAACCACA AGAAATTTGA TTCTGTAAAG AATCCTCTTT AGCTGTGGCC TGGCAGTATA	1680
	TAAATGGTGC TTTATTTAAC AGAATACCTG TGGAGGAAAT AAAGCACACT TGATGTAAAA	1740
40	ATAATGTTT TATTTTATT GACATGACTG ATTGATTGCT ATTCTGTGCA CTTAATTAAA	1800
	CTGATTGTGA TGACTTWAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	1851

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(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 3542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

60

TCCAATGCTG ATGAGCGTCT TCGCTGGCAG GCCAGCTCCT TGCCTGCTGA TGACCTTTGC	60
ACAGAAAATG CCATCATGCT GAAACGATTC AATAGGTATC CGCTGATCAT TGACCCCTCT	120
GGACAGGCCA CAGAATTCAT TATGAATGAA TATAAGGWTG GTAAGATCAC ACCGACCAGC	180

	TTCTGGATG ACGCCTTCAG AAAGAACTTA GAGAGTGCAC TGAGATTCGG TAACCCCTT	240
5	CTGGTCCAGG ATGTGGAAAG CTACGATCCA GTTTTGAACC CGGTGCTGAA CCGTGAAGTG	300
	CGGCGAACAG GGGGGAGAGT GCTGATCACT CTCGGGGACC AGGACATAGA CCTGTCGCCA	360
	TCGTTTGTC TCTTCCTGTC CACCCGGGAT CCAACTGTCT AGTTCCACACC AGATCTCTGT	420
10	TCCCGGGTTA CTTTGTGAAA CTTCACAGTT ACCCGTAGCA GTTTACAAAG CCAGTGTCTA	480
	AATGAAGTAC TTAAAGCAGA AAGACCTGAT GTGGACGAGA AACGATCTGA TCTTCTTAA	540
15	CTTCAAGGGG AATTTAGCT CCGTTTGCCT CAGCTGGAAA AATCTCTACT ACAAGCTCTG	600
	AACGAGGTGA AAGGGCGCAT TTTGGATGAC GACACGATCA TAACCACTCT GGAGAACCTG	660
	AAGAGAGAGG CTGCAGAGGT CACCAGGAAA GTTGAGGAGA CGGACATTGT CATGCAGGAG	720
20	GTGGAGACCG TGTCCAGCA GTACCTCCCG CTCTCCACCG CCTGCAGCAG CATCTACTTC	780
	ACCATGGAGT CCCTCAAGCA GATACACTTC TTGTACCACT ACTCCCTCCA GTTTTCTCTG	840
25	GACATTTATC ACAACGTCCT ATACGAGAAC CCGAACCTGA AGGGTGTAC CGACCACACA	900
	CAGCGCCTGT CCAATTATAAC AAAGGACCTC TTCCAGGTGG CGTTTAACCG AGTGGCTCGA	960
	GGCATGCTGC ATCAGGACCA CATTACCTTT GCCATGCTGC TGGCAAGAAT CAAACTGAAG	1020
30	GGCACCCTGG GGGAGCCCAC CTACGATGCA GAATTCCAGC ACTTCTTGAG AGGAAATGAG	1080
	ATTGTCCTGA GTGCTGGCTC CACCCCCAGG ATCCAGGCC TGAATGTGGA GCAGGCGGAG	1140
35	GCGGTGGTGA GGCTGAGCTG CCTTCCCGCG TTTAAGGACT TGATTGCAA GGTTCAGGCA	1200
	GACGAGCAAT TTGGCATCTG GCTGGACAGC AGCTCCCGG AGCAGACTGT GCCCTACCTC	1260
	TGGAGTGAAG AAACACCTGC AACACCCATT GGCCAGGCCA TCCACCGCCT GCTCCTGATC	1320
40	CAGGCTTTCC GGCCCGATCG CCGTTGGCC ATGGCCACA TGTTGTTTC AACAAACCTT	1380
	GGGAGTCTT TCATGTCCAT CATGGAGCAG CCGCTCGACC TGACCCACAT TGTGGSCACA	1440
45	GAGGTGAAGC CCAACACTCC TGTCTTAATG TGCTCTGTGC CTGGTTATGA TGCCAGTGGA	1500
	CATGTCGAGG ACCTTGCAGC CGAGCAGAAC ACGCAGATCA CTTCAATTGC AATCGGCTCT	1560
	GCAGAAGGCT TTAACCAAGC AGATAAGGCA ATAAACACCG CTGTAAAGTC GGGCAGGTGG	1620
50	GTGATGCTGA AGAATGTGCA TCTGGCCCCA GGGTGGCTGA TGCAGCTGGA GAAGAAGTTG	1680
	CATTCCCTGC AGCCGCATGC CTGCTTCCGA CTCTTCTCA CCATGGAGAT CAACCCCAAG	1740
55	GTGCCTGTGA ATCTGCTCCG TCGGGCCGC ATCTTTGTGT TCGAGCCACC GCCAGGGRTG	1800
	AAGGCCAACA TGCTGAGGAC GTTCAGCAGC ATTCCCGTCT CACGGATATG CAAGTCTCCC	1860
	AACGAGCGTG CCCGCTGTGA CTTCTGCTG GCCTGGTTTC ATGCGATCAT CCAAGAACGC	1920
60	TTACGATACG CACCACTGGG GTGGTCAAAG AAGTATGAAT TTGGAGAGTC TGACCTGCCG	1980

	TCANYTTGCG ATACGGTGGA CACGTGGCTG GATGACACGG CCAAGGGCAG GCAGAACATC	2040
5	TCACCGGATA AGATCCCGTG GTCTGCACTA AAGACCTTAA TGGCCCAGTC CATTTATGGC	2100
	GGGCGCGTGG ACAACGAGTT TGACCGCGT CTGCTCAACA CCTTCCTGGA GCGCCTGTTC	2160
	ACAACCAGGA GTTTCGACAG TGAGTTTAAG CTGGCATGCA AGGTCGACGG ACATAAAGAC	2220
10	ATTCAAATGC CAGATGGCAT GCAGGCGAGA GGAGTTTGTG CAGTGGGTGG AGTTGCTCCC	2280
	CGACACCCAG ACGCCCTCCT GGCTGGGCCT GCCCAACAAC GCCGAGAGAG TCCTCCTTAC	2340
15	CACACAGGGT GTGACATGA TCAGTAAAAT GCTGAAGATG CAGATGTTGG AGGATGAGGA	2400
	CGACCTGGCC TACGCAGAGA CTGAGAAGAA GACGAGGACA GACTCCACGT CCGACGGGCG	2460
	CCCTGCCTGG ATGCGGACAC TGCACACCAC CGCGTCCAAC TGGCTGCACC TCATCCCCCA	2520
20	GACGCTGAGC CACCTCAAGC GCACCGTGGA GAATATCAAG GATCCTTTGT TCAGGTTCTT	2580
	TGAGAGAGAA GTGAAGATGG GCGCAAAGCT GCTTCAGGAC GTTCGCCAGG ACCTTGAGAA	2640
25	TGTCGTCCAG GTGTGCGAAG GAAAGAAGAA GCAGACCAAC TACTTGCGCA CGCTGATCAA	2700
	CGAGCTAGTG AAAGGGATCT TGCCTCGGAG CTGGTCCCAC TACACGGTGC CTGCCGGCAT	2760
	GACCGTCATC CAGTGGGTGT CCGACTTCAG CGAGAGGATC AAACAGCTGC AGAACATCTC	2820
30	ACTGGCAGCT GCATCTGGTG GCGCCAAGGA GCTAAAGAAC ATCCACGTGT GCCTGGGTGG	2880
	CCTGTTCTGT CCTGAGGCGT ACATCACTGC CACCAGGCAG TATGTGGCCC AGGCCAACAG	2940
35	CTGGTCCCTG GAGGAGCTCT GCCTGGAAGT CAACGTCACC ACCTCACAGG GCGCCACCCT	3000
	TGACGCTTGC AGCTTCGGAG TCACGGGTTT GAAACTTCAA GGGGCCACGT GCAACAACAA	3060
	CAAGCTGTCA CTGTCCAATG CCATCTCAAC CGCCCTTCCC CTGACGCAGC TCGCTGGGT	3120
40	CAAGCAGACA AACACCGAGA AGAAGGCCAG TGTGGTAACC TTACCTGTCT ACCTGAACCT	3180
	CACCCGTGCA GACCTCATCT TCACCGTGGA CTTCGAAATT GCTACAAAGG AGGATCCTCG	3240
45	CAGCTTCTAC GAGCGGGGTG TCGCAGTCTT GTGCACAGAG TAACTTTTC TAGCTGCCCC	3300
	TTTCTGTAAT AGTGAAAGTT GGTATTTAAC ATTTATTTCAT TTTTAAAATA TTTGGAAGGT	3360
	CTGAGCTTGT GAAAAGAAAG TGGTTGGTCT GAGGTTGGAG GAAGCTGAAT GGAATCTGAC	3420
50	GGTTGGGAGT GGTGGAATT GGAAGGATAC CAGGAGGTAT TTGGGAAGGC CAATGGCGTG	3480
	GCTCCTTTGA GGAAATAAAA CACTAAGCAT GAAAAAATAA AAAAACTTA CAANCCNCAA	3540
55	GG	3542

(2) INFORMATION FOR SEQ ID NO: 64:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

5 AGGTGATTTT AATGATAGGT GTCATATATA GGACGGATAA TCTGTTTACA TTCTGTTCTT 60
 10 CTCGATGCAC TCACAAGCGG GTAAC TAGGT GACAAGAAAA CAAAGATCTT ATTCAAAAGA 120
 GGTCTTACAG CAACCCAACG TCTCATCTTC CCATAGTAAA GATGACGGCG CCTTGAGGTA 180
 15 AGCTACAGGC AACACCACTT CCGCGTTTCT CTGCGCCCT GGTCCAAGAT GCGCGATGAA 240
 GCCACGCGAC GTGTTGTGTC TGAGATCCCG GTGCTGAAGA CTAACGCCGG ACCCGAGAT 300
 20 CGTGAGTTGT GGGTGCAGCG ACTGAAGGAG GAATATCAGT CCCTTATCCG GTATGTGGAG 360
 AACACAAGA ATGCTGACAA CGATTGGTTC CGACTGGAGT CCAACAAGGA AGGAACTCGG 420
 TGGTTTGAA AATGCTGGTA TATCCATGAC CTCCTGAAAT ATGAGTTTGA CATCGAGTTT 480
 25 GACATTCCTA TCACATATCC TACTACTGCC CCAGAAATTG CAGTTCCTGA GCTGGATGGA 540
 AAGACAGCAA AGATGTACAG GGTGGCAAA ATATGCCTGA CGGATCATTT CAAACCTTTG 600
 30 TGGGGCCAGG AATGTGCCA AATTGGACT AGCTCATCTC ATGGCTCTGG GGCTGGGTCC 660
 ATGGSTGGCA GTGGAAATCC CTGATCTGAT TCAGAAGGGC GTCATCCAAC ACAAAGAGAA 720
 ATGCAACCAA TGAAGAATCA AGCCACTGAG GCAGGGCAGA GGGACCTTTG ATAGGCTACG 780
 35 ATACTAWTTT CCTGTGCATC AACTTAACT CATCTAACTG TTCCCGGAC ANCCTCCACT 840
 CTAGTTGTTA CTAAGTANTG CAGTAGCAIT NTGGGAAGA ACA 883

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(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

45 GGCACGAGGT GGCCTCTACC CTGGGCTCAT CTGGCTACAC AGGGACTCTA AACGCTTCCA 60
 55 GATTCCCTGG AAACATGCCA CCCGGCATAG CCCTCAACAA GAAGAGGAAA ATACCATTTT 120
 TAAGGCCTGG GCTGTAGAGA CAGGAAGTA CCAGGAAGGG GTGGATGACC CTGACCCAGC 180
 TAAATGGAAG GCCCAGCTGC GCTGTGCTCT CAATAAGAGC AGAGAATTCA ACCTGATGTA 240
 60 TGATGGCACC AAGGAGGTGC CCATGAACCC AGTGAAGATA TATCAAGTGT GTGACATCCC 300

5 TCAGCCCCAG GGCTCGATCA TTAACCCAGG ATCCACAGGG TCTGCTCCCT GGGATGAGAA 360
 GGATAATGAT GTGGATGAAG AAGATGAGGA AGATGAGCTG GATCAGTCGC AGCACCATGT 420
 TCCCATCCAG GACACCTTCC CCTTCCTGAA CATCAATGGT TCTCCCATGG CGCCAGCCAG 480
 TGTGGGCAAT TGCAGTGTGG GCAACTGCAG CCCGGAGGCA GTGTGGCCCA AACTGAACC 540
 10 CCTGGAGATG GAAGTACCCC AGGCACCTAT ACAGCCCTTC TATAGCTCTC CAGAACTGTG 600
 GATCAGCTCT CTCCCAATGA CTGACCTGGA CATCAAGTTT CAGTACCGTG GGAAGGAGTA 660
 15 CGGCAGACC ATGACCGTGA GCAACCCTCA GGGCTGCCGA CTCTTCTATG GGGACCTGGG 720
 TCCCATGCCT GACCAGGAGG AGCTCTTTGG TCCCGTCAGN CTGGAGCAGG TCAAATTCCC 780
 AGGTCCTGAG CATATTACCA ATGAGAAGCA GAAGCTGTTC ACTAGCAAGC TGCTGGACGT 840
 20 CATGGACAGA GGA CTGATCC TGGAGGTCAG CGGTCATGCC ATTTATGCCA TCAGGCTGTG 900
 CCAGTGCAAG GTGTACTGGT CTGGGCCATG TGCCCCATCA CTGTGTGCTC CCAACCTGAT 960
 TGAGAGACAA AAGAAGGTCA AGCTATTTTG TCTGGAAACA TTCCTTAGCG ATCTCATTGC 1020
 25 CCACCAGAAA GGACAGATAG AGAAGCAGCC ACCGTTTGAG ATCTACTTAT GCTTTGGGGA 1080
 AGAATGGCCA GATGGGAAAC CATTGGAAG GAAACTCATC TTGGTTCAGG TCATTCCAGT 1140
 30 AGTGGCTCGG ATGATCTACG AGATGTTTTT TGGTGATTTT ACACGATCCT TTGATAGTGG 1200
 CAGTGTCGC CTGCAGATCT CAACCCAGA CATCAAGGAT AACATCGTTG CTCAGCTGAA 1260
 GCAGCTGTAC CGCATCCTTC AAACCCAGGA GAGCTGGCAG CCCATGCAGC CCACCCCCAG 1320
 35 CATGCAACTG CCCCTGCCC TGCTCCCCA GTAATTGTGA ATGCCATCTT CTTCCTTCTC 1380
 TTTTATAA TATTGTACAT ATGGATTTTT TTATTGTTA GATTAAACCA GCTTTTAAAT 1440
 40 CTCTGTTTTT TGTGACAGTG TTAGAAGTTT GTGATTCTCC AAATATGCCT AGATTTAAAG 1500
 CTGATTTAAT TTATGGAAAA AAAAAAAAAA AAAAAAAAAA A 1541

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(2) INFORMATION FOR SEQ ID NO: 66:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 732 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAAAATGAA TGTTAGAAGG TGCCTGCCGA GCGGGACAG AGTGTMTGCT CGCGCTGGAG 60
 60 AAGGCTCTGC TCAGCCCTGA GAGTCCCTTC CTGCCCCACC GATACTGGCA CTTTAAAAAG 120

GAAGCTGACC GCACAGTGTC CAGACGAATT GGCCCCCAGA AGATGGGGAG TTCTGTCCTG 180
CCCTTCTGTG TCTGCGTGAC CTCACCCAGC CTAGGAGGGA GGTGCATTCA GGGTAGATTT 240
5 GCCTCTCATT CAAAGTTCTG GGGCTTTGGG CGGAAAACAG CCAGCTTTGG CGCTGTTGGG 300
GAGACTCCTC CAGACCAGGA ACCCCAGAAG GAGACAGAGC CTGCCACATC CTCCCACGCC 360
10 AGGCCCTGGG CCAGGGTGAT TGGACTGAGA ATTTGGCCAC AACCAAATG ATGCTGGCTG 420
GAACCAGAGG CCAGAAAGCC TGGCCTTGTC CCCATGTGGG AGCCCTGTCC TCAGCCCTCT 480
TGTCCCTTG AGCTCAGTGA ATTCCCACCA GGTGCCCACA GTCCTGGAC TTCAAATTCT 540
15 ATATATGAG AGAGTTGGAG AGTATATCAG AGATATTTTT GGAAAGGAGT TGGTCTATGC 600
AATGTCAGTT TGAATCTTC TTGAAAGTTT AATGTTTTTA TTAGGAGATT TAAAGAAAAT 660
20 AAAGGTCTAC AATATCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
AAAAAAAAAA AA 732

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(2) INFORMATION FOR SEQ ID NO: 67:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

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TTAAGGAATT CGGCMCGATC CCGGCAAGTA ACATGACTAA AAAGAAGCGG GAGAATCTGG 60
GCGTCGCTCT AGAGATCGAT GGGCTAGAGG AGAAGCTGTC CCAGTGTCCG AGAGACCTGG 120
AGGCCGTGAA CTCCAGACTC CACAGCCGGG AGCTGAGCCC AGAGGCCAGG AGGTCCCTGG 180
AGAAGGAGAA AAACAGCCTA ATGAACAAAG CCTCCAACTA CGAGAAGGAA CTGAAGTTTC 240
TTGGCAAGA GAACCGGAAG AACATGCTGC TCTCTGTGGC CATCTTTATC CTCCTGACGC 300
TCGTCTATGC CTA CTGAGACC ATGTGAGCCT GGCAC TTCCC CACAACCAGC ACAGGCTTCC 360
ACTTGGCCCC TTGGTCAGGA TCAAGCAGGC ACTTCAAGCC TCAATAGGAC CAAGGTGCTG 420
GGGTGTCCC CTCCCAACCT AGTGTTCAAG CATGGCTTCC TGGCGGCCCA GGCCTTGCCT 480
CCCTGGCCTG CTGGGGGGTT CCGGGTCTCC AGAAGGACAT GGTGCTGGTC CCTCCCTTAG 540
CCCAAGGGAG AGGCAATAAA GAACACAAAG CTGAAAAAAA AAAAAAAAAA AACTCGTAGG 600
GGGGGCCCGT ACCCAATCGC CCTNTCGTG 629

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

10 CTGCTAGCCG GCCGGCGCAG GCTGCCGAGC GGGTGAGCGC GCAGGCCAGG CCAAAGCCCT 60
 GGTACCCGCG CGGTGCGGGC CTCAGTCTGC GGCCATGGGG GCGTCCGCGC GGCTGCTGCG 120
 15 AGCGGTGATC ATGGGGGCCC CGGGCTCGGG CAAGGGCACC GTGTGCTCGC GCATCACTAC 180
 ACACCTCGAG CTGAAGCACC TCTCCAGCGG GGACCTGCTC CGGGACAACA TGCTGCGGGG 240
 CACAGAAATT GCGTGTTAG CCAAGGCTTT CATTGACCAA GGGAAACTCA TCCCAGATGA 300
 20 TGTCATGACT CGGCTGGCCC TTCATGAGCT GAAAAATCTC ACCCAGTATA GCTGGCTGTT 360
 GGATGGTTTT CCAAGGACAC TTCCACAGGC AGAAGCCCTA GATAGAGCTT ATCAGATCGA 420
 25 CACAGTGATT AACCTGAATG TGCCCTTTGA GGTCAATAAA CAACGCCTTA CTGCTCGCTG 480
 GATTCATCCC GCCAGTGGCC GAGTCTATAA CATTGAATTC AACCTCCCA AAACTGTGGG 540
 CATTGATGAC CTGACTGGGG AGCCTCTCAT TCAGCGTGAG GATGATAAAC CAGAGACGGT 600
 30 TATCAAGAGA CTAAAGGCTT ATGAAGACCA AACAAAGCCA GTCCTGGAAT ATTACCAGAA 660
 AAAAGGGGTG CTGGAACAT TCTCCGGAAC AGAAACCAAC AAGATTGGC CCTATGTATA 720
 35 TGCTTTCCTA CAACTAAAG TTCCACAAAG AAGCCAGAAA GCTTCAGTTA CTCCATGAGG 780
 AGAAATGTGT GTAACATTA ATAGTAAGAT GGGCAAACCT CCTAGTCCTT GCATTTAGAA 840
 GCTGCTTTTC CTAAGACTTC TAGTATGTAT GAATTCCTTG AAAATTATAT TACTTTTATT 900
 40 TCTACTGATT TTATTTTGGA TACTAAGGAT GTGCCAAATG ATTCGGATAC TAAGATGCAT 960
 CGTTTGAAAT CATCTAGTGT GTTGATGCA GTTATCCTCA AAAACATCAG CGATGTCTGA 1020
 45 ACCTTTAAAA CATCTGTTAG AGCAAAATTA AAAGAGCATT TGGTAGTAAT CTAACCTTTT 1080
 GTTCAGTTAA TAAGTGGTTG ATAAAGTTTC CATATTTTTC TGGAAAAGTT AAAAAAGTT 1140
 ACATGTCATT TGGAGAAAAT ACGTAATCAG AAATTTGTGC ATAGATTGAT GCCAAAAAG 1200
 50 ACATTTCCAG CATGTGGAA CATGGTGAGA CACTATATAA AATTCCAGAA AGAAAGCAAC 1260
 TGGATTTACA GATTTATTGT GAGACACAAA TTCACTGCTG CCTTTTCACT AAGAAATGTA 1320
 55 TATGTTAACC ATATATGCTG TATTTATTTT GTCGTTAAGC ATACTTTCAG TTTACTCAGA 1380
 ATTTTCAATT TGCTATAAAG ATGTATCAAT TAGCATATAG AAAAATATTA CTTTAAGATG 1440
 ACTTGMTTCC TTTGAAAATA CCTGTGTACT GAGGGTTATG ATTTGTGTCA AAAATGACA 1500
 60

TAAGTGCTTT TACAAGCACC AAAGTTGAAT GAATTTTCAA CAAAATGTAA TTAAAGTCTA 1560
 TGTTTTCAGT TATGACTCAG GTTAAGAAAT GTGTTTTAGG ATCTACTTGC TGGTTTTTCT 1620
 -5 TTTTGATCCA AATGTGTGAT CTGCCCTGAT AAATAACAAG TTATNGTACC ATCTCCCCCG 1680
 CCAATAAAAA AAAAAAAAAA AAAAAAAAAAC TCGAGGGGGG GCCCGGTACC CAATTCTCCG 1740
 NAATAGGNAG T 1751

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(2) INFORMATION FOR SEQ ID NO: 69:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

25

GGCACGAGAT TATGTATTAA AATGTTTTTG AATGTGAAA TATTAGAATA TTGTTACTAT 60

TTGACCCAAC TCAAAATCTC CATGGGAAAA TACCTGTCGA TACCCACAGT ATTGTTGAAA 120

ATAATCAGAT GCAGTATCAC AGCTGTGTCA GACTCTAGTA CCAGTTGGGC AATCAAGGCA 180

30

CAGCTAAAAA TTGAAAACAA AGATCTGGAC AACAAAACAG CCAAAGGTGG GGGTCAAGAA 240

GCTCTGACGT GTACCTAGCT GTAGAATGCT ATGCACACGT GCCAGGTGTA GTGTGCATAT 300

35

CCAGGAAAAA CTGCAGAGAG CCCCACTCTT CACCTCTGGT TGACCATGAG CTCTGTGTAA 360

GCAGGAAGTG AAGGCTAAGG CAGATTTAAG CTCTGAAAGC ATTCCACAAC ATACACACAA 420

ATCGTGCAAA GCATTAAGGA AATCTTGTTA CTGCTAAGTG TTGCTGACCC AGGAACAAC 480

40

CCTACTCAGC TGGACTTAAA AATAAAAA 508

45

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

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TACATAGAGC AAAGAGAAAT TTCCAGAATT TCTARAATTC TGGAAGAGA ATTTTCCTGA 60

GATTGCAGAT TTGCTGTGT CCTCAGGTGA TGATGAGGGC TGTTTCCCC TGTTGTCTT 120

60

TCCTCACT CATGCTTCCT CTCCTAGAGT GTCTGGTGG CATGATCATG TGCTACCTAG 180

GCATTTCTTT CACTGATACA AGGAAACTG CAGGGTTAAA AAAAAAAAAA AAAAAAAAAA 240
NCNCG 245

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(2) INFORMATION FOR SEQ ID NO: 71:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATGTTCTCA TGAGGATGCA CTTGTGCTTC TGCAAGTATT GCTGCAGCTT CATAGTGA CT 60
20 CCCACCAGCA CCAGCAATAC AGCTAGCTAC CTGTGGCCTT GGATCTCAGC CAGCATGGCT 120
GGGAGAGGGA GCAGCTGGGC ATGTACCCTA AATGCTGTTA CCAGGAAGG ACTCCCAGAG 180
TGAAGACAAG TAGGGACTTC CTGCAGAGGT GGTACATGTG CTCTCTGTAT CCATACTTTT 240
25 TTTTTTTTTT TTTGAGATA GAGTTTCACC CTTGTTGCCC TGGCTGGAGT GCAATGGTGC 300
GATCTCAGCT CACTGCAACC TCTCTGCCTC CCGGGTTCAA GTGATTCTCC TGCCTCAGCC 360
30 T 361

35

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

45 AGGATCACAC AATAGAGAAC ACTGTAGTAA CATTTCCGTC TGCTCACAAG ACCCAGAACA 60
TTGATCAGTT TTGTGTGTG GTTTATTATT TTCTGTAA AAAATTGTGA AAAGTTTGT 120
TTAGCTAGAT GATATTTTAA TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACTACTT 180
50 AACACACATA CCTTATGTTT TGTMTTGT TTMTTACAC TCAGTATAAA TCAGGAGAAG 240
TTAGCCAACC ATCTAGCATT TAGAATCCTC TTTTATTG TCTTCTAAGG ATATGGATGT 300
55 TCCCATAACA GCAACAAAC AGCAACAAA ACATTTTATA AATATCACTT GATAGACTGT 360
AAGCACCTGC TTAACCTTGT GTCCCAAATA TTTAGTGTGT ATATATATAT ATATATATAC 420
60 ACACACACAC ACATATATAT TCAACAAATA AAGCAAATA TAACATGCAT TTCACATTTT 480

GTCTTTCCCT GTTACGATTT TAATAGCAGA ACTGTATGAC AAGTTTAGGT GATCCTAGCA 540
 TATGTTAAAT TCAAATTAAT GTAAAACAGA TTAACAACAA CAAAGAACT GTCTATTTGA 600
 -5 GTGAAGTCAT GCTTTCTATT ATAATAACTT GGCTTCGGTT ATCCATCAAA TGCACACTTA 660
 TACTGTTATC TGATTGTTTA TAATAAAGAA TACTGTACTT ATAAAAAAAA AAA 713

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(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAAAGTCAGA GCTGTCCAAT CCTCAGCAC CTMTTAGATT TGCTCCAAAT TAGAAAACGTG 60
 GGGACTATGT GTTCTGGGCA ATCACAGGTC TGGAAAATGG CTCTGCAGGC TCTTGATAGT 120
 25 GAGACAGTGG TCATCTTACC AGACATGCAT CTGATTTTAA GCCTCAGGCT AATCCACAAT 180
 GCTCGGCCAT GCCTATGATT AACAAACAAA AGCAAAATCT GCTTTTATAG TTTAGGAAAC 240
 30 CTGGATAGAA CAGTATTTTT CAGCATTCTT GGATAAAGCA GTTCTGCATT TTTAAATTGG 300
 GACTGCAGAA GTGACTGTCT ATAGTTGTGA AATACAAAAA ATGGTATGTT TGATCAGAAA 360
 AGGAAGCCCG TGCCTGGCAC TTGGAAAGAT ACTGAGCATC ATAACCCTAA TGAGAAAATG 420
 35 TAGGCTCTGT GAATGTTAAC TACAAATCAG GTTAGGAAAG CATATGACAC CCTTTGTCAA 480
 ACTAAGCTTC ACTAGGAGGA CCTGTGCTCA TAGAAGAATA TGCTTTAAAA GTATCAATTT 540
 40 TCCACAGTCG ATGATGGAGA AAAGTTCATT TGACCAGAA TGCTGATAGT CACAATACAC 600
 AGCCTGACAT ATATAACAAT ACAGTTTCT GTAAACAGAA GTTCTTCCTC TTCCAATTCA 660
 GGAGTCAGTC AGAGCATAAA TATTGCATGT TTCACCTTAG AAAGTGATTC ATTTTAGAAA 720
 45 GCAGATCTGG ATTATTTTGC AGGGTAGAAA TGAAGGCTAT TTCTGGCATT CTTGCTCAAA 780
 AAGTCAATAT ATGTACATTA AGTATAAAA AGGGTCTCTT TCACCTCTTT TGTTCGTAG 840
 50 CATGGCTAC ATAACTCGTG CC 862

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(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 4602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

- 5	GCGAGGGGGC GKGGGGAGCA GCGCCGARGC CGCCGCCTCC GCCTCCGCCG CCTAGGACTA	60
	GGGGGTGGGG GACGGACAAG CCCCAGTGCC GGGGAKACG GAAGAGCCGA GACCCCCGGA	120
	GCAGCAGGAC CAGGAAGGGG GAGAGGCGGC CAAGGCGGCT CCGAGGACC CGCAACAACG	180
10	GCCCCCTGAG GCGGTGCGG CGGCGCCTGC AGGGACCACT AGCAGCCGCG TGCTGAGGGG	240
	AGGTGCGGAC CGAGGCGGG CCGCTGCGRC CGCCGCGCMG CAGCTGTGTC CCGCCGGAGA	300
15	AGGCCGAGTA TCCCCGCCGG CGAGGAGCAG CCCAGCGCC AGGCCTCCCG ACGTCCCCGG	360
	GCAGCAGCCC AGGCCGCGAA GTCCCCGTCT CCAGTTCAGG GCAAGAAGAG TCCGCGACTC	420
	CTATGCATAG AAAAAGTAAC AACTGATAAA GATCCCAAGG AAGAAAAAGA GGAAGAAGAC	480
20	GATTCTGCCC TCCCTCAGGA AGTTTCCATT GCTGCATCTA GACCTAGCCG GGGCTGGCGT	540
	AGTAGTAGGA CATCTGTTTC TCGCCATCGT GATACAGAGA ACACCCGAAG CTCTCGGTCC	600
25	AAGACCGGTT CATTCGAGCT CATTTGCAAG TCAGAACCAA ATACAGACCA ACTTGATTAT	660
	GATGTTGGAG AAGAGCATCA GTCTCCAGGT GGCATTAGTA GTGAAGAGGA AGAGGAGGAG	720
	GAAGAAGAGA TGTTAATCAG TGAAGAGGAG ATACCATTCA AAGATGATCC AAGAGATGAG	780
30	ACCTACAAAC CCCACTTAGA AAGGGAAACC CCAAAGCCAC GGAGAAAATC AGGGAAGGTA	840
	AAAGAAGAGA AGGAGAAGAA GGAAATTAAA GTGGAAGTAG AGGTGGAGGT GAAAGAAGAG	900
35	GAGAATGAAA TTAGAGAGGA TGAGGAACCT CCAAGGAAGA GAGGAAGAAG ACGAAAAGAT	960
	GACAAAAGTC CACGTTTACC CAAAAGGAGA AAAAAGCCTC CAATCCAGTA TGTCCGTTGT	1020
	GAGATGGAAG GATGTGGAAC TGTCTTGCC CATCTCGCT ATTTGCAGCA CCACATTAAA	1080
40	TACCAGCATT TGCTGAAGAA GAAATATGTA TGTCCCCATC CCTCCTGTGG ACGACTCTTC	1140
	AGGCTTCAGA AGCAACTTCT GCGACATGCC AAACATCATA CAGATCAAAG GGATTATATC	1200
45	TGTGAATATT GTGCTCGGGC CTTCAAGAGT TCCACAATC TGGCAGTGCA CCGGATGATT	1260
	CACACTGGCG AGAAGCATTA CAATGTGAGA TCTGTGGATT TACTTGTCGA CAAAAGGCAT	1320
	CTCTTAATTG GCACATGAAG AAACATGATG CAGACTCCTT CTACCAGTTT TCTTGCAATA	1380
50	TCTGTGGCAA AAAATTTGAG AAGAAGGACA GCGTAGTGGC ACACAAGGCA AAAAGCCACC	1440
	CTGAGGTGCT GATTGCAGAA GCTCTGGCTG CCAATGCAGG CGCCCTCATC ACCAGCACAG	1500
55	ATATCTTGGG CACTAACCCA GAGTCCCTGA CGCAGCCTTC AGATGGTCAG GGTCTTCCTC	1560
	TTCTTCCTGA GCCCTTGGGA AACTCAACCT CTGGAGAGTG CCTACTGTTA GAAGCTGAAG	1620
60	GGATGTCAAA GTCATACTGC AGTGGGACGG AACGGGTGAG CCTGATGGCT GATGGGAAGA	1680

	TCTTTGTGGG AAGCGGCAGC AGTGGAGGCA CTGAAGGGCT GGTATGAAC TCAGATATAC	1740
	TCGGTGCTAC CACAGAGGTT CTGATTGAAG ATTCAGACTC TGCCGGACCT TAGTGGACAG	1800
- 5	GAAGACTTGG GGCATGGGAC AGCTCAGACT TTGTATTTAA AAGTTAAAAA GGACAAAAAA	1860
	AAAATCTAAA GCATTTAAAA TCTAGTGAAA TAACTGAAGG GCCTGCTCTT TCCATTGTGG	1920
10	ATCACAGCAC ACACATACAT ACACCCTCCA CCTCCCCATC CCTGTCTCTC CCTCTGTTC	1980
	TCCCCTTATA AAATTGATGT TGTCTTTACC AGAAAGGTAG ACAAAAAAGA AGCAGCAGCA	2040
	GCTCTTAAAG TGAGGGTTAT TCTCATACTC GGTTCAGCC ATCAGCAGAC TTCCTGCTCA	2100
15	TCGGCAGATC CCCCTTTCCA ACCTGTAACT CTGATGTGCT CTGGATCAGC TTTTAACTTT	2160
	TAATCATATA TTACTGTCTT CTAAATCCCT TCTCCTCTC TACTGCTGCC CTATGGTTCT	2220
20	GGCTCCTACC CCCTGCGGCA CACTTATCTT CAAATACCAT AGAATTCTAA TCTCTGAAAT	2280
	CATAGCTCTC CAGTGGCTTT TAAAGAAAGC TGGTCTCAG CACTAACAAA ATCACTACAA	2340
	TAGCCTAGTG CTTTTTTTGA AGCCTTTTTA GGAAGAATG TTAGGTTTCAT GGTAAGTAGT	2400
25	ATGCTCTTG AGATTTTTAC AGTGTGAAA CTTAAGAATT TTGAGAGGGT GAGGAGGGTT	2460
	GTTCAGAATC TAAATTACAG ATAGATGATT GTTCTGTG AATTGTTC TTTCTCTTT	2520
30	TTTTGTCCC TACCATTTC TTACATTTC CTGGGGCCC ATCTCTGGCT CCTTGCTTTT	2580
	TGTTCTTGC TTGCTTTAT CAGTTCATTC CAGCTCCCTG TTAGTGAAGG AACTGCTGT	2640
	TAGTGAAGGA ACAAAGTCTA TGAGTCTTAA AATTTTAAGT CAAAGAAAAC TGCTCTGTTT	2700
35	CCCCTTTAGT AACACTTCTG AAGAGGAAAA ACTTCAATAG CCAAAGTTAA TAATCCTATA	2760
	TAATAATTGC TTTGGCTTTC ACCTAAAATT CTGGGCATCA CAATTTCTT GGGATAGAGG	2820
40	TTGTGTTGGG GAATAGATTG CTTATTGCTG TTCACTGGAG AGAAAAGGTA GTGTTTTTGT	2880
	ACAAGGTCAT ACCGCCAGAA GCCCAAATC CTATTTTGGC TCATCTTCAG GTAAAGAGTA	2940
	ATTCCTATCC TGTGTGCTC AGAAGCTAGA ATCGAAGGCT TACCCTATTC ATTGTTTATT	3000
45	GTCAGAAATG CATGATGGCT CTTGGAAAGA ATGACGTTTT GCTGGAAAAA AAAAAARAA	3060
	CMGTTTGTGT TTCACAAACA TGGCTTATCA ATTTTTTCAA AGAATTCTTT TTTCCAAAA	3120
50	AGAGGAGTAA CAAAATGTCA TTTCTGAAAG AGGCTTACTT TATACCAACT AGTGTACAGCA	3180
	TTTGGGATGC CAGGGAACAG AGAGTGAGAC ACCTACAATC ACCAGTCTCA AATGCGCTAT	3240
	TGTTTCTTTT CAGAGTGTG CAGATTTGCC ATTTCTCCAT AATATGGGGA TAGAAAATGG	3300
55	AATAAAGATA GAAGGGATGT AGAATATGCT TTCCTGCCAA CATGGTTTGG AGTCGACTTT	3360
	GGTATATTGA CTAGATTGA AAATACAAGA TTGATTAGAT GAATCTACAA AAAAGTTGTC	3420
60	CTCCTCTCAG GTCCCTTTTA CACTTTTGA CTAAGTAGCA TCTATATTCC AACTTAGCT	3480

TTTTGTGAC ACTTATCCTT TGTCTCCGTA AATTTTCATTT GCAGTGGTTA GTCATCAGAT 3540
 ATTTTAGCCA CCTACACAAA AGCAAAGTGC ATTTTAAAAA ATCTTTCTGA GATGGGAGAA 3600
 -5 AATGTATTCT CCTTTCCTAT ACCGCTCTCC CAACAAAAAA ACAACTAGTT AGTTCTACTA 3660
 ATTAGAACT TGCTGTACTT TTTCTTTTCT TTTAGGGGTC AAGGACCCTC TTTATAGCTA 3720
 10 CCATTTGCCT ACAATAAATT ATTGCAGCAG TTTGCAATAC TAAAAATTTT TTTATAGACT 3780
 TTATATTTT CCTTTTGATA AAGGGATGCT GCATAGTAGA GTTGGTGTA TAAACTATC 3840
 TCAGCCGTTT CCCTGCTTTC CCTTCTGCTC CATATGCCTC ATTGTCCTTC CAGGGAGCTC 3900
 15 TTTTAATCTT AAAGTTCTAC ATTTCATGCT CTTAGTCAAA TTCTGTTACC TTTTAATAA 3960
 CTCTTCCAC TGCATATTTT CATCTTGAAT TGGTGGTCTT AAATTCGAA ACTGTAGTTG 4020
 AGATACAGCT ATTTAATATT TCTGGGAGAT GTGCATCCCT CTCTTTGTG GTTGCCCAAG 4080
 20 GTTGTTTTGC GTAACGAGA CTCCTTGATA TGCTTCAGAG AATTTAGGCA AACACTGGCC 4140
 ATGGCCGTGG GAGTACTGGG AGTAAAATAA AAATATCGAG GTATAGACTA GCATCCACAT 4200
 25 AGAGCACTTG AACCTCCTTT GTACCTGTTT GGGGAAAAAG TATAATGAGT GTACTACCAA 4260
 TCTAACTAAG ATTATTATAG TCTGGTTGTT TGAAATACCA TTTTTCCTC CTTTTGTGTT 4320
 TTTCCCACTT TCCAATGTAC TCAAGAAAAT TGAACAAATG TAATGGATCA ATTTAAAATA 4380
 30 TTTTATTTCT TAAAGCCTT TTTTGCCTGT TGTAATGTC AGGACCCTTC TCCTTTCATG 4440
 GGAGAGACAG GTAGTTACCT GAATATAGGT TGAAAAGGTT ATGTAAAAG AAATTATAAT 4500
 35 AAAAGGGATA CTTTGCTTTT CAAATCTTTG TTTTCTCTTA TTCTAGGTAA GGCATATTAA 4560
 AAATAATAT GTAAAGAAGA AAAATAAAG TTGCTTCAT GG 4602

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(2) INFORMATION FOR SEQ ID NO: 75:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGCGCCCCGG GCCGGCGGGT TTCTCTAACA AATAACAGA ACCCGCACTG CCCAGGCGAG 60
 CGTTGCCACT TTCAAAGTGG TCCCTGGGG GAGCTCAGCC TCATCCTGAT GATGCTGCCA 120
 55 AGGCGCACTT TTTATTTTAA TTTTATTTT ATTTTTCCTT TAGCATCCTT TTGGGGCTTC 180
 ACTCTCAGAG CCAGTTTTTA AGGGACACCA GAGCCGAGC CTGCTCTGAT TCTATGGCTT 240
 60 GGTGTGTTACT ATAAGAGTAA TTGCCTAACT TGATTTTCA TCTCTTAAAC CAAACTGTGT 300

5 GCCAAAAGAT ATTTGACCGT TTCCAAAATT CAGATTCTGC CTCTGCGGAT AAATATTTGC 360
 CACGAATGAG TAACTCCTGT CACCACTCTG AAGGTCCAGA CAGAAGGTTT TGACACATTC 420
 TTAGCACTGA ACTCCTCTGT GATCTAGGAT GATCTGTTCC CCCTCTGGAT GAACATCCTC 480
 TGATGATCAA GGCTCCCAGC AGGCTACTTT GAAGGGAACA ATCAGATGCA AAAGCTCTTG 540
 10 GGTGTTTATT TAAAATACTA GTGTCACTTT CTGAGTACCC GCCGCTTCAC AGGCTGAGTC 600
 CAGGCCTGTG TGCTTTGTAG AGCCAGCTGC TTGCTCACAG CCACATTTCC ATTTGCATCA 660
 TTACTGCCTT CACCTGCATA GTCACCTCTT TGATGCTGGG GAACCAAAAT GGTGATGATA 720
 15 TATAGACTTT ATGTATAGCC ACAGTTCATC CCCAACCCTA GTCTTCGAAA TGTTAATATT 780
 TGATAAATCT AGAAAATGCA TTCATACAAT TACAGAATTC AAATATTGCA AAAGGATGTG 840
 20 TGTCTTTCTC CCCGAGCTCC CCGTTTCCCC TTCAITGAAA ACCACCACGG TGCCATCTCT 900
 TGTGTATGCA GGGCTATGCA CCGCAGGCA CGTGTGTATG CACTCCCCGC TTGTGTTTAC 960
 ACAAGCTGTG GGGTGTACG CATGCCTGCT TTTTTCACCT AATAATACAG CTTGGAGAGA 1020
 25 TTTTGTATC ACATTATAAA TCCCACTCGC TCTTTTGTAT GGCCACATAA TAACTACTGC 1080
 ATAATATGGA TACGCCTTAT TTGATTTAAC TAGTTCCTA ATGATGGACT TTTAAGTTGT 1140
 30 TTCTTTTTTT TTTCTTTTTT GCTACTGCAA ACGATGCTAT AATAAATGTC CTTATCAAAA 1200
 AAAAAAAAAA AAAAAAAAAA AAAAAANCCC NGGGGGGGGG CCCCGGGAAC NCAAT 1255

35

(2) INFORMATION FOR SEQ ID NO: 76:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GGCACGAGAG AAATGTTTGA TTCTCTTTCC TATTTTAAGG GATCTTCTCT CTGTTGATG 60
 TTGAAACTT ACCTTAGTGA AGATGTGTTT CAACATGCTG TTGTCCTTTA CCTGCATAAT 120
 50 CACAGCTATG CATCTATTCA AAGTGATGAT CTGTGGGATA GTTTTAATGA GGTCAAAAC 180
 CAAACACTAG ATGTAAAGAG AATGATGAAA ACCTGGACCC TGCAGAAAGG ATTTCTTTTA 240
 55 GTGACTGTTT AAAAGAAAGG AAAGGAACCT TTTATACAAC AAGAGAGATT CTTTTTAAAT 300
 ATGAAGCCTG AAATTCAGCC TTCAGATACA AGGTACATGC CCTCTTTCTT TTCATGCCAT 360
 60 CTCTTTTGCA CTCTCAGGTG GAAATATTTT GAAGTGTGTT ATAATCATAA GTTCTTGTGA 420

AACCTAACAA GATTATCCCT TCCTAAGAAT ACTTAACCTT CCTACCAAAT TAAAA

475

5

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

15

TTCTCTCTGC TCTTCGACTG CACCGCACTC GCGCGTGACC CTGACTCCCC CTAGTCAGCT 60

CAGCGGTGCT GCCATGGCGT GGCGGCGGCG CGAACCRGCG TCGGGGCTCG CGGCGTGTTC 120

20

GCTCTGGCGT TGCTCGCCCT GGCCCTGTGC GTGCCCGGGG CCCGGGGCCG GGCTCTCGAG 180

TGGTTCTCGG CCGTGGTAAA CATCGAGTAC GTGGACCCGC AGACCAACCT GACGGTGTGG 240

AGCGTCTCGG AGAGTGCCCG CTCGGCGGAC AGCTCGCCA AGGAGGGCGC GCATGGCCTG 300

25

GTGGGCGTCC CGTGGGCGCC CGGCGGAGAM CTCGARGGCT KCGCGCCCGA CACGCGCTTC 360

TTCGTGCCCAG AGCCCGGCGG CCGAGGGGCC GCGCCCTGGG TCGCCCTGGT GGTCGTGGGG 420

30

GCTGCACCTT TCAAGGACAA AGTGCTGGTG GCGGCGCNGA ANGAA 465

35

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1907 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

45

ACATGCAGCC CAACTACAGA TTCTTATGGA ATTCCTCAAG GTTGCAAGAA GAAATAAGAG 60

AGAGCAACTG GAACAGATCC AGAAGGAGCT AAGTGTTTTC GAAGAGGATA TTAAGAGAGT 120

50

GGAAGAAATG AGTGGCTTAT ACTCTCCTGT CAGTGAGGAT AGCACAGTGC CTCAATTGTA 180

AGCTCCTTCT CCATCACACA GTAGTATTAT TGATTCCACA GAATACAGCC AACCTCCAGG 240

TTTCAGTGGC AGTTCTCAGA CAAAGAAACA GCCTTGGTAT AATAGCACGT TAGCATCAAG 300

55

ACGAAAACGA CTTACTGCTC ATTTTGAAGA CTTGGAGCAG TGTTACTTTT CTACAAGGAT 360

GTCTCGTATC TCAGATGACA GTCGAACTGC AAGCCAGTTG GATGAATTTT AGGAATGCTT 420

60

GTCCAAGTTT ACTCGATATA ATTCACTACG ACCTTTAGCC ACATTGTCAT ATGCTAGTGA 480

TCTCTATAAT GGTTCAGTA TAGTCTCTAG TATTGAATTT GACCGGGATT GTGACTATTT 540
 TCGGATTGCT GGAGTTACAA AGAAGATTAA AGTCTATGAA TATGACACTG TCATCCAGGA 600
 5 TGCAGTGGAT ATTCATTACC CTGAGAATGA AATGACCTGC AATTCGAAAA TCAGCTGTAT 660
 CAGTTGGAGT AGTTACCATA AGAACCTGTT AGCTAGCAGT GATTATGAAG GCACTGTTAT 720
 10 TTTATGGGAT GGATTCACAG GACAGAGGTC AAAGGTCTAT CAGGAGCATG AGAAGAGGTG 780
 TTGGAGTGTT GACTTTAAAT TGATGGATCC TAAACTCTTG GCTTCAGGTT CTGATGATGC 840
 AAAAGTGAAG CTGTGGTCTA CCAATCTAGA CAACTCAGTG GCAAGCATTG AGGCAAAGGC 900
 15 TAATGTGTGC TGTGTTAAAT TCAGCCCCTC TTCCAGATAC CATTTGGCTT TCGGCTGTGC 960
 AGATCACTGT GTCCACTACT ATGATCTTCG TAACACTAAA CAGCCAATCA TGGTATTCAA 1020
 AGGACACCGT AAAGCAGTCT CTTATGCAAA GTTTGTGAGT GGTGAGGAAA TTGTCTCTGC 1080
 20 CTCAACAGAC AGTCAGCTAA AACTGTGGAA TGTAGGGAAA CCATACTGCC TACGTTCCCTT 1140
 CAAGGGTCAT ATCAATGAAA AAAACTTTGT AGGCCTGGCT TCCAATGGAG ATTATATAGC 1200
 25 TTGTGGAAGT GAAAATAACT CTCTCTACCT GTACTATAAA GGACTTTCTA AGACTTTGCT 1260
 AACTTTTAAG TTGATACAG TCAAAAGTGT TCTCGACAAA GACCGAAAAG AAGATGATAC 1320
 AAATGAATTT GTTAGTGCTG TGTGCTGGAG GGCCTACCA GATGGGGAGT CCAATGTGCT 1380
 30 GATTGCTGCT AACAGTCAGG GTACAATTAA GGTGCTAGAA TTGGTATGAA GGGTTAACTC 1440
 AAGTCAAATT GTACTTGATC CTGCTGAAAT ACATCTGCAG CTGACAATGA GAGAAGAAAC 1500
 35 AGAAAATGTC ATGTGATGTC TCTCCCCAAA GTCATCATGG GTTTTGGATT TGTTTTGAAT 1560
 ATTTTCTCTT TTTTCTCTT TCCCTCCTTT ATGACCTTTG GGACATTGGG AATACCCAGC 1620
 CAACTCTCCA CCATCAATGT AACTCCATGG ACATGCTGC TCTTGGTGGT GTTATCTAAT 1680
 40 TTTTGTGATA GGGAAACAAA TTCTTTTGAA TAAAAATAAA TAACAAAACA ATAAAAGTTT 1740
 ATTGAGCCAC AGTTGAGCTT GGAAAGTTT TGTCAAATGC NGCAAGAGAT AACTCTTTTT 1800
 45 ANGAAGTAGC ATATGTGAAC TATAATGTAA CAGTGAATAA TTTGTAAAGT TCGTATTTCC 1860
 CAACCTCTTT GGGAAATTACA CATATCAATA TAAACAAAAT ATAAAGT 1907

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(2) INFORMATION FOR SEQ ID NO: 79:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

	GCTGGGGTGT CCCCKCSGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA	60
5	CCCATGACTG ATGCTTATAA ATTTGTCAAA GGCAAACGAC CAATTATCTC CCCAAACCTT	120
	AACTTCATGG GGCAGTTGCT AGAGTTCGAG GAAGACCTAA ACAACGGTGT GACACCGAGA	180
	ATCCTTACAC CAAAGCTGAT GGGCGTGGAG ACGGTTGTGT GACAATGGTC TGGATGGAAA	240
10	GGATTGCTGC TCTCCATTAG GAGACAATGA GGAAGGAGGA TGGATTCTGG TTTTTTTTCT	300
	TTCTTTTTTT TTTTGTAGTT GGGAGTAAGT TTGTGAATGG AAACAACTT GTTTAAACAC	360
15	TTTATTTTTA ACAAGTGTA GAAGACTATA ACTTTTGATG CCATTGAGAT TCACCTCCCA	420
	CAAACCTGACA AATTAAGGAG GTTAAAGAAG TAATTTTTTT AAGCCAACAA TAAAAATATA	480
	ATACAACTTG TTTCTCCCCC TTTTCCTTTT AAGCTATTIG TAGAGTTTAT GACTAAATAG	540
20	TCTGTGCAGG TTCATAGACC GAAGATACTA CACACTTTAA ACCAATTAAA AAGAACCAAA	600
	AGTAAATAGA AAAGACATTG AATCACCAAG GCCTGGGATC AACCTGGGCT GTCCACACAG	660
25	AAAACAAAAA CCCAACCAAA CCAAGCCCTG TTGTGCTCAC TGGTGCAAAG AGAAGATCAG	720
	GGCAGCTTAA GTGGTCTAAG RATCCTTCAG GCATTCTTTA AGGAGAAAAA GGATACCTTT	780
	GATTTTGIGT GTTTCATGCT CTGGATTTTT TTTTTTTTTC CTCTCTGGG TTTAAGAGAT	840
30	TTTTTTTGAA ATAGTGAGGA ACTGACCATT ATATGCCTTC ACTGGCTTCT TGTGCAATAA	900
	TATGATGTTT TAAGTGTGCA AACAAGTTAG AGCTGGCAGC TGAATGATAG ACAAATAGTG	960
35	CAAATTTGCC AGCTTGAGGA TAGAAAGGAA TTCAACAATA TATCAAATAC TTTCTTCCC	1020
	ACCTTTTTTC TTTTTTTTTT TTTTCTCTGA TTTGATCTG GTTACAGTGC CATAAACCTT	1080
	GTTACATATG TATATCAGAA TGTAAGAAAA AAAAATTTAT TTAATAATAT TTTTCGCAAA	1140
40	AAAAAANNA AAAAATCGA GGGGGGCC	1168

45 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

55	AGAAAATCAC ATCCTAACAA AGAAGTCTGT CTAAGACAGT ACATCTCCTG TTGAACTTGC	60
	ATCTTTCCAC AGGACTTTCT GTTTTATAGG ATGAGACTAT TCTCTGCTTC ATCAAGGAAA	120
60	GAGAAATGTT CAGGGTTGTA GGGATGGCAC ACTTATTAGT TCTGCCTGTC TGAAAGGTTC	180

	CTGCAGGACA GTTTGGTCAG AGCTGCAATT CTTAGTCCAT GGTCTAATGC TTGAGTATCT	240
	CTTCTTTCCC TTTCTGTCT CAGGAATCAG CTGAGAATTC ATTCGATTGT CATGCCTCTA	300
-5	GCCCCTACT GTGATTTGTT GGTGCACTT TCATTTGCTT TAGTTCTAGA ATCACCTGTT	360
	GACTCCTCAG ACTTCACCTA ACTTTGGAAA CTCTCTTTTG GAGGCTTCTC ATTTCCCCCT	420
10	AATTCTGTGC TGCCTGAGCC CTAGAATTTT CCCACCAACG AATTATTCCA GGTAGATCCT	480
	AAGTTGCTGG ATCTAGTTGA TATTTAAACA ATATCTAGTT GATATTTCTC ATTCAGTTGG	540
	ATCCAGAAAC CAGTATCTCT NAAAAACAAC CTCTCATACC TTGTGGACCT AATTTTGTGT	600
15	GCGTGTGTGT GTGCGCGCAT ATGTATATAG ACAGGCACAT CTTTTTACT TTTGTAAAAG	660
	CTTATGCCTC TTTGGTATCT ATATCTGTGA AAGTTTAAAT GATCTGCCAT AATGTCTTGG	720
	GGACCTTTGT CTTCGTGTGA AATGGTACTA GAGAAAACAC CTATATTATG AGTCAATCTA	780
20	GTGGTTTFA TTCGACATGA AGGAAATTTT CAGATAACAA CACTAACAAA CTCTCCCTTG	840
	ACTAGGGGGA CAAAGAAAAG CAAACTGAC CATAAAAAAC AATTACCTGG TGAGAAGTTG	900
25	CATAAACAGA ATTAGGTAGT ATATTGAAGA CAGCATCATT AAACAGTTAT GTTGTCTCC	960
	TTGCAAAAAA CATGTACTGA CTTCCTGTTG AGTAATGCCA AGTTGTTTTT TTTATTATAA	1020
	AACTTGCCCT TCATTACATG TTTCAAAGTG GTGTGGTGGG CCAAATATT GAAATGATGG	1080
30	AACTGACTGA TAAAGCTGTA CAAATAAGCA GTGTGCCTAA CAAGCAACAC AGTAATGTTG	1140
	ACATGCTTAA TTCACAAATG CTAATTTTCAT TATAAATTGT TTTGCTAAAA TACACTTTGA	1200
35	AACTATTTTT CTGTATTCCA AGAGCTGAGA TCTTAGATTT TATGTAGTAT TAAGTGAAAA	1260
	AATACGAAAA TAATAAACAT TGAAG	1285

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(2) INFORMATION FOR SEQ ID NO: 81:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

	TCTCCAGCCC CAATTTCTAC GCGCACCGGA AGACGGAGGT CCTCTTTCTT TGCCTAACGC	60
	AGCCATGGCT CGTGGTCCCA AGAAGCATCT GAAGCGGGTG GCAGCTCCAA AGCATTGGAT	120
55	GCTGGATAAA TTGACCGGTG TGTTTGCTCC TCGTCCATCC ACCGGTCCCC ACAAGTTGAG	180
	AGAGTGTCTC CCCCTCATCA TTTTCTGAG GAACAGACTT AAGTATGCCC TGACAGGAGA	240
60	TGAAGTAAAG AAGATTTGCA TGCAGCGGTT CATTAAATC GATGGCAAGG TCCGAACTGA	300

	TATAACCTAC CCTGCTGGAT TCATGGATGT CATCAGCATT GACAAGACGG GAGAGAATTT	360
5	CCGTCTGATC TATGACACCA AGGGTCGCTT TGCTGTACAT CGTATTACAC CTGAGGAGGC	420
	CAAGTACAAG TTGTGCAAAG TGAGAAAGAT CTTTGTGGGC ACAAAGGAA TCCCTCATCT	480
	GGTGACTCAT GATGCCCGCA CCATCCGCTA CCCCAGATCC CTCATCAAGG TGAATGATAC	540
10	CATTGAGATT GATTAGAGA CTGGCAAGAT TACTGATTTT ATCAAGTTCC ATTCACCCAG	600
	CCAGGTGGTC TCGTCACCTC AGAGGCTCCG CAGACTCCTG CCCAGGCCAG GACTGAGGCA	660
15	AGCCTCAAGG CACTTCTAGG ACCTGCCTCT TCTACCAAG ATGAACTCAC TGGTTTCTTG	720
	GCAGCTACTG CTTTTCCTCT GTGCCACCCA CTTTGGGGAG CCATTAGAAA AGGTGGCCTC	780
	TGTGGGGAAT TCTAGACCCA CAGGCCAGCA GCTAGAATCC CTGGGCCTCC TGGCCCCSGG	840
20	GGAGCAGAGC CTGCCGTGCA CCGAGAGGAA GCCAGCTGCT ACTGCCAGGC TGAGCCGTCG	900
	GGGACCTCG CTGTCCCCGC CCCCAGAGAG CTCCGGGAGC CCCCAGCAGC CGGGCCTGTC	960
25	CGCCCCCAC AGCCGCCAGA TCCCCGCACC CCAGGGCGCG GTGCTGGTGC AGCGGGAGAA	1020
	GGACCTGCCG AACTACAAC TGAACCTCTT CGGCCTGCGC TTCGGCAAGC GGGAGGCGGC	1080
	ACCAGGGAAC CACGGCAGAA GCGCTGGGCG GGGCTGAGGG CGCAGGTGCG GGGCAGTGAA	1140
30	CTTCAGACCC CAAAGGAGTC AGAGCATGCG GGGCGGGGGC GGGGGCGGG GACGTAGGGC	1200
	TAAGGGAGGG GGCCTGGAG CTTCCAACCC GAGGCAATAA AAGAAATGTT GCGTAACTCA	1260
35	AAAAAAAAA AAAAAAANC TCGGGGGGGG	1290

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

50	TTTATTGTAT TCTGTAACTA TAGAACTTCT ATTTWATTCT TTTTGGACT TGCTAAGTTG	60
	TCTTTWATGG TTTTWAGTTC CATGCTGAAG TTTTCAGTAT TGACTTATCC CCTTGAACAT	120
	GAGTTGTTTT ATAGACTCTR ATGATTCAAA AATCTTACAT CTTTGGTAG TCTCTTTCAT	180
55	TGTYCACATG TTTCTGTTGA TTCTWACTCA TGGTATTTTA ATTCTTCGTT WTTTTTTTTC	240
	TGTTWAGAWA CATCTTTTGA AAAATAATTT GGAGGAATAT TTGATTCTTA TGAACAAGGC	300
60	ATTACTCACC AGAGAAGATT TTTTGTGTYT ACCARGTGCC TARGAATGCT AACAGTCTGG	360

5 GAMCACATAG AMCACCAGGT GATGAGACAA TCCTGGGART CCTGTTTTAC TTTGSSCCAT 420
 CTTTTCTCCC AACCTGTGG GAATARTCAT YCATATCCTA RCTGCAGGCT ARAAGGTGGT 480
 TTATCAGAGC CCAACTTCGA GGGCTCTGGG CTTTAGCTAC TGTCACCCCA TCATAACTGA 540
 GCTTCATGGA TTGATTCTCT TTTTATCTTT CAGATTTTCT TTTAAAAATC TTTGTTTTTT 600
 10 TTTTCTTCC GAAAGATTCC CCCAACATTA CCATTCCCCA CCTTCCGTTG AATTTTTTTG 660
 GCTCTCATTT TGAATTTTTC AAGA 684

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(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2024 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

25

CTGCAGGAAT TCGGCACAGC TGGCTGGAG GCTTCATCTT TGCCGCCGCT GCCGTCGCCT 60
 TCCTGGGATT GGAGTCTCGA GCTTCTTCG TTCGTTCTGYC GCGGGTTTCG CGCCCTTCTC 120
 30 GCGCCTCGGG GCTGCGAGGC TGGGAAGGG GTTGGAGGGG GCTGTTGATC GCCGCGTTTA 180
 AGTTGCGCTC GGGCGGCCA TGTGGCCCG CGAGGTCGAG CGCCTAGTGT CGGAGCTGAG 240
 CGGCGGGACC GGAGGGGATG AGGAGGAAGA GTGGCTCTAT GGCGATGAAA ATGAAGTTGA 300
 35 AAGGCCAGAA GAAGAAAATG CCACTGCTAA TCCTCCATCT GGAATTGAAG ATGAAACTGC 360
 TGAAAATGGT GTACCAAAAC CGAAAGTGAC TGAGACCGAA GATGATAGTG ATAGTGACAG 420
 40 CGATGATGAT GAAGATGATG TTCAATGTCAC TATAGGAGAC ATTAACACGG GAGCACCACA 480
 GTATGGGAGT TATGGTACAG CACCTGTAAG TCTTAACATC AAGACAGGGG GAAGAGTTTA 540
 TGGAAGTACA GGGACAAAAG TCAAAGGAGT AGACCTTGAT GCACCTGGAA GCATTAATGG 600
 45 AGTTCCACTC TTAGAGGTAG ATTTGGATTG TTTTGAAGAT AAACCATGGC GTAAACCTGG 660
 TGCTGATCTT TCTGATTATT TTAATTATGG GTTTAATGAA GATACCTGGA AAGCTTACTG 720
 50 TGAAAAACAA AAGAGGATAC GAATGGGACT TGAAGTTATA CCAGTAACCT CTACTACAAA 780
 TAAAATTACG GTACAGCAGG GAAGAACTGG AAACCTCAGAG AAAGAACTG CCCTTCCATC 840
 TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG 900
 55 GAGATTACCT GGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 960
 CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 1020
 60 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA 1080

- 5 CATTCCACCT CCTCCATTTT TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 1140
 TCCACCACCG GGTTTTCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 1200
 AGAAAGTGGA CATTCCTCTG GTTATGATAG TCGTTCTGCA CGTGCAATTC CATATGGCAA 1260
 TGTTCGCTTT CCCCATCTTC CTGGTTCTGC TCCTTCGTGG CCTAGTCTTG TGGACACCAG 1320
 10 CAAGCAGTGG GACTATTATG CCAGAAGAGA GAAAGACCGA GATAGAGAGA GAGACAGAGA 1380
 CAGAGAGCGA GACCGTGATC GGGACAGAGA AAGAGAACGC ACCAGAGAGA GAGAGAGGGA 1440
 15 GCGTGATCAC AGTCTACAC CAAGTGTMTT CAACAGCGAT GAAGAACGAT ACAGATACAG 1500
 GGAATATGCA GAAAGAGGTT ATGAGCGTCA CAGAGCAAGT CGAGAAAAAG AAGAACGACA 1560
 TAGAGAAAGA CGACACAGGG AGAAAGAGGA AACCAGACAT AAGTCTTCTC GAAGTAATAG 1620
 20 TAGACGTCGC CATGAAAGTG AAGAAGGAGA TAGTCACAGG AGACACAAAC ACAAAAAATC 1680
 TAAAAGAAGC AAAGAAGGAA AAGAAGCGGG CAGTGAGCCT GCCCCTGAAC AGGAGAGCAC 1740
 CGAAGCTACA CCTGCAGAAT AGGCATGGTT TTGGCCTTTT GTGTATATTA GTACCAGAAG 1800
 25 TAGATACTAT AAATCTTGTT ATTTTCTGCG ATAATGTTTA AGAAATTAC CTTAAATCTT 1860
 GTTCTGTTTG TTAGTATGAA AAGTTAACTT TTTTCCAAA ATAAAAGAGT GAATTTTCA 1920
 30 TGTTAAGTTA AAAATCTTTG TCTTGACTA TTTCAAAAT AAAAAGACAG CAATGACTTT 1980
 ATATCCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCC 2024

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(2) INFORMATION FOR SEQ ID NO: 84:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 931 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CGCGCCMATA GCCGACGGG GATCTGAGCT GGCAGGATGA ATGTGGGGGT GGCACACAGC 60
 GAAGTAAACC CCAACACCCG AGTGATGAAT AGCCGAGGCA TCTGGCTGGC CTACATCATC 120
 50 TTGGTAGGAT TGCTGCATAT GGTCTACTC AGCATCCCCT TCTTCAGCAT TCCTGTTGTC 180
 TGGACCCTGA CCAACGTCAT CCATAACCTG GCTACGTATG TCTTCCTTCA TACGGTGAAA 240
 55 GGGACACCCT TTGAGACTCC TGACCAAGGA AAGGCTCGGC TACTGACACA CTGGGAGCAA 300
 ATGGACTATG GGCTCCAGTT TACCTCTTCC CGCAAGTTCC TCAGCATCTC TCCTATTGTG 360
 CTCTATCTCC TGGCCAGCTT CTATACCAAG TATGATGCTG CGCACTTCCT CATCAACACA 420
 60

GCCTCATTGC TAAGTGTACT GCTGCCGAAG TTGCCCCAGT TCCATGGGGT TCGTGTCTTT 480
 GGCATCAACA AATACTGAGG GATGGGTTTT GGGACAGCTC CATGGGCATG GGGAAGGCAC 540
 5 TGAAACAGAG GACTATAAAA CATCCTTCTC TTATTCTCCA TACTGTCTTC TACACCTTTA 600
 AAGCCTGAGA ACTATACAAC CTTTCCCAGA CTCCAAGAA GAGAAGAGAT TGGCAAATGG 660
 GGCTCCTGGG CCCAGTCTCG CTAGTGGCAA GTTTCCTTGA ATCAGGAAGG CAGGTGAGGT 720
 10 AAGGGCCAAA TCACTCTCCT CCATAGCAGG AAGCCATTG GGCAGCTCCT TTGGTGATTA 780
 CATCTTCCA TATCTTTTAC ACTTACCACC TTCCAGCTCT GTTTTGCTGT GTATTTTTCT 840
 15 TACAATAATT TTTTTCAGCT ATAGCTGCAG TTTAATCAGG ATGGGTAGAG AGCTGTCCTC 900
 ATAAGGCTGG GGGTGGGAAG ATGGAATACT G 931

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(2) INFORMATION FOR SEQ ID NO: 85:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CGGGGCCGGC GGGGTCTTCA GGGTACCGGG CTGGTTACAG CAGCTCTACC CCTCACGACG 60
 CAAACATGGC AGCGCAGAAG GACCAGCAGA AAGATGCCGA GGCGGAAGGG CTGAGCGGCA 120
 35 CGACCCTGCT GCCGAAGCTG ATTCCCTCCG GTGCAGGCCG GGAGTGGCTG GAGCGGCGCC 180
 GCGCGACCAT CCGGCCCTGG AGCACCTTCG TGGACCAGCA GCGCTTCTCA CGGCCCCGCA 240
 40 ACCTGGGAGA GCTGTGCCAG CGCCTCGTAC GCAACGTGGA GTACTACCAG AGCAACTATG 300
 TGTTCTGTGT CCTGGGCCTC ATCCTGTACT GTGTGGTGAC GTCCCTATG TTGCTGGTGG 360
 CTCTGGCTGT CTTTTTCGGC GCCTGTTACA TTCTCTATCT GCGCACCTTG GAGTCCAAGC 420
 45 TTGTGCTCTT TGGCCGAGAG GTGAGCCCAG CGCATCAGTA TGCTCTGGCT GGAGGCATCT 480
 CCTTCCCCTT CTTCTGGCTG GCTGGTGCGG GCTCGGCCGT CTTCTGGGTG CTGGGAGCCA 540
 50 CCCTGGTGGT CATCGGCTCC CACGCTGCCT TCCACCAGAT TGAGGCTGTG GACGGGGAGG 600
 AGCTGCAGAT GGAACCCGTG TGAGGTGTCT TCTGGGACCT GCCGGCCTCC CGGGCCAGCT 660
 GCCCCACCCC TGCCCATGCC TGTCTGCAC GGCTCTGCTG CTCGGGCCCA CAGCGCCGTC 720
 55 CCATCACAAAG CCCGGGGAGG GATCCCGCCT TTGAAAATAA AGCTGTTATG GGTGTCATTC 780
 AGGAAAAAAA AAAAAAAGG GGGGCCCTC TAGGGGTCAA AGTTA 825

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(2) INFORMATION FOR SEQ ID NO: 86:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

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CATGTAAAAG GATGAAATGT GACTTCTGGT GTTTTTTTAT TTCTATGGAG GGACTTTCTG      60
15 GGGACGGTTT CTGGCTCTCA GGCTCTGAGA AGCTGCAGTT TATGAGTGGC TCTGTGTGTG      120
CTGCCACCTA CTGGAGAAGC CATAAGCTGC AGCTTTAGGA AAAGGGAACC CGGGGCAGAG      180
20 TGTGGGGAAG TGGGATGGCA GCATGGCAGG GCTTTGGAAA ATGAGAGGTG AGAGTKTKTC      240
CAGGAAGGGT GTAAGGAGAG GATGGATCCT GATACATGGA TTCAGGATCA TTAGGGTCCT      300
GTCTGGGACA CTGGCCTTCC TGCTTACCTG CTCTTTCCTT CCTCCTTGGT CGGAGGAGGG      360
25 GCTGGCTCAC TGCTCTGGCT TCATTTTCCA GAGCTGCCTG CTGCAGTCAC ACTTAGGTCA      420
TCTTCTCTCA CTTTCTCCTT TTGCCGATT AGTGGACGTG ACAGAGATGT GAATGGGGCA      480
30 GGGATGTCCT TTGATGGCAT CAAGACTTTA GCTTCTGGTG CGCTGTGTCC CAGCTCTGAT      540
TTCAGTTGCA GCCGTGATGG AMAGTTNGCA TGGAAGCTGA GACTCTCACT GACAGTGAAA      600
CCCTCAAATG AACACAATCC CTGCTTTCCT GCCAAGGATC CTTGTAGGGT NCCCCAGCT      660
35 TCCCCACTTT TTTTCTGTGT CCGACAAAG AAACACAGAG TAACTTGATT GCCCTGTGAC      720
CTGGECCAGT GCATTTCCTT TGCAGGCTTG AGCCCAAGCC AGAGCCTTGA AAAGGTATTC      780
40 AGGTGTGTGC CAAAACACT GAAAAAACT GCCCTGGCCC TGAACCAAAT ACCTTGAACC      840
CTCGTAAACT CCATACCCTG ACCCCCTTGT TTTGGATATA CCCAGGTAGA ACAACTCTCT      900
CTCACTGTCT GTTGTGAGGA TACGCTGTAG CCCACTCAT T AAGTACATTC TCCTAATAAA      960
45 TGCTTTGGAC TGATCACCTT GCCAGTCTTT TGTCTTGGGC AATCTATACT TTTNCTCAGA      1020
GGTCCCAAG GCCTACTGAA GGGACTTAAC ATACTCTTAA TGGCTTTCCT CTCTCTTGT      1080
50 TTACCTTATG CCCTCACTTC CTGAGTTAAC CTCCCAAATA CAGGATTCAC CTGTACCCAA      1140
GCCCTTAGCT TCAAGAATAC AGGATCACCT GTACCCAAGC CCTTAGCTCA AGCTCTGCTT      1200
TGGAAGAACC CAAACTAAGA CAGTGCTCCT GGTGCCCT      1238

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(2) INFORMATION FOR SEQ ID NO: 87:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1460 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

	ATTGCCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA TCCCCGAGA GCATTCTCTGG	60
10	CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTCGGGAGG CCAGTTATTC CACCATCGCG	120
	CCCCTCTCA TTGCCGACCT CTTTGTGGCC GACCAGCGCG ACCGGATGCT CAGCATCTTC	180
15	TACTTTGCCA TTCCGGTGGG CAGTGGTCTG GGCTACATTG CAGGCTCCAA AGTGAAGGAT	240
	ATGGCTGGAG ACTGGCACTG GGCTCTGAGG GTGACACCGG GTCTAGGAGT GGTGGCGGTT	300
	CTGCTGCTGT TCCTGGTAGT GCGGGAGCCG CCAAGGGAG CCGTGGAGCG CCACTCAGAT	360
20	TTGCCACCCC TGAACCCAC CTCTGGTGG GCAGATCTGA GGGCTCTGGC AAGAAATCCT	420
	AGTTTCGTCC TGTCTTCCCT GGGCTTCACT GCTGTGGCCT TTGTACCGG CTCCCTGGCT	480
25	CTGTGGGCTC CGCATTCTCT GCTGCGTTCC CGCGTGGTCC TTGGGGAGAC CCCACCCTGC	540
	CTTCCCGGAG ACTCCTGCTC TTCTCTGAC AGTCTCATCT TTGGACTCAT CACCTGCCTG	600
	ACCGGAGTCC TGGGTGTGGG CCTGGGTGTG GAGATCAGCC GCCGGCTCCG CCACTCCAAC	660
30	CCCCGGGCTG ATCCCTGGT CTGTGCCACT GGCCTCCTGG GCTCTGCACC CTTCTCTTTC	720
	CTGTCCCTTG CTTCGCCCCG TGGTAGCATC GTGGCCACTT ATATTTTCAT CTTCATTGGA	780
35	GAGACCCTCC TGTCCATGAA CTGGGCCATC GTGGCCGACA TTCTGCTGTA CGTGGTGATC	840
	CCTACCCGAC GCTCCACCGC CGAGGCCTTC CAGATCGTGC TGTCCACCT GCTGGGTGAT	900
	GCTGGGAGCC CCTACCTCAT TGGCCTGATC TCTGACGCC TGCGCCGAA CTGGCCCCC	960
40	TCCTTCTTGT CCGAGTTCCG GGCTCTGCAG TTCTCGCTCA TGCTCTGCGC GTTTGTGTTGG	1020
	GCACTGGGCG GCGCACTTCC TGGGCACCGC CATCTTCATT GAGGCCGACC GCCGGCGGGC	1080
45	ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGTCC ACAGACGACC GGATTGTGGT	1140
	GCCCCAGCGG GGCCGCTCCA CCCGCGTGCC CGTGGCCAGT GTGCTCATCT GGAGAGGCTG	1200
	CCGCTCACCT ACCTGCACAT CTGCCACAGC TGGCCCTGGG CCCACCCAC GAAGGGCCTG	1260
50	GGCCTAAACC CCTTGGCCTG GCCAGCTTC CAGAGGGACC CTGGGCCGTG TGCCAGCTCC	1320
	CAGACACTAC ATGGGTAGCT CAGGGGAGGA GGTGGGGGTC CAGGAGGGGG ATCCCTCTCC	1380
55	AACAGGGGCA GCCCAAGGG CTCGGTGCTA TTGTAAACGG GATTAAAATT TGTAGCCAGA	1440
	AAAAAAAAA AAAAAAAAAA	1460

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(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1395 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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CAGGTGCAAA GTGGGAAGTG TGAGTCCTCA GTCTTGGGCT ATTCGGCCAC GTGCCTGCCG 60
 GACATGGGAC GCTGGAGGGT CAGCAGCGTG GAGTCCTGGC CTTTTCGTC CACGGGTGGG 120
 AAATTGGCCA TTGCCACGGC GGAAGTGGG ACTCAGGCTG CCCCCCGGC GTTCTCATC 180
 CGTCCACCGG AYTCGTGGG GCTCGCACTG GCGCTGATGT AGTTTCCTGA CCTCTGACCC 240
 GTATTGTCTC CAGATTAAAG GTACGACATT TGGAGGCCCC AGCGAGAAAC GTCACCGGGA 300
 GAAACGTCAC CGGCGAGAG CGGKCCCGCT GTGTGCTCCC CCGGAAGGAC AGCCAGCTTG 360
 TAGGGGGGAG TGCCACCTGA AAAAAAATT TCCAGGTCCC CAAAGGGTGA CCGTCTTCCG 420
 GAGACAGCGG ATCGACTACC ATGTGGGTGC CCACAAAAAT TYCACCTYTG AGTCCTCAAC 480
 TGCTGACCCC GGGGTCACTT CCAGAGAGAA GGAATCCCTC CTGCTTGGAA GAGACCTCAC 540
 ACCGTCATCA CGATGCCAAC GGCTCTGAAG GTGGATGGCA TTCTGCGTG GATTTCATCAC 600
 TCCCGCATCA AAAAGGCCAA CRGAGCCCAA CTAGAAACAT GGGTCCCCAG GGCTGGGTCA 660
 GGCCCTTAA AACTGCACCT AAGTTGGGTG AAGCCATTAG ATTAATTCTT TTTCTTAATT 720
 TTGTAAAACA ATGCATAGCT TCTGTCAACT TATGTATCTT AAGACTCAAT ATAACCCCT 780
 TGTATAACT GAGGAATCA ATGATTGAT TEECCAAAA CACAAGTGGG GAATGTAGTG 840
 TCCAACCTGG TTTTACTAA CCTGTTTTT AGACTYTCCC TTTCTTTAA TCACTCAGCC 900
 TTGTTTCCAC CTGAATTGAC TCTCCCTTAG CTAAGAGCGC CAGATGGACT CCATCTTGGC 960
 TCTTTCNACT GGCAGCCGCT TCCTYCAAGG ACTTAACTTG TGCAAGCTGA CTCCCAGCAC 1020
 ATCCAAGAAT GCAATTAACT GATAAGATAC TGTGGCAAGC TATATCCGCA GTTCCCAGGA 1080
 ATTCGTCCAA TTGATTACAC CCMAAGCCC CGCGTCTATC ACCTTGTAAT AATCTTAAAG 1140
 CCCCTGCACC TGGAATATT AACGTTCTG TAACCATTTA TCCTTTTAA TTTTTTGCCT 1200
 ACTTTATTTT TGTAATAATG TTTTAACTAG ACCCCCCCTC TCCTTTCTAA ACCAAAGTAT 1260
 AAAAGCAAA CTAGCCCTT CTTAGGCCG AGAGAAATTC GAGCGTTAGC CGTCTCTTGG 1320
 CCACCAGCTA AATAAACGGA TTCTTCATGT GTAAAAAAA AAAAAAAA CTCCGAGGGG 1380
 GGGCCCGGTA CCAA 1395

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1186 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

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5      GGCACGAGCC GGCAAGCCGA GCTAGGGTGA AACTGGGGG CGCACCAGGA TGTNNGACAG      60
      AAAAGCAGAA GATGAGACTC TGTTCAATTCA CTTTTCCTAG GCCCATCCTG TGGTCATCTT      120
15     TCCCCCTCCC ATCATACCTC CTCCTTCCTG GAGCCTCTGC OGGCTTGGCT GTAATGGTGG      180
      CACTTACCTG GATATTTTCA TGGGAGGATG AAAGGCGAGA CTCACCCTAC GCGGTGGGAC      240
20     AGATGGGGAG AGGAAAAAGG CAGAGATGGC CAGGAGAGGG GTGCAGGACA AACCAGAGAG      300
      GTTGGGTCAG GGGAAAAGG TGGGAGAGAA GAGGGGTGCA GGCCCTGCAG GCCGGTTAGC      360
      CAGCAGCTGC GGCTTCCCCG GGCCCTTGGC ATCCAACCTC GCAGACAGGG TACCAGCCTC      420
25     CTGGTGTGTA TCATAGGATT TGTTACATA GTGTTATGCA TGATCTTCGT AAGGTTAAGA      480
      AGCCGTGGTG GTGCACCATG ACATCCAACC CGTATATATA AAGATAAATA TATATATATA      540
30     TGTATGTAAA TTATGGCAG AGAAATTATA GCACTGAGGG CCCTGCTGCC CTGCTGGACC      600
      AAGCAAACT AAGCCTTTTG GTTTGGGTAT TATGTTTCGT TTTGTTATTT GTTTGTTTTT      660
      GTGGCTTGTC TTATGTCGTG ATAGCACAAG TGCCAGTCGG ATTGCTCTGT ATTACAGAAT      720
35     AGTGTTTTTA ATTCAATCAAT GTTCTAGTTA ATGCTTACCT CAGCACCTCC TCTTAGCCTA      780
      ATTTTAGGAG GTTGCCCAAT TTTGTTTCTT CAATTTTACT GGTACTTTT TTGTACAAAT      840
40     CAATCTCTTT CTCTCTTTCT CTCCTCCCCA CCTCTCACC TTGCCCTCTC CATCTCCCTC      900
      TCCCGCCCTC CCTCTCTCC TCTGGCTCCC CGTCTCATTT CTGTCCACTC CATTCTCTCT      960
      CCTCTCTCC TGCTCTCTGC TGCCCCCTCC CCAGCCCACT TCCCCGAGTT GTGCTTGCCG      1020
45     CTCCTTATCT GTTCTAGTTC CGAAGCAGTT TCACTCGAAG TTGTGCAGTC CTGGTTGCAG      1080
      CTTCGCGCAT CTGCCTTCGT TTCGTGTAGA TTGACGCGTT TCTTTGTAAT TTCAGTGTTT      1140
50     CTGACAAGAT TAAAAAAGG AAAAAGGAAA AAAAAAAGG AAAAAA      1186

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(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1821 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

- 5	AAAACATGCT TTCAGGGCGT CCCCTATGTA TTCGGGGGGC CCACGGACAC TCAGGCTGGA	60
	KATCCGTCCT CACTGCGCTC AAGATGGCCT CAGCAGACAC CAGTTACCCA GCTGAAAGTC	120
	ACAATCCCTC CCAGAAGTCT CCCAACACTA GTGCTGACCA GAGGTGGGGC TCTCAGGCTA	180
10	GGAGTTTCAC ACACAATGAC AGGCTGCTGG GGGACATTGC AGGACCCCTT TTCCTYTCCT	240
	CTCCATGCTA GAAGCCAGCC CTAGGMAGCT GCAGTTACTC CCTGTGACTC AGCAGCAGGC	300
15	TGATTCAACA CAGCTGCCCA CACAAAGCCA GTGGTAATAC ATCTGTTTAC CTTTCCCTAT	360
	CACCCAGACA CAAGCCCCTT TCCCAGGTCA AACCACAGGC CGATGCATCT CCAGTTTGAC	420
	AGTCAAATCA CTACTTCCAT TGCTACTTTA GATCAGCCAA AGTGGTGACT GCTGCAGTGT	480
20	GTGGCTATCC CTACAAGGCC CACCCAAGGG ATGCCCAAAG CCCAACCTTC TCCAGGGCTG	540
	CAGCAGNAGC AACCCACCA GCCTAAGTCC AGCAGAGGAC CTCCCACCA ATGTCTTGTT	600
25	CTAATTAGAA GGGGAAGTTA GCCACAGAAA ATCAACTTAT CTATAATTAC AAAATCTCT	660
	TGACTCACCT TAAAGTTCCT ATTGACATCT ACTGCTTTTA AACCTATTG AAAACTCTGA	720
	TACTAAAACA AATGACACTC TAAGAAAGTT TGGGAGCCCC ATGCTGAGAA CCATTCTGT	780
30	GCAGTGAGGA TGTTTCCAGA AGCTACTTAC CTACATGTGA ATGTGCCATT TTCTTTCCTT	840
	TTGTAGAGAA AATCCCCTTT ACTTTTGGGA ACAGTAATGG CAGCTTCTAG TACAGCCATT	900
35	ACAGTTTCAT ATGAGAAAAA TTAAGAATAA CTATAAAATT GTTAAATAT CCAATAATGG	960
	ATAATGATGG CCAGAAGATT TAACATACAA AGTAATTCTC AATGTAAAGC TATTCAGCTC	1020
	TTCCAGGTTG AATGCCCTGT AACCACCCCT GACCTTCCAC ATCATCTTCA AAAAGCAGTT	1080
40	TCTCTGTTCC CCATGATTCT CCTATAAGGT AACTCTTTAG TCCTCCATT AGCACATTTT	1140
	AAATCCTCCA AAGAATAAGT ATCATGTGAT TATTTTAGCT TTACAAAAA AAAGTTGAAT	1200
45	GGCGTTTAT TTTCATGGCC TATAAGCAGG TACCTTAGTA GGCAGATAT AGGAAAAACA	1260
	AATTAGAGCA AACAAATCC TCTACAAATC CAAGGCAGGA AAAGTGGTGG CAGAGTGACT	1320
	CATTCTCCTG TCCCTCCCAT CAGGTCAAAT CAGGAGGCTG CAGTGAATGC CTGTTCTTTG	1380
50	AATGTGTAGC AGTTGTTCTT GTAACCTTTT AAAACTTGGC TATAGGCTGT TTAGCACAGT	1440
	ACAGATTAAA GATACAGTTA CGTAAACAGC AAAGTAATTT TATAGTGCTT CATCCATTTA	1500
55	TCATGCTTTG GTTTGCTAAT TTTTTCACAT ACCTTTTCT ATCACAGTCT GTTGCTTTTG	1560
	TACACATTTT TCATATTGGG GTTCGACAGG TAAACACAAA CTGCTATTTT AGTAGAAAAA	1620
60	GTTATTGTTA TGGAATATTA AACCCAATAA ATTGTATAAA GGGTAAAAA AAAAAAAAAA	1680

AAAAAAAAA AAAAAAAAAA AAAAAAATTC CTGCGGGCCG CANGCTTTTT CCCTTTGGGT 1740
 GAGGGGTAT TTTNGGCTTG GGCACGGGC CCTTCGTTTT TACAACGTCG TGANGGGGGG 1800
 5 AACCCGGGGG GGGTTTCCCC C 1821

10 (2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 862 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

20 TGCCCTTTTT CCCACCGATT CGGGGCMNIGG TGAAGGTGGG AGATGTGAAC TCCAATTAAG 60
 GGACTGGAGA GAGGTGAAGA ATTTTGCAAG TGGGAGATTT GGATTGAAT GTGGACTTGT 120
 AAATGACTTG ACCTTGCCAT CTGTGTTCAA GGTACGGTT TGCTGTGGG TTCCTGGAG 180
 25 AGCTTACTCA CCCCGGAGTC TTTTCTTTCT CTGCTCCAA GAAGAGCCCT GTTGGTGCTT 240
 TACCACCGCT TGGAGTCTCC CGAGGACACA AACAGGCAGA GAGGGACGTG TAGGGAGAGT 300
 30 TCTTTCCTGT TTTCTGTGCT TTCCTTTTAA CAGGACTCCC GGAAGGCCAC TCATGGCCAT 360
 GCCAGGAGCT TTCTCAGAAA CAGTCATAAA CGATCTCTTG AGTCTCTTTC TTGTCTCTCC 420
 AGCTGAGCTT TCTTATTCCA CCCTTCTTGG TGCTATAGG AATGCATGAG AAGACCCTGG 480
 35 GACGTTTTTC TGCTCTCTTC TGGCCCTCCA TGGAGCCATG GGCCTCGGCC TCGGCGGCTC 540
 CTCACCTCA CAATTTATTT CCTCCTCCCG TGCCAGCCCT TCTTTTGTGT CTGAAACCGG 600
 40 TTTTAAATG TGAATCTCCC AGAGAAGAAG CCGCTGGCTG TATGAAACTT GACGGCGCTT 660
 TTGTAAGGTG CCACCCCAA ACTTTAAGGT AGCTAAACCA ATTTTAAAA GATTCAATGG 720
 45 CTTGTTTCATC CTCCAGATGT AGCTATTGAT GTACACTTCG CAACGGAGTG TCTGAAATTG 780
 TGGTGGTCCT GATTATAGG ATTTATAAT TAAATGTCT GCTGAATAAA AAAAAAAAAA 840
 AAAAATCGA GGGGGGCCCG GT 862

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

	CTGAGGCGAG TGAAGTGGAC TCTGAGGGCT ACCGCTACCG CCACTGCTGC GGCAGGGGCG	60
- 5	TGGAGGGCAG AGGGCCGCGG AGGCCGCGAGT TGCAAACATG GCTCAGAGCA GAGACGGCGG	120
	AAACCCGTTT GCCGAGCCCA GCGAGCTTGA CAACCCCTTT CAGGACCCAG CTGTGATCCA	180
10	GCACCGACCC AGCCGGCAGT ATGCCACGCT TGACGTCTAC AACCCTTTGT AGACCCGGGA	240
	GCCACCACCA GCCTATGAGC CTCAGCCCC TGCCCCATTG CCTCCACCTT CAGCTCCCTC	300
	CTTGCGAGCC TCGAGAAAGC TCAGCCCCAC AGAACCTAAG AACTATGGCT CATACAGCAC	360
15	TCAGGCCTCA GCTGCAGCAG CCACAGCTGA GCTGCTGAAG AACAGGAGG AGCTCAACCG	420
	GAAGGCAGAG GAGTTGGACC GAAGGAGCGA GAGCTGCAGC ATGCTGCCCT GGGRGGCACA	480
20	GCTACTCGAC AGAACAATTG GCCCCCTCTA CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT	540
	TTCCAGGACA TCTCCATGGA GATCCCCCAA GAATTTGAGA AGACTGTATC CACCATGTAC	600
	TACCTCTGGA TGTGCAGCAC GSTGGNTCTT CTCCTGAAYT TCMTCGSCTG CCTGGCCAGT	660
25	TCTGTGTGGA AACCAACAAT GCGAGGCTT TGGGTT	696

30 (2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1886 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

40	CAGGCCACTG ACGCTTCTTT GCGAGGGATG CAGGAGGTCC TACAGAGAAA GCGCTTCTT	60
	GCATKTCAGA GGGCCACAG CCTGTCACCC ACAGATCACC AAGCAGCTTT CTACCTGGCT	120
45	CTGCAGCTTG CCATCTCCAG ACAGATCCA GAGGCTCTGG GGTATGTCCG CCAAGCTCTT	180
	CAGCTTCAAG GTGACGATGC CAACTCCCTG CACCTCCTTG CCCTCCTGCT GTCAGCACAG	240
	AAGCATTACC ATGACGCTCT GAACATCATC GACATGGCCC TGAGTGAATA CCCAGAAAAT	300
50	TTCATACTAC TGTTTTCCAA AGTGAAGTTG CAGTCACTCT GCCGAGGCCG GGACGARGCA	360
	CTGCTGACTT GTAAGCACAT GCTGCAGATA TGGAAATCCT GCTACAACCT CACCAACCCC	420
55	AGTGATTCTG GACGTGGGAG CAGCCTCTTA GATAGAACCA TTGCTGACAG ACGACAGCTT	480
	AATACAATTA CTTTGCCAGA CTTGAGCGAT CCCGAGACAG GCTCCGTCCA TGCCACATCG	540
	GTAGCAGCCT CAAGAGTGA GCAGGCACTG TCGGAAGTGG CTTCGTCTCT GCAGAGCATG	600
60	CCCCTAAGCA GGGCCCGCTG CACCCCTGGA TGACGCTGGC ACAGATCTGG CTCCATGCAG	660

CTGAAGTCTA TATCGGCATC GGAAGCCTG CAGAAGCCAC AGCCTGTACC CAAGAAGCTG 720
 CCAACCTCTT CCCAATGTCC CACAATGTCC TCTACATGCG CGGCCAGATT GCTGAGCTCC 780
 5 GGGGAAGCAT GGACGAGGCG CGGCGGTGGT ATGAAGAGGC CTTAGCCANT CAGCCCCACC 840
 CACGTGAAGA GCATGCAGCG ACTTGGCCCT GATCCTTCAC CAGYTAGGCC GYTACAGTYT 900
 10 GGCGGAGAAG ATCCTCGGG ACGCGGTGCA GGTGAAGTCG ACAGCCCACG AGGTCTGGAA 960
 CGGGCTGGGC GAGGTCTCTC AAGCTCAGGG CAACGATGCG GCGGCTACGG AGTGCTTCTT 1020
 GACAGCCTTG GAGCTGGAGG CCAGCAGCCC CGCCGTGCCC TTCACCATCA TCCCCCGCGT 1080
 15 GCTCTGAGCA GGCGCCTGCC AGCCTCACCT GCCGCTCAGC CTNCAGAGGC CCTGCCGGGC 1140
 ACCAGGGCTT GTGCCATCGC CCCAAGGGGA TGAATCTGCC GCACTGAGGC CAGGGACGAG 1200
 20 TGTTCAGTGG GCCACAGTGA ACCAACCAAA CCAACCCGA ATCATCGCTC TCGCCATGTG 1260
 CGTTCTCTT GTTTTTTTTG CCAGCCCAAT GGTAGTTTCT GAACCTATTG ACATTGTTCA 1320
 AAATGGATCA TGTGCCATAT TTTGTTAGTT GACATCTGAG TTTTCAGTAA AATGATTATG 1380
 25 GAATTAATCA GCAAATGTAG AAGAATATAT TCAAAGTTAA AATTCAAGTG CAGCACAGAT 1440
 TATTTTTATC AGAGCTGTAA AGAAAACAAC TGTCTTTTTC TCCCCACCAC CCCTCCTGCC 1500
 30 CCACTTTGGC CCAGAAACCA AATGTGAAGT TCCTGTCTCC CACCTCAGCA CTAGTCCATG 1560
 CCAGGACACC AGCTGACAAT TTCTTGGTTT TACTGTCAAT AATTGTACCA TGTGATCAAT 1620
 TACTGTCTCT ACTTAGAACA AAGCCTGAGT CCGAGAATAT TTATATTTTA CCAATATATG 1680
 35 CCTGTTACAA GAGAAGGAAA TATGAGTTAT TTAAGTTTAA CTTTTTTATG TGAATTCAGA 1740
 GTTATTTTAT CGAGGGAAAT ATGTACAAAG AAGCTTCAAA TGAATATTT ACCGACATTC 1800
 40 CTTATACATG ACAGACACTT GGCTACATGG GAAGATGATG TTAATAATAA AATGATTTTT 1860
 AAATGGAAAA AAAAAAAAAA AAAAAN 1886

45

(2) INFORMATION FOR SEQ ID NO: 94:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CTCAGCTACC GTATACAGTA GGACATAACC CCATTCACA TGCACTACAC TGAGACTTGC 60
 CTCTCTCCC CCCACATTGA AGATGTTCTT TTTTCATAAC TATATACTAT TCCATTGCAT 120
 60

	GAATATTCTG TAATTTATTT AATCCCCTAT GGATTGATAA TTAGGTTTCAT TATAGATAGA	180
	AGTGTAATTA ACATTCCTGT ACATGTATTT TGCTACTTGT GTGGGTATTT CTGTAGGATG	240
-5	AATAACTAGA AATTTATGCG ATCAGGTTTC ACATTTGCAG TTTTGAAAAC TACTACCAA	300
	AAGATTTTAC CAATTTACAA CTCCATCATT AGTAAGAATG CCTGTTTGCC TATAGTCTGC	360
10	CAACCCTGAA TCCTTAAAAA TTTTGGCCAA TCTGGTAGGC AAAATTTCCTT TCTTTTCTTT	420
	GAATATTAAT GAGGAGGAAC ATCTTTTCAT GTTCTTGGC CATTTGCATT TCCTATTATG	480
	AATTGCTTTT GCCCATTTTC CTTTMTTAA TTATGAAAGT CTAATGACTA CCTTCTCATT	540
15	GTATAAAAAA CACAGTTCTT TGAATAGAGA GACCCTTTTC TCCAATGCTA CCAATCACAT	600
	TCCACTTACC ACAGTTTAAC ATACATCCTC TAGTCACCTT TCCGTACGAA TATACATACA	660
20	CATAAAAACA CTTTTTACAT AAATAGGATC TCATATTCTG TAGCTMTTAA AAATTTTGGT	720
	CTCAAAAAA GATAACAGGT CTTTAAATTT CTTTAATGGT TGAATATGAT TAAATACTAT	780
	GAAAATGCCA TTATTTATTC CCTTAATTTT TTCTCTCTG CTATTACATT GCCAAAGTAA	840
25	ACATCCTATT CAGATGTCTT TGTGCATGTG TGTGAATATT TCTTTAGTCT GGAGTCCAGT	900
	AAGGTGGATT TTTGGATCAA AGGTTTGTG CTCTGTCCAC CTTCAGTCTT CCCAAAGGCC	960
30	TTCATAACTG TATTTTCACC AAGTGATGG AGAATGTTC TTTCCCCATA TAACCATACC	1020
	TACACTTGAT AGTTTTATC TGTGGGCGA AAAAGAACCT TTTCTTATTT TGCATTTCCC	1080
	TGATTATAAA AAAAAATGGT GAGATTGGGG TTATTTTCAT GTTTATTGGC CATTTATAGT	1140
35	TTACTGTGGA TTGTTGTAT CCCTTACCTG CTTTCTATG GGTATGTGT GGATATATG	1200
	TTTTTATTTG TTCAGCATCT CCTTCCCCAT CTCTGGTAA CACAACCTTT ATTTATTTGT	1260
40	GGGGAACCTA TTCCCTGTGG CTTAGGTGAG CATGTGACCA GGCCTGGCCT CCTGAGTCCC	1320
	ACAGCTTCCT AGCCACAGTG ATAAAAGAAT GGGTATATAA CTTAAGCCAG GCTAAGGAAA	1380
	GCCCTTAACA GAACTTCTGC TGGAACTACT GGAAAGAAGG CTTTATGGAG ATCCCAGGAA	1440
45	CCAAGGACCA TGTAAGCCTG AATTGTGCC ATGTGGAGAG AGTCTGTCTG AGGAGAACT	1500
	CGGATGCTAG CAGAAATGGA AAGAGAACTA AGTTCTGATG TCATTTTCTT GGAGGCCCTA	1560
50	GATCCAGCTG TGCCTAAAGC CTGCCCTACT CCGGACTTTA AAGTTTGTG AGCCAATAAA	1620
	GTCCCTTTCT TGTTTAAGAT AATTGAATTG AGTTTCTGTT CTGATTAATA TAGGTTATTT	1680
	GTATTTCTT ATTGATTTGT AGAAAACCTT TGTAATTTTA AATTCTAGAC TTTATGCACT	1740
55	ATATAAGTTA ATAAAATTAG CATGGCCTTC CATG	1774

60 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

10	GGCACGAGCG AAGGCAAGGG GGCACCAGCT CAGGACTGCA TCTGCCTGCC ATTTCCCTTC	60
	CACTCCTCCT TTCTGGAGTC TGACATTAGA AAGCCAGCGA GAAGGAAGAT TCAAACAACC	120
15	AACCTGATT TCCTGCTTCT CTTTTCATG AGTGTTCCTG TGGTCTCTGC ACCTCCTTTC	180
	TGTCCCCCGG CAGAGGGCAG TAGAGATGGC CGGCCCAAGG CCTCRGTGGC GCGACCAGCT	240
	GCTGTTCATG AGCATCATAG TCCTCGTGAT TGTGGTCATC TGCCTGATGT TATACGCTCT	300
20	TCTCTGGGAG GCTGGCAACC TCACTGACCT GCCCAACCTG AGAATCGGCT TCTATAACTT	360
	CTGCCTGTGG AATGAGGACA CCAGCACCTT ACAGTGTAC CAGTTCCCTG AGCTGGAAGC	420
25	CCTGGGGGTG CCTCGGGTTC GCCTGGGCCT GGCCAGGCTT GCGGTGTACG GGTCCCTGGT	480
	CCTCACCTTC TTTGCCCCC AGCCTCTCCT CTTAGCCCAG TGCAACAKTG ATGAGAGAGC	540
	GTGGCGSCTG GCAGTGGGCT TCCTGGCTGT KTCCTCTGTG CTGCTGGCAG GCGGCCTGGG	600
30	CCTCTTCCTC TCCTATGTGT GGAATGGGTC ARGCTCTCCC TCCCGGGGCC TGGGTTCCTA	660
	GCTCTGGGCA GCGCCCAGSC CTTACTCATC CTCTTGCTTA TAGCCATGGC TGTGTTCCTT	720
35	CTGAGGGCTG AGAGGGCTGA GAGCAAGCTT GAGAGCTGCT AAAGGCTTAC GTGATTGCAA	780
	GGGTTCAGTT CCAACCATGG TCAGAGGTGG CACATCTGCT CAGCCATCTC ATTTTACAGC	840
	TAACGCTGAT CTCCAGCTCC AGCGATGGAA CCCACTACAG AGGAGGTGGG GCCCCGTGTG	900
40	CAAAGAGGCC GAGGGGCAGC AAGGGCAGMC AGGGCACCTG TGAATTCTTA GTACAAGATT	960
	GTCTGTCTCT CAGGACTTCC AAGGCTCCCA AAGACTCCCT AAACCATGCA GCTCATTTGTC	1020
45	ACACCAATTC CTGCTTTAAT TAATGGATCT GAGCAAATCT TCCTCTAGCT TCAGGAGGGT	1080
	GGGAGGGGAG TGATTGCTGT CATGGGGCCA GACTTCCAGG CTGATTTGCC AAATGCCAAA	1140
	ATGAAACCTA GCAAAGAAGT TACGGCAACA AACGAGGACA TTAAAAGAGC GAGCACCTCA	1200
50	GTGTCTCTGG GGACATGGTT AAGGAGCTTC CACTCAGCCC ACCATAGTGA GTGGGCCGCC	1260
	ATAAGCCATC ACTGGAACTC CAACCCAGAG GTTCCAGGAG TGATCTCTGA GTGACTCAAC	1320
55	AAAGACAGGA CACATGGGGT ACAAAGACAA GGCTTGACTG CTTCAAAGCT TCCCTGGACC	1380
	TGAAGCCAGA CAGGGCAGAG GCGTCCGCTG ACAAATCACT CCCATGATGA GACCTGGAG	1440
	GACTCCAAAT CCTCGCTGTG AACAGGACTG GACGGTTGCG CACAAACAAA CGCTGCCACC	1500
60	CTCCACTTCC CAACCCAGAA CTGGAAAGA CATTAGCACA ACTTACGCAT TGGGGAATTG	1560

	TGTGTATTTT CTAGCACTTG TGTATTGGAA AACCTGTATG GCAGTGATTT ATTCATATAT	1620
-5	TCCTGTCCAA AGCCACACTG AAAACAGAGG CAGAGACATG TACTCTGGTG TGATCTCTTG	1680
	TCCTCAGTGT CTCTTCTGGG CTCTGTCCC TCTTGCTTTA TAGCTAGCTG CCCGGGGACC	1740
	AAGGTACAGG TGAAAGCAAG GTAGCAGCTT GCGGGAGGAG GCCTGTCTGG CTTACCAGTC	1800
10	TATACACTGT GGCCTCAACC TCCCAGACAG GGCAGAGAAC TGTGGGCAGC TCGTTTGCTT	1860
	TCTAGGCTGG CTGGAGAGGT GGGAGCTCAT TGATAGACTC ATGATGGAAA CTATTTTGA	1920
15	AACAGGCTTC CTCCTTCAGG AGAGATCATG CGGACTAAAC TGTAGCAATT CCAGTGCACC	1980
	TGGCAGTGAT CCTTTCTTT GCAAAGTACT GTCTCTTTGG TTCCAGTAAG TTGGACCACC	2040
	ACATGACATY ATTTTCCCTG GAACCTGGTC ACTGACTAAC ACAGACAATT GGGACTCCAG	2100
20	AGCCTCAAGA GCCAGGAGAG GGCACAGTAC ATACAGAGGG AGTCAAATGG GATCTCATTT	2160
	TGAGTCCTGC CTCCGCACA CTCAGAACGG CANCCCCAAG GCCCGGAGTG TCCAGGGCTT	2220
25	CTGGCCTGAG GTGAATCTGC CAGGCCAAG AAGGCACAAA GGTAGGAGCA CAGAGAGCCC	2280
	CATTCCACA GCGGKCGGC CCAGCAGCAC CAGTGAAGC TCAGCTGTCC TCCAGCTGCT	2340
	CTCGGCAGAC AGTTCAGTGC ACAGTTTATG CCCTAGCTGA AAAAGATCTC CCGGACGTAT	2400
30	TTCAGCACAT CCTCTCCTC CTCCTCCTCA GGGCTCCTGC TACAGGCAGA GCTGGAACCC	2460
	CCCGCCTCT GGAAGGGCT GAGGCCTGGA GYCACTGCCT GTC	2503

35

(2) INFORMATION FOR SEQ ID NO: 96:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

	CTGGAAGCC GAGGGTAGCC GAGCGGGCG GCGCTCTGG AGCGCGGGT GCTCGGGCTG	60
50	CCGTCCGCTC CGCCAGAAGC ACCGAGCAGC CGAGCCGGG CCCGCCGCC TCCTCCTCCA	120
	TGAGGCCCGA GTGAGGCGCG GCGCTATAG CCGACCCGCG GCGCTTCCC CCCGCGTCTT	180
	ATCGCGAGCG CACGACMAGC GCCCCCTGGA GGAGGAGGCG GAGGAGGAGG AGCATGTCGG	240
55	ACGGTTTCGA TCGGGCCCCA GGTGCTGGTC GGGGCCGAR CCGGGGCTG GGCCGCGGAG	300
	GGGGCGGGC TRAGGCGGC GGTTYCCGA AMGGARCGGR GCCTGCTGAG CGGRCGGGC	360
60	ACCAGCCGCC GCAACCCAAA GCCCCGGGCT TYCTGCARCC AMCGCCGCTG CGCCARCCCA	420

	GGACGACCCC GCCGCCAGGG GCCCAGTGCG AGGTCCCCGC CAGCCCCCAG CGGCCTTCCC	480
	GGCCCGGGGC GCTCCCAGAG CAAACGAGGC CCCTGAGAGC TCCACCTAGT TCACAGGATA	540
-5	AAATCCCACA GCAGAACTCG GAGTCAGCAA TGGCTAAGCC CCAGGTGGTT GTAGCTCCTG	600
	TATTAATGTC TAAGCTGTCT GTGAATGCCC CTGAATTTTA CCCTTCAGGT TATTCTTCCA	660
10	GTTACACAGA ATCCTATGAG GATGGTTGTG AGGATTATCC TACTCTATCA GAATATGTTT	720
	AGGATTTTTT GAATCATCTT ACAGAGCAGC CTGGCAGTTT TGAAACTGAA ATTGAACAGT	780
	TTGCAGAGAC CCTGAATGGT TGTGTTACAA CAGATGATGC TTTGCAAGAA CTTGTGGAAC	840
15	TCATCTATCA ACAGGCCACA TCTATCCCAA ATTTCTCTTA TATGGGAGCT CGCCTGTGTA	900
	ATTACCTGTC CCATCATCTG ACAATTAGCC CACAGAGTGG CAACTTCCGC CAATTGCTAC	960
20	TTCAAAGATG TCGACTGAA TATGAAGTTA AAGATCAAGC TGCAAAAGGG GATGAAGTTA	1020
	CTCGAAAACG ATTTATGCA TTTGTACTCT TTCTGGGAGA ACTTTATCTT AACCTGGAGA	1080
	TCAAGGGAAC AAATGGACAG GTTACAAGAG CAGATATTCT TCAGGTGGT CTTGAGAAT	1140
25	TGCTGAATGC CCTGTTTTCT AATCCTATGG ATGACAATTT AATTTGTGCA GTAAAATTGT	1200
	TAAAGTTGAC AGGATCAGTT TTGGAAGATG CTTGGAAGGA AAAAGGAAAG ATGGATATGG	1260
30	AAGAAATTAT TCAGAGAATT GAAAACGTTG TCCTAGATGC AAAGTGCAGT AGAGATGTAA	1320
	AACAGATGCT CTGAAGCTT GTAGAACTCC GGTCAAGTAA CTGGGGCAGA GTCCATGCAA	1380
	CTTCAACATA TAGAGAAGCA ACACCAGAAA ATGATCCTAA CTACTTTATG AATGAACCAA	1440
35	CATTTTATAC ATCTGATGGT GTTCTTTTCA CTGCAGCTGA TCCAGATTAC CAAGAGAAAT	1500
	ACCAAGAATT ACTTGAAAGA GAGGACTTTT TTCCAGATTA TGAAGAAAAT GGAACAGATT	1560
40	TATCCGGGGC TGGTGATCCA TACTTGGATG ATATTGATGA TGAGATGGAC CCAGAGATAG	1620
	AAGAAGCTTA TGAAAAGTTT TGTTTGGAAT CAGAGCGTAA GCGAAAACAG TAAAGTTAAA	1680
	TTTCAGCATA TCAGTTTTAT AAAGCAGTTT AGGTATGGTG ATTTAGCAGA ACACAAGAGA	1740
45	GCAAGAAAAT GTGTCACATC TATACCAAAT TRAGGATGTT GAGTTATGTT ACTAATGTAT	1800
	GCAACTTTAA TTTTGTTTAA CACTATCTGC CAAAATAAAC TTTATTCCCT ATAACTTAAA	1860
50	ATGTGTATAT ATATATAATA GTTATTATG TACAGTTAAT TCTACTGTTT TGGCTGCAAT	1920
	AAAATCGATT TTGAAATAAA TGAAATGTTG AAAATTTTGC TAGTTGGTTA GATGCTTATC	1980
	CTTTAAATTC TACTTTTCTT GAGGGGAAAA AGTCTTCGTC TGGAAATACA TATTACTGCA	2040
55	AAAATGTAGC ATCCTTTTTT AGGTAGGAGT ATTATAGCTT YCATTTTAGT TKGACATTTA	2100
	GTGTCCCAAT GAATTGAATT TCAAATATGA ATCATAATCT TGAAAATCTT TAGCACTAAA	2160
60	GTCTTGGGAA TATATCAACA ACTGATTTAC ATATGCAGAT GCTATTTGNA TACCAAGGGC	2220

TTTTAAATG TCATGGGGG GAAAAACCCA ACTTGGTGA ACTCCCAGCT AAACAACCAA 2280
 GACTTCACTG GAAGATTTAT TCCAATTCTA GGAATTGTTT TTTTATTATTT TTATTTTTTTC 2340
 5 AACTGRCTAA CTTCAATTACC TTAAAGCCTA GAACATTATT CTGCTTTATT TATATGGCTT 2400
 TCTCACTTTT ATTTTGTAGC AKGGGTGCA TCGACTTTT TACTAGAGAA TTTTACTAGA 2460
 10 TATTTGTCAT TCAAGTTTTC ATCTGCTTTA TAATTGATAC ACCTTGAGGG TCACTTTTCT 2520
 AATACTTTTA CTATAATGTG GTACCACCTC AGCCCTAATA AATAATATTT TTACCTAATG 2580
 TCAAATCTTT TTCCAGCTAA CTAAAACTG TGTACAAAAG GATTGCTTGT AAATATGCAT 2640
 15 GTAAATAGTT CTGTTAATAA CCCACTGTTT TACATTTGGT ACATCTGTGT CTGCTAATAC 2700
 AGTTAGCTTT CTCACTTTTC TGCTTGTGTTG TTCAGTCTGA ATTAAAATTA GACTTTGAAA 2760
 ATAAAGCTTA AAAAAAAAAA AAAAAAAAAA AAAAAGCTCGA G 2801
 20

(2) INFORMATION FOR SEQ ID NO: 97:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

35 ATGGAGCCAA AGACAATCAC TGATGCTTTG GCTTCTAGTA TAATTAAGAG TGTGCTGCCT 60
 AATTTTCTTC CATACAATGT CATGCTCTAC AGTGATGCTC CAGTGAGTGA ACTGTCCCTC 120
 GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG AACAGGGACA CACGAGGCAG 180
 40 TGGCTGAAGG GGCTGGTGCG AGCGTGGACT GTGACCGCCG GATACTTGCT GGATCTTCAT 240
 TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG CAAATCAACA AGTTAACAAT 300
 AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG GAGAAGGCCT TCATGCAGCC 360
 45 CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGYTTTC AGCYTTACCG CCGACCTTTA 420
 AATTTTCCAC TCAGGATATT TCTGTTGATT GTCTTCATGT GTATAACATT ACTGATTGCC 480
 50 AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT GGTTAATGTC GTTTTGGACG 540
 GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTG TGCTCTATGT TTGCTGGCTA 600
 ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCTC AGGGACGCAG AGTGATCTTC 660
 55 CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT TGATAGTTGC GGTGCTGTTG 720
 GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC TGGTCATTGT GGCTCCCCTG 780
 60 AGGGTTCCCT TGGATCAGAC TCCTCTTTTT TATCCATGGC AGGACTGGGC ACTTGGAGTC 840

CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC CTCAGTGGTG GTTGAAAAC 900
 GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG ACCTTCACTA TATTGTTTCGT 960
 -5 AAAC TGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC TGTGTGTACC TTATGTCATA 1020
 GCTTCTGGTG TTGTTCTTTT ACTAGGTGTT ACTGCGGAAA TGCAAAACTT AGTCCATCGG 1080
 10 CGGATTTATC CATTTTTACT GATGGTCGTG GTATTGATGG CAATTTTGTG CTTCCAAGTC 1140
 CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA AGTACCTTGT GGGTCAACGA 1200
 CTCGTGAACT ACGAACGGAA ATCTGGCAAA CAAGGCTCAT CTCCACCACC TCCACAGTCA 1260
 15 TCCCAAGAAT AAAGTAGTGT TCTCAACAAC TTGACCTTCC CCTTTACATG TCCTTTTTTG 1320
 TGGACTTCTC TCTTTGGAGA TTTTCCCAG TGATCTCTCA GCGTTGTTTT TAAGTTAAAT 1380
 20 GTATTTGACT TGTGTTCTCA GCATTGAGAG AGCAGCGGTG TAAGATTCTG CTGTTCTCCC 1440
 TGGATCTTCT GACATTACTG CTGTCTGAGA TTTGTATATG TGTAATACA AGTTCCTTGA 1500
 TACCCTAAAA CCTTGGATTA AACAGAATGT GCATTGTACA TCTTTAAACA AAATGTATAT 1560
 25 TAATTTATTA AATCTAGTTG TCACTTTAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC 1620
 GGTACCCAAA T 1631

30

(2) INFORMATION FOR SEQ ID NO: 98:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAGCTGGG CGAGAAGTAG GGGAGGGCAC GAGCCGCCG GGTGGCGGTT GCTATCGCTT 60
 45 CGCAGAACCT ACTCAGGCAG CCAGCTGAGA AGAGTTGAGG GAAAGTGCTG CTGCTGGGTC 120
 TGCAGACGCG ATGGATAACG TGCAGCCGAA AATAAACAT CGCCCTTCT GCTTCAGTGT 180
 GAAAGGCCAC GTGAAGATGC TGCGGCTGGA TATTATCAAC TCACTGGTAA CAACAGTATT 240
 50 CATGCTCATC GTATCTGTGT TGGCACTGAT ACCAGAAACC ACAACATTGA CAGTTGGTGG 300
 AGGGGTGTTT GCACTTGTGA CAGCAGTATG CTGTCTTGCC GACGGGGCCC TTATTTACCG 360
 55 GAAGCTTCTG TTCAATCCCA GCGGTCTTFA CCAGAAAAAG CCTGTGCATG AAAAAAAGA 420
 AGTTTTGTAA TTTTATATTA CTTTTTAGTT TGATACTAAG TATTAAACAT ATTTCTGTAT 480
 TCTTCCAAA AAAAAAAAAA AAAA 504
 60

(2) INFORMATION FOR SEQ ID NO: 99:

-5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

15	GGCACGAGGG AGGGAGCCCT CTCGTTGGG TGA CTCTTGT GTGCCCTTTA GACAGGCTGG	60
	CCTGCCGGTT CCACAGGGTA CAGTTAGGAC TTGAGTCTTT CTTTTCTGT TTTGAGTTGG	120
	TGAGTGAGTG ATAGGGTAAC ATGGGCCTTC AGGATGACCC CTTGGAAC TGCCGAGTTC	180
20	CTTAAATCTC AGCTGGGATC CTGGACCTGG GAGGCCCTG TGAGGGCCAG CTC TGAAAA	240
	ACCTGGGAGT TGATGCCGGA GCTGTGGAAG AACTCTGCTC GAGGGCAGG TGCCCTGGAA	300
	CACTGGTAGT TCTGGGGCTG GGAGGGAGAG GGGCTCCGGC TTTCTCTGAA ATGAACACTG	360
25	CTCTTCAGCA GTTCAAGTAC TTGTTCTCAA AACATTTTCT AATTGATTGG TAGGTTTCA	420
	TAAGCATTGT TTCTTTAAGG CATGGAAGG GAAGAATGCT CAAGCAAGTC ATGTTTGT	480
30	TCAGTGGGAT GGGCCCGCGT TCTCACTGCT GGGGGCTTCC CCTTCATGTG GCACCTTGT	540
	GCAGGGGCCA CCAGGCAGAC TCTTCCACC TTCTCCACT GAAGCACCAA GGGGCTTGA	600
	ACCGTAATTT GGCTAATCAG AGGCATTTT TTTGTCTAG TATCTTTCAC ACTTGTCCAA	660
35	CCGTCTTATT TTTTAAAAG TTCTGTTGCT TGTATTAAAC CGAACTAGA GAGAAATAGT	720
	TTCTGAAGCC AGTTTATTGT GAAGATCCCC AAGGGGAGGT TCGGTAGAGA AAAATAGTAA	780
40	GCTGGTTTAG AAACGACGA GGGCAAACAG CCAGGACGCA TTGGAGAGGA ATTTGCCAAA	840
	GATCTACCTT GAGATAACGC CTGTCCAGTG TCTTCACCAC GTGAATAACC AGCGCTCCAA	900
	AGTGTTTTTC TGCTTTGAAA AAAAAATTC CACAAGCTTT TAAAGGTGCA TTTAAGAATC	960
45	CATGTGACTT TAGAATGGAA CTGCCGGCCC TGGCAACTGT CACGTGTGCT AGAAGGTTG	1020
	ATGCCTCTGG AATGCATGTG ATACTCATCT CCATTTTGT TCTTGATTG CATTMTTGT	1080
50	CTTTTAGCAG ATCTGTCCCT GTGGGTGGTG TCTAAGAAGT CGGACACCTT GGTTTTGTG	1140
	TTAGATTGAG CTGGGCAGCT GCAATCAGCT TCTTTATATG CAAATTAGGC ACGACCCATC	1200
	TGTGGTTCTT GGTGGTGGC TAATGAAGTG AGGGGAGGGA GGGATGTCAC CCCAAAAGTA	1260
55	GGCCCTCCCA TTGGCTTTGG CCAGGCCAGA CACTTCACAT CGTTTACATG GTTCTGTGTA	1320
	ATTTTAAAGT TTATGTGTAT AAAGCGAAGC TGTTTCTGTG AACTGTATA TTTTGTAAT	1380
60	AAATATATTG CTACTTGAAA AAAAAAAAAA AAAAAA	1416

-5 (2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2847 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

15 GGCTAGGACA ATTTTGGTGC TTTACCTATC TCTGCAAAGA CTGGAGAATT TGGCATACCA 60
 TTAATTACAA CCACCAATCA TATCCAACAA AAGTACCCTA AAAGAAGGAC CAGTGGCCAC 120
 TCTCGAAAAA ATTTAAGTAT CAGAAGATTA AAAAGATTTT AGGATTTGGA AGCTTGTATT 180
 20 GTCTTTCCCC AATAATCATT GTTTGATCTC CAAATAGTAG CCTTATATTA GCAATRGACA 240
 GATCATTGGT TCTCCATATC TGATCATATG TTACTACTTT GGAATCAGTA TTTGGGCAAA 300
 25 TTCAAGCATT TATGCAGTGG ATATAAATGG AAATATAAAA ATATTGCCA ACCTGTCTCA 360
 GTAACCTATC ATATCTCTGT GNATCCTCAA GGAAAGCACT TTTGCTTTTA CTTAGAAAGC 420
 GTTTCAGATT TGCTTTTATAG ACTCCTGCTG TCTTCAGTAC CTGATAAAAC TTTAACCAGG 480
 30 GAAGCATTAA ACACAGTGCA GCAGCTTTTG CCCAGGCTTC TAAGTTCCTG CCGGCAGCAT 540
 TTATCAATGT AAGAACTAGG ATGCTTCCTG CAGTGGCACT ACCTTCCCCT AGAGCTGGAG 600
 35 CATGCTGCTT GGCCTTAAGC CCCAGCATGA TGAGGCTTCC CTCCTGCCAG GTCAGTAAAA 660
 GTTAGAGAGC TCAGAATTGG GTCTTGCCCTG GGTGCAGGTG GCAGGGTTTG CTGAAACCCC 720
 TAAAGAGAAG TCACCAAGGG AGGCAGGTAA TGAATGTTTC CAGAATCAGT CKGATACTCA 780
 40 TAGCAATTTT TGGCTATCTT TCAAATGTTG AATTTCCTGA TGCTGAGAGG GACTTTGATT 840
 TGATATCATT AAATCCAGGA CAGTCCCAAG AAGTGCTTGG AGTCTCGGCT CTGACAGCCC 900
 45 AAGAAGGGAA ATAACTTGTA TTAAGGAACA ACTATGAGCC AGGCCCTGAG CTGTCTCTTA 960
 GATAATAAAA CAGATGGGGA GTGGAAGAGT CATTTGCTTC AAGTTATACA GCTAGGAAAT 1020
 ACTCAAGCCA AATCTTGAAC GCAGCTCCCC CTAATTCCTG GGACAGGCAC TTTGTACCAC 1080
 50 ACACCATGGT CCACCTAAAA ACAGAAGGAT AAAAAGACTT CAGGTTTTC CACTGTGTGC 1140
 TGACCATCCC AATTATGAA TCTTCTTCAA AATGACATTT CACAGTTATA GTTAGGGCTC 1200
 55 AGAAATGGCA TTGAGGTAGC CTTATTTCTC CCCTTTAGCA GATGCTTTAA GTACACATTG 1260
 CTGACTTGAG CCCACCCCCA GGAGTTAGGA GAACATTTCC TTTTTCATGC CATCTTCCAT 1320
 60 AAATAAGGTG TTTCTTGGCC TTCAAAGATA TAGAACTTTG CAGCAGTAGT AAAAGTGAAG 1380

	GGTGTCTGTC TCTCTACTCA ACTTTATTTG AAAATGTCTG CAGCTTCACT CCTGTAGAAA	1440
	AGGAAATCTT CATATTTTAG TAAACTTAGC CGCCAGTGTA CTCTGTGAGG ATGTGGCAAT	1500
- 5	TCAAAGTCCA GTGAATCTGG CTCTCTTACT GATTCTCTGGT TTTAGTGTGT GTGTGGGGG	1560
	AGTGTGTACC TATATATAAA GGACAAGTGT GATATGTGTG TATATGTATA TACATACATA	1620
10	CATGTCCACA CACACACACA CAATATTTGA GAGCTAAGGA AAACCTCAAAG CAGCCCCCTC	1680
	ATTATCTTGC GTACTACTTC AAAGATTTCT GTCAGCCCTA ATTACAAGTG TCACCATATA	1740
	GTTGGGGCTT AGGTACTTGC TTACAGGAAG AGCAATTCCC TAGCAAAGGT CATTAGCTCC	1800
15	TAAGGCACTG AGTCAAAGTG ACAGCCCTGA AGGAAATTGC ACTCCAGCCC TCCTCCAGGA	1860
	TGTCTAATAA GATGGGAAAC TTGGATGCCC AGCCATTTTG GTGACCTGAG AGTCTAACTA	1920
20	CTCCAGTTAG ACCTAAGGGC ACAAATGCAG AATTCATGAC CTTGTAGTTG TGGCAGGGTC	1980
	TAGGAAGTCC TCTCTCCCA AGTAGAAAAT ATTCTCTTGC CATTCTGAA ATTCCACATT	2040
	CATATAATGG CTGTGCAATA CATGCTTCTC AATAAGAAAA TTAAGTGCAT GTTTACTGTG	2100
25	TGCTGATCAC ATCAGATTTT TATGTTTAAA AAAATCTCAT TATGGNITGA GTCCAGCCCA	2160
	GCTCTAAGAG AAAAAGAAGG CCCATATGGG AGACTTCAGT CTCATTATTA TTGCCTTTAT	2220
30	CCAGCAGTGC TTATRAAGCC CCCTACCCCTG TCCCATTCCA GAAACCATAA GACTCAGGCA	2280
	GTTCTTGATT CTGGAGGCCT GCCTGGTAAG ATAAGATAGT ATAATTGGA ACTGAGAACA	2340
	TACCAGAAAC AGCAGAACGA GGGCCAGAGC AGAAAAATGA AAATAAGTGG AGACACTTAT	2400
35	GGATACATTG GTGCAAAAAA AGCCACGGGS CCCATACTGG GCTTGATATG ACTTTGAGGG	2460
	GACAGCAGAT TAATACTTAA TGAGGGTTAA ACCTGACCAG TCTTTCTACA GTGACAGGCC	2520
40	ACACTGCATG AATGGGGAGA ACCAATGAAT CCATTGTCCT CTGCCTATTT TCCTGTGCAC	2580
	AGTCACATTC CCTCCTTAGG AATCTTCCCC TTCCACCCCTT TACATTAAAC AAGGGAACAC	2640
	TGAATCTTTC AAGGGAATTA CACGTTTGGG TTAATGTTTC AGTATATCAT TTTCACTG	2700
45	TAAATTATTT TGTAAAGAG AGTTACTGCT ATCCAGGAT GTTCGGACTT GGTGCCCCTG	2760
	TGCATTTGGA AATCAATAAA CTATTACTGG AAATGCCAAA AAAAAAAAAA AAAAAAAAAAN	2820
50	NAAAAAATC GAGGGGGGCC CGTACCC	2847

55

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

5	GAGATTGGTG GAGGAGAGTA AATAATCTAG AGGCAAGAGT TCACTGAGGG CCAAGGGGGA	60
	CCCCCAGAAA AAGGTATGGA GCTAACTCAT CTCTTTTACA AGGGGTGGCC ATGACTTACT	120
	GTTGCAAAGT ACTCAGTGTA TATTTAATGT TGATTGTGA ATTTTAGTTA CGAGAGGGAA	180
10	GAACAATTTT ACTTCTGTCC TTATTTCACT TGCTGAAAAG CTGTGGGACA AAATGTATGG	240
	AATAGACAAG GCCACTTTCT TTGTGATTTT TGCTTTTCAT GCATATTATT TTATTTACCC	300
15	ATAATTTCCA AGAGGTTTGG CGTTCGCCTC TCCTGCTTTT TTCTTTTCATC CACCCCTTTC	360
	CTTTTTTTGG AAGGGGGTTA TATATGAGAG TTCATTGAAG AAGTCCAGTG AGGCTGAAGT	420
	AAAGGGGCAA GATAGGGCAG TTAATAAAG AGCACTTTAT TTCTTTGAAG CCTTCTAAG	480
20	AAAGAAATGG GGGTGCGAGT GGCTTGAATC TCCCATGATG TTGGAGGGCA CTTAGTGGGG	540
	TTGAAGTATG ACATAATATT TCCCATTGGG GAAAGGAGAA TTTCTCTTAG AGGGTGGCAA	600
25	AATGCCPTTG CCCAGTGTCC CTATTTTAGG CATCTTTTCC TTCCTTATTC CTTCAGTCA	660
	GGGTGTGTCC TATACAAAAC TTCCCATCAG TTCTCCTCAA TATCCCCAT TTGTAAATGA	720
	TCACCTCTCT TTTCTAAACC CTMTTCCTGT TCAGATCCAT ACAGGATTTG CAAGGGTAGG	780
30	ATCATACATG CAAATGCCCC TTGTTTCTCT GTGTCTTCTG CAACTAGTC TCATGAAGAA	840
	TTCTGGCGTG CAGCAGGGTA GCTGAAGTTT GGGTCTGGGA CTGGAGATTG GCCATTAGGC	900
35	NTCNCTGAGA TTCCAGCTCC CTTCCACCAA GCCAGTCTT GCTACGTGGC ACAGGGCAAA	960
	CCTGACTCCC TTGGGGCCTC AGTTTCCCCT CCCCTTCATG AAATGAAAAG AATACTACTT	1020
	TTTCTGTGTG GTCTAGCATT GCTGGACACA AAGGTAGTC ATTATTGTTG TATTGGGTGA	1080
40	TGTGTGCAAA ACTGCAGAAG CTCACTGCCT ATAAGAGGAA ATAAGAGAGA AAGTGGAGGA	1140
	GAGGGACAAA AGGAGTAATT ATTTGGTATA GATCCACCCA TCCCAACCTT TCTCTCCTCA	1200
45	GTCCCTGCTC CTCATGTTTC TGGTTTGGTG AGTCCTTTGT GCCACCACCC ATAATGCTTT	1260
	GCATTGCTGC ATCCTGGGAA GGGGTATAT GGTCTCACA GTTGTGTGCA TTGTTTTTTT	1320
	GCATGCTTTC TTAATAAAAA AAAAAAAAAA ATGTTTANAG TTTTATCTTA AAAAAAAAAA	1380
50	AAAAAAAAA ACCC	1394

55 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

-5	GGMRCGAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC CGGATTATTC TATTTCCTCT	60
	CCCTCTCTCC CGCCCCGTAT CTCTTTTCAC CCTTCTCCCA CCCTCGCTCG CGTACCATGG	120
	CGGAGCGTCG GCGGCCACTC AGTCCCATTC CATCTCCTCG TCGTCCTTCG GAGCCGAGCC	180
10	GTCCGCGCCC GCGGCGGCGG GGAGCCCAGG AGCCTGCCCC GCCCTGGGGA CGAAGAGCTG	240
	CAGCTCCTCC TGTGCGGTGC ACGATCTGAT TTTCTGGAGA GATGTGAAGA AGACTGGGTT	300
15	TGTCTTTGGA CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCAGTGTG ATCARTGTGG	360
	GTTTCTTAMC TCATCCTGGC TCTTCTCTCT GTCACCATCA RCTTCAGGAT CTACAAGTCC	420
	GTCATCCAAG CTGTWCAGAA RTCAGAARAA GGCCATCCAW TCCAAAGCCT ACCTGGACGT	480
20	AGACATTACT CTGTCTCAG AAGCTTTCCA TAATTACATG AATGCTGCCA TGGTGACAT	540
	CAACAGGGCC CTGAAACTCA TTATTCTCTT CTTTCTGGTA GAAGATCTGG TTGACTCCTT	600
25	GAAGCTGGCT GTCTTCATGT GGCTGATGAC CTATGTGGT GCTGTTTMA ACGGAATCAC	660
	CCTTCTAATT CTGTCTGAAC TGCTCAITTT CAGTGTCCCG ATTGTCTATG AGAAGTACAA	720
	GACCCAGATT GATCACTATG TTGGCATCGC CCGAGATCAG ACCAAGTCAA TTGTTGAAAA	780
30	GATCCCAAGC AAAA	794

35

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

45

	TTTGCTTGCT AGTCTGAACC AAAGAGTTGT TTGGGCATTT GCTGTGTTGG CCATTTCTGG	60
	AGCAAGAGGG TCTTCTTCCT CCTTCCCCCA GCCAGCCAGC TGTCTGGGG CCAGGCTTTC	120
50	CTGGGTGGAA AGAAGTATAC CTTTCCCTGG GGCCCTAGGA TAGCAAAGTG AGCCATAGTG	180
	GGCCAGGCTG CCCTCCATGC TGGGCCCCAG CCCAGGCTCG CACTGCGCTG GATCACCTTC	240
	TTTGAGCCTT AGCCATCTCC TGTGAGGTAG GAATGAACTT GCCAGCCTTC AGGYTCGTTC	300
55	AGCTATGACC ATCTGTGCGG TCAGGGTACA CTCAGCTCTC CTCCCCAACT CCAGCAGCCT	360
	TTAAGAAGTG TCCCTTTGGC GCCCCCTGGA GGCAGAGCAC TGAGCTGGAC CCTGGGTAGA	420
60	CTCCACAGG GAGGACGGAG CTGGCCTCAG GAGTGGGACA CCCAGACTTG GCAGGGCCTT	480

CAAGAGGCCT GTGTGGGGGC CCCAGGAATC CTTAGCTGAA GCGGGGAGAC TCACTCTCCA 540
 TCTCAGGAAA TTCTAGCCCT TGCCCTCAGG GAGCCACGGT TGAGGGTGAG GCCCAACACC 600
 -5 TGCCTTAGGG CCCTGGGTGG GCAAGTCTGG GCCCTGGGGT AGGGAGGGAG ACTCAGGCCC 660
 ACACTTGGGT ATTTTCTAAT TTCAGACAAA CACACACTCA GCGCGCACTC ACTGATTCTT 720
 10 ACACATTGCC AAGATTTCAC ACATGTGACC AGGGGCCACC AAAGTCCCTG TGACCTTTGT 780
 GACTAGGATC CTAATTCTC TATTTCTCC TGGGTGCCTG GGTCTGTGTC ACCTGGGGCA 840
 GTGTGGATAA TGTTTAGTTC TGTGACACTG TTTTGTGGG GTGGCACCTG GTTCTCGAT 900
 15 GCCTGGGCTG GTGTCAGGCC CAGGACTGTA GTGCTGGGAG CAGTAAAGCT CAGCTCTGTG 960
 TAATGAGTGA TGCTATGGCT TGCTCGTGTC TTATGATCCA ATCCTTTTCT ACATCAGCCC 1020
 20 TTGTTTGTGTT TTATGGCTAG TCTTATCTGG CCTGGTTATT TCCTTGCGGG GAGGAGAGGG 1080
 TTTGCTAATC TGCTCCCAGC CCAACCTATT ACCACCCAC CTCGCTGGGA CCTACTGCTC 1140
 GGGAGGCAGC AGACAGGGAG CCACCAGCAG TGGCTTCCTG GCCCTGTGCT GGGGGTGGGG 1200
 25 GGAAGCTGGG GGCACATGTG GCCCTGCCT TCTGAGCAGC TCCCAGTGCC AGGGCTTTGA 1260
 GACTTTCCCA CATGATAAAA GAAAAGGGAG GTACAGAAGT TCCAATTCCC TTTTATTATT 1320
 30 GCTGGTTGGT ATCTGTAAAT GTTTAATAAA TATCTGAGCA TGTATCTATC AACGCCAAGA 1380
 ATTTCAAAGT CTCCTTCAAC AATATGAGGC TTTTAGGATG TTTATATTCC TTCATCCCTC 1440
 TTGTTTCCCA GGTTTTGAG GGAAGGAGG TCTGGAATTA TAGATACAGC TTATTATTAA 1500
 35 ATTTGTTCTT GCATAAAAAA AAAAAAAAAA AACNCNNGG GGGG- 1544

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(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

50

ACCCAGCGCT CCGNCTTGTC CACCCGGGGG CGTGGGAGTG AGGTACCAGA TTCAGCCCAT 60
 TTGGCCCCGA CGCCTCTGTT CTCGGAATCC GGGTGCTGCG GATTGAGGTC CCGGTTCTTA 120
 55 AGGTGGGTCG CTGTCCACCC GGGGGCGTGG GAGTGAGGTA CCAGATTCAG CCCATTGGC 180
 CCCGACGCCT CTGTTCTCGG AATCCGGGTG CTGCGGATTG AGGTCCCGGT TCCTAACGGA 240
 CTGCAAGATG GAGGAAGGCG GGAACCTAGG AGGCCTGATT AAGATGGTCC ATCTACTGGT 300

60

CTTGTCAGGT GCCTGGGGCA TGCAAATGTG GGTGACCTTC GTCTCAGGCT TTCCTGCTTT 360
 TCCGAAGCCT TCCCCGACAT ACCTTCGGAC TAGTGCAGAG CAAACTCTTC CCCTTCTACT 420
 -5 TCCACATCTC CATGGGCTGT GCCTTCATCA ACCTCTGCAT CTTGGCTTCA CAGCATGCTT 480
 GGGCTCAGCT CACATTCTGG GAGGCCAGCC AGCTTTACCT GCTGTTCTTG AGCCTTACGC 540
 10 TGGCCACTGT CAACGCCCCG TGGCTGGAAC CCCGCACCAC AGCTGCCATG TGGGCCCTGC 600
 AAACCGTGGG AGAAGGAGCG AGGCCTGGGT GGGGAGGTAC CAGGCAGCCA ACAGGTTCCC 660
 GATCCTTAAC GCCAGNTGCG AGAGAAGGAC CCCAAGTACA GTGCTCTCCG CCAGAATTTT 720
 15 TTCCGCTACC ATGGGCTGTC CTCTCTTTGC AATCTGGGCT GCGTCCTGAG CAATGGGCTC 780
 TGTCTCGCTG GCCTTGCCCT GGAAATAAGG AGCCTCTAGC ATGGGCCCTG CATGCTAATA 840
 AATGCTTCTT CAGAAAAAAA AAAAAAAAAA A 871
 20

(2) INFORMATION FOR SEQ ID NO: 105:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGACAGAGTT ATAGCATGGC ATTCATACTT TTGTTTTATT GCCTCATGAC TTTMTTGAGT 60
 35 TTAGAACAAA ACAGTGCAAC CGTAGAGCCT TCTTCCCATG AAATTTTGCA TCTGCTCCAA 120
 AACTGCTTTG AGTTACTCAG AACTTCAACC TCCCAATGCA CTGAAGGCAT TCCTTGTCAG 180
 40 AGATACCAGA ATGGGTTACA CATTTAACCT GGCAACATT GAAGAACTCT TAATGTTTTT 240
 TTTTAAATAA GAATGACGCC CCACTTTGGG GACTAAAAAT GTGCTATTGC CGAGAAGCAG 300
 45 TCTAAAATTT ATTTTTTTTAA AAAGAGAAAC TGCCCCATTA TTTTGGTGGG GTTGGTTTTT 360
 AATTTNTAAT NTGAAAAAAT TTTTGGGGT TTTTGGGGCC ATGG 404

50

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

60

	GTCAGACAGG TGGAGCCGCC GGGGCAGGAG TCTCAAAGAG CCAGGCTCCA GGAGAGGAAG	60
	GGCTCTRCGA GAGGAGAGAG GAGAGCGCTG GAGAGGAGAG GCTGGAGAGT CCTTAGCCAG	120
- 5	GATGGAGGCT GTTGTGAACT TGTACCAAGA GGTGATGAAG CACGCAGATC CCCGGATCCA	180
	GGGCTACCCT CTGATGGGGT CCCCCTTGCT AATGACCTCC ATTCTCCTGA CCTACGTGTA	240
10	CTTCGTTCTC TCACTTGGGC CTCGCATCAT GGCTAATCGG AAGCCCTTCC AGCTCCGTGG	300
	CTTCATGATT GTCTACAACT TCTCACTGGT GGCACTCTCC CTCTACATTG TCTATGAGTT	360
	CCTGATGTCG GGCTGGCTGA GCACCTATAC CTGGCGCTGT GACCCTGTGG ACTATTCCAA	420
15	CAGCCCTGAG GCACTTAGGA TGGTTCGGGT GGCTGGCTC TTCCTCTTCT CCAAGTTCAT	480
	TGAGCTGATG GACACAGTGA TCTTTATTCT CCGAAAGAAA GACGGGCAGG TGACCTTCCT	540
20	ACATGTCCTC CATCACTCTG TGCTTCCCTG GAGCTGGTGG TGGGGGGTAA AGATTGCCCC	600
	GGGAGGAATG GGCTCTTTCC ATGCCATGAT AAATCTTCC GTGCATGTCA TAATGTACCT	660
	GTACTIONGGA TTATCTGCCT TTGGCCCTGT GGCACAACCC TACCTTTGGT GGAAAAAGCA	720
25	CATGACAGCC ATTCAGCTGA TCCAGTTTGT CCTGGTCTCA CTGCACATCT CCCAGTACTA	780
	CTTTATGTCC AGCTGTAACCT ACCAGTACCC AGTCATTATT CACCTCATCT GGATGTATGG	840
30	CACCATCTTC TTCATGCTGT TCTCCAACCT CTGGTATCAC TCTTATACCA AGGGCAAGCG	900
	GCTGCCCCGT GCACTTCAGC AAAATGGAGC TCCAGGTATT GCCAAGGTCA AGGCCAACTG	960
	AGAAGCATGG CTTAGATAGG CGCCACCTA AGTGCCTCAG GACTGCACCT TAGGGCAGTG	1020
35	TCCGTCAGTG CCTCTCCAC CTACACCTGT GACCAAGGCT TATGTGGTCA GGACTIONGACA	1080
	GGGACTGGC CCTCCCTCC CCACAGCTGC TCTACAGGGA CCACGGCTTT GGTTCCTCAC	1140
40	CCACTTCCCC CGGGCAGCTC CAGGGATGTG GCCTCATTGC TGTCTGCCAC TCCAGAGCTG	1200
	GGGGCTAAAA GGGCTGTACA GTTATTTCCC CCTCCCTGCC TTAAACTTTG GGAGAGGAGC	1260
	ACTCAGGGCT GGCCCCACAA AGGGTCTCGT GGCCTTTTTC CTCACACAGA AGAGGTCAGC	1320
45	AATAATGTCA CTGTGGACCC AGTCTCACTC CTCCACCCCA CACACTGAAG CAGTAGCTTC	1380
	TGGGCCAAAG GTCAGGGTGG GCGGGGGCCT GGAATACAG CCTGTGGAGG CTGCTTACTC	1440
50	AACTTGTGTC TTAATTAAAA GTGACAGAGG AAACANAAA AAAAAAAAAA AAAAACTCGA	1500
	GGGGGGCCCG TACCCAAATC GCCGGTATGA TCGTAAACAA TC	1542

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(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2327 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

-5	GGTAGCTCAN TGCAGTGAAA TAGTCTTACT GGAAACAAAG CCCTTTATCA AGAATAATTA	60
	ACTCTTCCCT TTTCTTTTGG GAGAGGTGCT TTGTTTCTGA TCGGACCATT TCACTGCAGC	120
10	AAGCAACACA GTATTCTRAG CAGAAGATCG GGACTTGAGG CCATGTTGCG GAGGGCCAGT	180
	RACATTATCT GGACTCTGGA GTGTGAGGAA TATGGACTCC ACTCTTCACT ATATTCACAR	240
	CGATTGAGAC TTGAGCAACA ATAGCAGTTT TAGCCCTGAT GAGGAAAGGA GAACTAAAGT	300
15	ACAAGATGTT GTACCTCAGG CGTTGTTAGA TCAGTATTTA TCTATGACTG ACCCTTCTCG	360
	TGCACAGACG GTTGACACTG AAATTGCTAA GCACTGTGCA TATAGCCTCC CTGGTGTGGC	420
20	CTTGACACTC GGAAGACAGA ATTGGCACTG CCTGAGAGAG ACGTATGRGA CTYTGCCCTC	480
	AGACATGCAG TGGAAAGTTC GACGGAATC TAGCATTTCTC CATCCACGRG CTTCAGTTA	540
	TTCTTGAGGA TCAATTGACA GCTGCAGATC TGGTTCCAAT TTTTAATGGA TTTTAAAAG	600
25	ACCTCGATGA AGTCAGGATA GGTGTTCTTA AACACTTGCA TGATTTTCTG AAGCTTCTTC	660
	ATATTGACAA AAGAAGAGAA TATCTTTATC AACTTCAGGA GTTTTTGGTG ACAGATAATA	720
30	GTAGAAATG GCGGTTTCGA GCTGAAGTGG CTGAACAGCT GATTTTACTT CTAGAGTTAT	780
	ATAGTCCCAG AGATGTTTAT GACTATTTAC GTCCCATTCG TCTGAATCTG TGTGCAGACA	840
	AAGTTTCTTC TGTTCGTTGG ATTTCCTACA AGTTGGTCAG CGAGATGGTG AAGAAGCTGC	900
35	ACGCGGCAAC ACCACCAACG TTCGGAGTGG ACCTCATCAA TGAGCTTGTG GAGAACTTTG	960
	GCAGATGTCC CAAGTGGTCT GGTGCGCAAG CCTTTGTCTT TGTCTGCCAG ACTGTCATTG	1020
40	AGGATGACTG CCTTCCCATG GACCAGTTTG CTGTGCATCT CATGCCGCAT CTGCTAACCT	1080
	TAGCAAATGA CAGGGTTCCT AACGTGCGAG TGCTGCTTGC AAAGACATTA AGACAACTC	1140
	TACTAGAAAA AGACTATTTT TTGGCCTCTG CCAGCTGCCA CCAGGAGGCT GTGGAGCAGA	1200
45	CCATCATGGC TCTTCAGATG GACCGTGACA GCGATGTCAA GTATTTTGCA AGCATCCACC	1260
	CTGCCAGTAC CAAAATCTCC GAAGATGCCA TGAGCACAGC GTCCTCAACC TACTAGAAGG	1320
50	CTTGAATCTC GGTGTCTTTC CTGCTTCCAT GAGAGCCGAG GTTCAGTGGG CATTGCCCAC	1380
	GCATGTGACC TGGGATAGCT TTCGGGGGAG GAGAGACCTT CCTCTCCTGC GGACTTCATT	1440
	GCAGGTGCAA GTTGCCCTACA CCAATACCA GGGATTTCOA GAGTCAAGAG AAAGTACAGT	1500
55	AAACACTATT ATCTTATCTT GACTTTAAKG KKWAWKMMWW KCTCAGMSRA TTATAMTTSW	1560
	CWMMRARGSM WYMAAWSCTK SWGCTCYWCC KSRSTGRMKG MMRCTCTAGA AYTRGYRGAK	1620
60	CMYYYYSGCT KMWGGAAKKS GGCASGAGCC AGAGACCTGC ATTGCTTTCT CCTGGTTTTA	1680

TTTAACAATC GACAAATGAA ATTCTTACAG CCTGAAGGCA GACGTGTGCC CAGATGTGAA 1740
 AGAGACCTTC AGTATCAGCC CTAACCTCTC TCTCCCAGGA AGGACTTGCT GGGCTCTGTG 1800
 -5 GCCAGCTGTC CAGCCCAGCC CTGTGTGTGA ATCGTTTGTG ACGTGTGCAA ATGGGAAAGG 1860
 AGGGGTITTTT ACATCTCCTA AAGGACCTGA TGCCAACACA AGTAGGATTG ACTTAAACTC 1920
 10 TTAAGCGCAG CATATTGCTG TACACATTTA CAGAATGGTT GCTGAGTGTC TGTGTCTGAT 1980
 TTTTTCATGC TGGTCATGAC CTGAAGGAAA TTTATTAGAC GTATAATGTA TGTCTGGTGT 2040
 TTTTAACTTG ATCATGATCA GCTCTGAGGT GCAACTTCTT CACATACTGT ACATACCTGT 2100
 15 GACCACTCTT GGGAGTGCTG CAGTCTTTAA TCATGCTGTT TAAACTGTTG TGGCACAAGT 2160
 TCTCTGTGCC AAATAAAATT TATTAATAAG ATCTATAGAG AGAGATATAT ACACTTTTGA 2220
 20 TTGTTTTCTA GATGTCTACC AATAAATGCA ATTTGTGACC TGTAAAAAAA AAAWAAAAAA 2280
 ACTCGAGGGG GGCCCGGTAC CCAAATCGCC GATATGATCT AANCATC 2327

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(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 1062 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGCCGAG GCGCAACAGC CGTCTGTGCA GCTCTGGGTC CAACCGGACT AGCGAANATC 60
 TTCCTCATCC TCATCATCGT CTTCCTCATC CCGATCTCGG TCCAGGTCCC TCTCCCCCCC 120
 40 ACACAAGAGG TGGCGAAGGT CCAGCTGTAG TTCTCTGGA CGTTCTCGAA GATGCTCTTC 180
 CTCTTCTTCG TCATCATCTT CCTCTTCGTC TTCCTCATCC TCATCATCCA GTTCTCGAAG 240
 45 CCGCTCACGA ATCCCCATCC CCCCGCCGGA GRAAGTGACA GGAGGCGGCG GTACAGCTCT 300
 TATCGTTCAC ATGACCATTA CCAAAGGCAA AGAGTGCTAC AAAAGGAGCG TGCAATAGAA 360
 GAAAGAAGGG TGGTCTTCAT TGGAAAGATA CCTGGCCGCA TGA CTGATC AGAGCTGAAA 420
 50 CAGAGGTTCT CCGTTTTTGG AGAGATTGAG GAGTGACCA TCCACTTCCG TGTCCAAGGG 480
 GACAACTACG GCTTCGTCAC TTATCGCTAT GCTGAGGAGG CATTTCAGC CATTGAGAGT 540
 55 GGCCACAAGC TCGGCAGGC AGATGAGCAG CCCTTTGATC TCTGCTTTGG GGGCCGAAGG 600
 SWGTNCTGCA AGAGGAGCTA TTCTGATCTT GACTCCAACC GGAAGACTT TGACCCAGCA 660
 CCTGTAAAGA GCAAATTTGA TTCTCTTGAC TTTGACACAT TGTGAAACA GGCCAGAAG 720
 60

AACCTCAGGA GGTAACCTTG GGCCCTTCCC TGCTATCCTT TTTCTCCTTT GGAGGTGCCC 780
 AACCTCCTCC ACCCCCTTCC CCTACTCTAG GGGAGAGAGC TGCTAGTGAG ATGACTGTTT 840
 - 5 TATAAAGAAA TGGAAAAAAG TGAAATAAAA AATATGTTGA ATCAGATTTT TTAAAAGGGG 900
 TATTTGTTTT TTTATAACAG GTATTGAAAC AAGTTAACTT GCATTCTAT GTAAGATAGG 960
 AGGGGCTGAG GGGATCCCCA GTGTTTGAA CATAAGTCAC TATGCAGACT AATAAACATC 1020
 10 AACTAGAGAG NAAAAAAAAA AAAAAAAAAA ATTTAAAAAA CT 1062

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

25

GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGAAGA 60
 GCACCTACCT GTGTGGTGA GGTGTTGTTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
 30 AGGCTTCCTG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTC AACTATGAT 180
 AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG 240
 TGGATTTTCT TCCAAAATGA AAGTTGTTGC TTCTAGACTT TYAAGMKMRA TWKCCCMK 300
 35 YWAWCKGAAC AMAMKCTGSW CYTCCWSYGC SKTRRMKRYC GYKSTATRRC WARWKSAYM 360
 CCYGKMTGS RRGTAWYTSK TGCAYKAGGG AACAAATGAG GAAGTTTGT CTTTTTCCA 420
 40 TCGATACCA CAACTGCTTT TAGAACTTGA CAACGTAATT TCTGTTCTTT TTCAGAACAG 480
 TAAAGAAAGG GGTAAAGAAC TGAAGGAAAT CTGCCATTCT CAGTGGACAG GCAGGCATGA 540
 TGCTTTTGAA ATTTTAGTGG AACTCCTGCA AGCACTTGTT TTATGTTTAG ATGGTATAAA 600
 45 TAGTGACACA AATATTAGAT GGAATAACTA TATAGCTGGC CGAGCATTG TACTCTGAGT 660
 GCAGTGTGAG ATTTTGATTT CATTTGTTACT ATTGTTGTTT TTAAAAATGT CCTATCTTTT 720
 50 ACAAGAGCCT TTGGGAAAAA CYYCMAGGGG CAAACCTCTG ATGTCTTCTT TGCKKMSRT 780
 ARMTTTTGAY ATRMARYACT RMTKSAYTY AAYGRWGTGA CWSGAWAATA TTRAASYTA 840
 TACAATKAAT YWTRRYTSM KRMAGMYAAT CCGAAAYTGT GGMAAMYAAA CTTGATATTC 900
 55 AAATGAAACT CCCTGGGAAA TTCCGCAGAG CTCACCAGGG TAACTTGGA TCTCAGCTAA 960
 CCTCTGAGAG TTAATAATAA GAAACCCTAA GTGTCCCAAC AGTGGAGCAC ATTATTCAGG 1020
 60 AACTTAAAGA TATATTCTCA GAACAGCACC TCAAAGCTCT TAAATGCTTA TCTCTGGTAC 1080

	CCTCAGTCAT GGGACAACCTC AAATTCAATA CGTCGGAGGA ACACCATGCT GACATGTATA	1140
-5	GAAGTGACTT ACCCAATCCT GACACGCTGT CAGCTGAGCT TCATTGTTGG AGAATCAAAT	1200
	GGAAACACAG GGGGAAAGAT ATAGAGCTTC CGTCCACCAT CTATGAAGCC CTCCACCTGC	1260
	CTGACATCAA GTTTTTTCCT AATGTGTATG CATTGCTGAA GGTCCGTGTG ATTCTTCCTG	1320
10	TGATGAAGGT TGAGAATGAG CGGTATGAAA ATGGACGAAA GCGTCTTAAA GCATATTTGA	1380
	GGAACACTTT GACAGACCAA AGGTCAAGTA ACTTGGCTTT GCTTAACATA AATTTTGATA	1440
15	TAAACACGA CCTGGATTTA ATGGTGGACA CATATATTAA ACTCTATACR AKTAMGTCAG	1500
	MGCTYYCTAC AKAYRAYTCM SWAWMTGTGG AAARYWSSA MGMSWGCWKK TMMRRITMCG	1560
	GMWWTYYMK RKTYGAYMYW YGCGWMCAG AAAAAGCCGT AAGGTGTATG TAGACCACTT	1620
20	AATCACTAAA TATCTTTGCC TATAGGACTC CATTGAATAC ATTAGCCATT GATAATCTAC	1680
	CTGTTTAAAT GGCCCTGTG TGAAGTCTCA AGCTTTGAAG ACCTACCTGT TCTTCCAGAA	1740
	GAGAACGTTG AAAGTGCCAT GTTTCCTTTT GCGTGATCTC TGTGATGGC ACTCTGGAAT	1800
25	TGTTTCCAGT TTAAKTCATT TTAGACATAG CATTATTAT CACTGTGGAT CTCTACTTGT	1860
	TGGGTGTTAT GAATTCCTTG AAGAATATAT TTTGAAGAGG TGTGGGAGGA AGGAATACAT	1920
30	TTTATAAAAT GTTGTAGTGA AGCCACAAT TGACCTTKGA CTAATAGGAG TTTTAAGTAT	1980
	GTTAAAAATC TATACTGGAC AGTTACAAGA AATTACCGGA GAAAAGCTTG TGAGCTCACC	2040
35	AAACAAGGAT TTCAGTGTAG ATTTTGTCTT TCTTGAACCT AAAGAAACAA ATGACAAAGT	2100
	TTGAATGGAA AAGCCTGCTG TTGTTCCACA TCTCGTTGCT GTTTACATTC CTTTGTGGAG	2160
	CCTACATCTT CCTAAGCTTT TTAGCAGGTA TATGTTGAAC ACTTCTGTTT CATGGTTGAG	2220
40	ACAGAATCAG AGGCCATGGA TACTGACAAC TGATTTGTCT GTTTTTTTTC TCTGTCTTTT	2280
	TCCATGACTC TTATATACTG CCTCATCTTG ATTTATAAGC AAAACCTGGA AAACCTACAA	2340
45	AATAAGTGTT GTGGTTTATC TAGAAAAATA TGGAAAATAT TGCTGTTATT TTTGGTGAAG	2400
	AAAATCAATT TTGTATAGTT TATTTCAATC TAAATAAAAT GTGAATTTTG TTWWATTAAA	2460
	AATTWGSAC AAABTBGHGG GGGDTCCAAA CHTWVTCGHG KAAMTTCTCT WAARMATYTK	2520
50	ATAAACMSCT TCACAATTC	2539

55 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

5	AGCATGAAGC CGATGGCCGT GGTGGCCAGT ACCGTCCTGG GCCTGGTGCA AAACATGCGT	60
	GCGTTTGGCG GGATCCTGGT GGTGGTCTAC TACGTATTTG CCATCATTTGG GATCAACTTG	120
10	TTTAGAGGCG TCATTGTGGC TCTTCCTGGA AACAGCAGCC TGGCCCCCTGC CAATGGCTCG	180
	GCGCCCTGTG GGAGCTTCGA GCAGCTGGAG TACTGGGCCA ACAACTTCGA TGACTTTGCG	240
	GCTGCCCTGG TCACTCTGTG GAACTTGATG GTGGTGAACA ACTGGCAGGT GTTCTGGAT	300
15	GCATATCGGC GCTACTCAGG CCCGTGGTCC AAGATCTATT TTGTATTGTG GTGGCTGGTG	360
	TCGTCTGTCA TCTGGGTCAA CCTGTPTCTG GCCCTGATTC TGGAGAACTT CCTTCACAAG	420
20	TGGGACCCCC GCAGCCACCT GCAGCCCCCTT GCTGGGACCC CAGAGGCCAC CTACCAGATG	480
	ACTGTGGAGC TCCTGTTTCTG GGATATTCTG GAGGAGCCCG GGGAGGATGA GCTCACAGAG	540
	AGGCTGAGCC AGCACC CGCA CCTGTGGCTG TGCAGGTGAC GTCCGGGCTG CCATCCCAGC	600
25	AGGGGCGGCA GGAGAGAGAG GCTGGCCTAA CACAGGTGCC CATCATGGAA GAGGCGGCCA	660
	TGCTGTGGCC AGCCAGGCAG GAAGAGACCT TTCTCTGAC GGACCACTAA GCTGGGGACA	720
30	GGAACCAAGT CCTTTGCGTG TGGCCCAACA ACCATCTACA GAACAGCTGC TGGTGCTTCA	780
	GGGAGGCGCC GTGCCCTCCG CTTTCTTTTA TAGCTGCTTC AGTGAGAATT CCCTCGTCTGA	840
	CTCCACAGGG ACCTTTTCTG CAAAAATGCA AGAAGCAGCG GCCTCCCTTG TCCCTGTCAG	900
35	CTTCGGTGGT GCCTTTGCTG CCGGCAGCCC TTGGGGACCA CAGGCCTGAC CAGGGCCTGC	960
	ACAGGTAAAC CGTGAGTCTG TCTCATCTAT TCACAGCTGG GAATGATACT AATACCTCCG	1020
40	ATTTTAGCCC AGCACCACAG GGTACGTTCC AGTTTTTCTC TCTTTCCATA GCTGTAAGGC	1080
	CCTTCTGGG AATGGTTCTC ATTCTCCTTA ATCTATTATT GGGTCAGTTT TCCTGCATGT	1140
	CCCCAGCCTC CCATCACTGC CACCCACTCC CCACAGAGAT GCCCTGCTCA TCCGACTGGG	1200
45	GCTTTGACTC CCACACTGTG TACCCCTCTT GTGTGGACGC CCTGCTGCCA AAACCTTCAG	1260
	CAAACAGCTT TCCAAATGGA AGTTGTCACT GTCAGGCCTT TACAATCAGC AACAGCAAAA	1320
50	TCTACATGCT GCTGAGGGTC CTGCCTCATT AAGATGCAAT AAATATGTAA GTACATAAAA	1380
	ACAGCAATAG AAGAAACGTA ATGCTTTTATT CTCAAATATG ATGTCTACAT AGAAAAGCCA	1440
	AAATATTAA GAATAGTAAG AATTCACCCA GCACCTTTGGG AGGCCGAGGC GGGTGGATCA	1500
55	TGAGGTCAGG AGATCGAGAC CATCCTGGCT AACAGGTGA AACCCCGTCT CTACTAAAAA	1560
	TACAAAAAAT TGGCCGGGCG CAGTGGCGGG CGCCTGTGGT CCCAGCTACT GGGGAGGCTG	1620
60	AGGCAGGAGA ATGGCGTGAA CCCGGGAAGC GGAGCTTGCA GTGAGCCGAG ATTGCGCCAC	1680

TGCAGTCCGC AGTCCAGCCT GGGCGACAGA GCGAGACTCC GTCTCAAAAA AAAAAAAAAA 1740

AAAAAAAAA A 1751

-5

(2) INFORMATION FOR SEQ ID NO: 111:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AATGTTGTGG TGGTAGCATT TGGGTTAATT CTRATTATAG AGTCTCTTGG AGAGCAATGT 60

20

CCATAAACTA ATCCCAAACA ACATTGTCTT TTTRATGTTG TAGTGAACAG CAGAGAATTT 120

CAAAGGACCT TGCTAATATC TGTAAGACGG CAGCTACAGC AGGCATCATT GGCTGGGTGT 180

25

ATGGGGGAAT ACCAGCTTTT ATTCATGCTA AACAACAATA CATTGAGCAG AGCCAGGCAG 240

AAATTTATCA TAACCGGTTT GATGCTGTGC AATCTGCACA TCGTGCTGCC ACACGAGGCT 300

TCATTCGTTA TGGCTGGCGC TGGGGTTGGA GAACTGCAGT GTTGTGACT ATATTCAACA 360

30

CAGTGAACAC TAGTCTGAAT GTATACCGAA ATAAAGATGC CTTAAGCCAT TTTGTAATTG 420

CAGGAGCTGT CACGGGAAGT CTTTTTAGGA TAAACGTAGG CCTGCGTGGC CTGGTGGCTG 480

35

GTGGCATAAT TGGAGCCTTG CTGGGCACTC CTGTAGGAGG CCTGCTGATG GCATTTTACA 540

AGTACTCTGG TGAGACTGTT CAGGAAAGAA AACAGAAGGA TCGAAAGGCA CTCCATGAGC 600

TAAAACTGGA AGAGTGGAAG GGCAGACTAC AAGTTACTGA GCACCTCCCT GAGAAAATTG 660

40

AAAGTAGTTT ACAGGAAGAT GAACCTGAGA ATGATGCTAA GAAAATTGAA GCACTGCTAA 720

ACCTTCCTAG AAACCCCTCA GTAATAGATA AACAAGACAA GGACTGAAAG TGCTCTGAAC 780

45

TTGAAACTCA CTGGAGAGCT GAAGGGAGCT GCCATGTCCG ATGAATGCCA ACAGACAGGC 840

CACTCTTTGG TCAGCCTGCT GACAAATTTA AGTGCTGGTA CCTGTGGTGG CAGTGGCTTG 900

CTCTGTCTTT TTTCTTTTCT TTTTAACTAA GAATGGGGCT GTTGTACTCT CACTTTACTT 960

50

ATCCTTAAAT TTAAATACAT ACTTATGTTT GTATTAATCT ATCAATATAT GCATACATGA 1020

ATATATCCAC CCACCTAGAT TTTAAGCAGT AAATAAAACA TTTTCGCAAAA GATTAAAGTT 1080

55

GAATTTTACA GTTAAAAAAA AAAAAAAAAA AAAAAA 1117

60

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

10 GGCAGAGGTT TTCTTATATT TTAAGTAAAT TTAAAGTGGC TATCAGAATA TTTATTCTTG 60
TTTGAGACTA CCAACATAAC TACGTGTGTA AGGTGCTTCA CAGAGAATAT ATTGCCTTTA 120
ATGTGAAATA ATTTTCACCA ATGTTGCTAA CTTTAATAAA GTATAAAATT TGTAGAATAT 180
15 TCAGTTAAGT AGTTGGTAAC CCTTTTCTAT TTTAGTAAAA CTTAATGCAT GTTTACTTTT 240
TTTTGAAAGA TGCAGACAAT CTCTTTGAAC ATGAATTGGG GGCTCTCAAT ATGGCTGCAT 300
TACTACGAAA AGAAGAAAGA GCAAGTCTTC TTAGTAATCT TGGCCCATGT TGTAAAGCGT 360
20 TGTGCTTCAG ACGGGATTCT GCAATTCGAA AGCAGCTTGT TAAAAATGAG AAGGGCACCA 420
TAAAACAAGC TTACACGAGT GCTCCAATGG TAGACAATGA ATTACTTCGA TTGAGTCTTC 480
25 GGTATTTTAA GCGGAAGACT ACTTGCCATG CTCCAGGACA TGAAAAGACT GAAGATAATA 540
AACTTTCACA GTCCAGTATC CAACAGGAAC TGTGTGTGTC TTAAGACCGA AGTTACAATA 600
TGGTATTTTT GGTACTGTCT TCCTTCAGCA GTGCATATTC TTTTGCAAAG TTCTTTGGTT 660
30 TGACAAGCAT TAGTGACAAA GGCAGAAAAG ATTTATCAGC CATGCTAAAA GAGTGAAGAA 720
TTTTGATCTT TAGAGACACT AGTTTTGGCC AACTTAAGAT TTTACGTTAA TTTTACATA 780
35 GTATTTGACA CTCATGCAAA ATAATGTGAA AACATCTAGA TTTAGTAGTT TATTCTGCGC 840
CTTTTGTTAA AACTGAAGAT TTTGAAAAT GGTGTCACT GCTCTCCAG CCTATGAATA 900
TTTTTGTGAA ATGGAACCAT GGATTTATGT CTGGATCATC CATACAGAAC CAACAATTTT 960
40 ATTCAAAAAC AATGTGTTCA TCAAAGTAAT TGCTCACATT GTGCAGTACT ATGTTGTACA 1020
GACCACGTGA AAGGGAATGC TGGTCTAGCT GCGTGGTAT GTTTATAGGC GAATTTCAGC 1080
45 AGAAGGAAGC CAAAATAGTT TTTTCCTTTT GAAAGTTTTT TAAAAATTAT TTCATGGGTC 1140
TTTTTTTAA TTAATATGTG TGCATTGTTA CAATGTATGT TGGGATGTCT TTTGACCCTA 1200
AATGCTTTTT TTGTTATCAG AGATTGTGTA CTATTTTAT TTTAATAAAA TGTATCTTCC 1260
50 CTTTTMAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 1313

55

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

-5	ACAGGGACAG AATACTTTCT TTCCTTCCTT CAAGTACAAG AAGGCTTTCT CTACCATTG	60
	CGTCTACACT TTATTTTAAA AGCTATCCTT TTCTAGTAGT ATTTTATCAT GGCAATGGCA	120
10	TGATGACAAC AACAGTCTTT CATTACAGAC TGAAGGGAAG CATGTCCTTA CTTAAAATAG	180
	TTCTGCTACT TTCCTCCTA TTATAAGGAA ATTTTACAGA TTCTAAAAAT ACCTTAATTT	240
15	TTCTTTGATT TTTATTTTAC CAAGTCACAA ATGTCTTTT GATGTTTTGA GAATTGTTCT	300
	CATAGAATCA CAAATACTGA CATTTCATTA GATGATTATT TTCCTAGAAT CCCCAGAG	360
	CAGTGGCAGT CCATGGCTTG GTGAAGCTA GAAATTTTCC TGCCCTGGT GACCTGGTAA	420
20	GCCTCCTGCT CGGAACCGTG TGAGTGGGTG AGGAAGATGA GAGATGGTCA GATGGAAGAG	480
	AGRAATACAT GAACTGCTCT GGCCTCTCTG GTTCTGTTCT TGGCCAGAG TTTTGAAAA	540
25	GCAGCGGANA TNGACTGACT TCACATGCTC AGCTTTCTCA GCCTTTTGTT TATTTTGTG	600
	TCCTTAGATT TCCCTGTTGT AAAAGGGGCA AGAAAAGTAA CTCATCATCT CTAACACACC	660
	ATGGCAGCTT AGCCAGGTAG TCTTAGTGGT GGTGTTTAGG CATAAGATAT GCTGATCATC	720
30	AGTCTCAGGC CACAGTTTCC TTCACTAATC GTCCAGCTTG AGTGTCTGT TCTCTTCCTG	780
	CCCATTTCCT TGAACCTCCT GCTCTAGCCT TGGCGGAGGG AGAGTGCTAT TTGCTTTTGT	840
	TCTCCCTCTG TCTTAGGAAA AGCCATCTTT AATATAGTTC TTCACCACTG TTGGGGTTGT	900
35	<u>TTTGIGATT</u> <u>TTTTTTCTT</u> <u>CGAAGA</u> <u>ACT</u> <u>CCTGGT</u> <u>TGTT</u> <u>ATTGGATT</u> <u>TT</u> <u>GTATTTAAT</u>	960
	ACAAATTATT GAATTTTATA AGCTTGTA CAATATTTAA TTAGTGTGAA AGGAAACAAA	1020
40	GAATGCAGGA AAAATAATTT AATATCAACC TCAGTTGACA AGGTGCTCAG ATTATTCAAT	1080
	TCGGGATCCT CCTTTTGTTA GGTTTTGTAG ACAACCCTAG ACCTAACTG TGTCACAGAC	1140
45	TTCTGAATGT TTAGGCAGTG CTAGTAATTT CCTCGTAATG ATTCTGTTAT TACTTTCCTA	1200
	TTCTTTATTC CTCTTCTTC TGAAGATTAA TGAAGTTGAA AATTGAGGTG GATAAATACA	1260
	AAAAGGTAGT GTGATAGTAT AAGTATCTAA GTGCAGATGA AAGTGTGTTA TATACATCCA	1320
50	TTCAAAATTA TGCAAGTTAG TAATTACTCA GGGTTAACTA AATTACTTTA ATATGCTGTT	1380
	GAAYCTACTC TGTTCCCTGG CTAGAAAAAA TTATAAACAG GACTTTGTAG TTTGGGAAGC	1440
55	CAAATTGATA ATATTCTATG TTCTAAAAGT TGGGCTATAC ATAAATTATT AAGAAATATG	1500
	GATTTTATT CCCAGGATAT GGTGTTTATT TTATGATATT ACGCAGGATG ATGTATTGAG	1560
	TAAATCAGT TTTGTAAATA TGTAATATG TCATAAATAA ACAATGCTTT GACTTATTTT	1620
60	CAAAAAAAA AAAAAATAAA NTTCGAGGGG GGGC	1654

-5 (2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

15 GGCAAACTTT CCCCCAANGC TTCGAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60
 GGGTTCGCNC GCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120
 CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180
 20 CTGCMCCTCA TCTTCCTGCG CCGACCTGCG CGGGTAAGG GGWAGTTTCA GACTGTGAAG 240
 GACGTCGTGC TGGACTGCCT GTTGGACTTC TTACCCGAGG GGGTGAACAA AGAGAAGATC 300
 25 ACACCACTCA CGCTCAAGGA AGCTTATGTG CAGAAAATGG TTAAAGTGTG CAATGACTCT 360
 GACCGATGGA GTCTTATATC CCTGTCAAAC AACAGTGGCA AAAATGTGGA ACTGAAATTT 420
 GTGGATTCCC TCCGGAGGCA GTTTGAATTC AGTGTAGATT CTTTTCAAAT CAAATTAGAC 480
 30 TCTCTTCTGC TCTTTTATGA ATGTTCAAGAG AACCCAATGA CTGAGACATT TCACCCACACA 540
 ATAATCGGGG AGAGCGTCTA TGGCGATTTC CAGGAAGCCT TTGATCACCT TTGTAACAAG 600
 35 ATCATTGCCA CCAGGAACCC AGAGGAAATC CGAGGGGGAG GCCTGCTTAA GTACTGCAAC 660
 CTCTTGGTGA GGGGCTTTAG GCCCGCCTCT GATGAAATCA AGACCCCTCA AAGGTATATG 720
 TGTTCAGGT TTTTCATCGA CTTCTCAGAC ATTGGAGAGC AGCAGAGAAA ACTGGAGTCC 780
 40 TATTTGCAGA ACCACTTTGT GGAATTTGGA AGACCGCAAG TATGAGTATC TCATGACCCT 840
 TCATGGAGTG GTAAATGAGA GCACAGTGTG CCTGATGGGA CATGAAAGAA GACAGACTTT 900
 45 AAACCTTATC ACCATGCTGG CTATCCGGGT GTTAGCTGAC CAAAATGTCA TTCCTAATGT 960
 GGCTAATGTC ACTTGCTATT ACCAGCCAGC CCCCTATGTA GCAGATGCCA ACTTTAGCAA 1020
 TTACTACATT GCACAGGTTT AGCCAGTATT CACGTGCCAG CAACAGACCT ACTCCACTTG 1080
 50 GCTACCCTGC AATTAAGAAT CATTTAAAAA TGTCTGTGG GGAAGCCATT TCAGACAAGA 1140
 CAGGAGAGAA AAAAAAAAAA AAAAAAAAAA A 1171

55

(2) INFORMATION FOR SEQ ID NO: 115:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

	GGTCTGCGCC GGAAGTGCAT GAGCTGCCGA TGTGGTGCCTT AGTGATTGCG GTTTCGGTCCG	60
10	CTCTCCCGTG TTTCCCGGGC TGGGTATTTG CCTCGCACCA TGGCGCCCAA GGGCAAAGTG	120
	GGCAGCAGAG GGAAGAAGCA GATATTTGAA GAGAACAGAG AGACTCTGAA GTTCTACCTG	180
15	CGGATCATAC TGGGGGCCAA TGCCATTTAC TGCCTTGTGA CGTTGGTCTT CTTTACTCA	240
	TCTGCCTCAT TTTGGGCCTG GTTGGCCCTG GGCTTTAGTC TGGCAGTGTA TGGGGCCAGC	300
	TACCACTCTA TGAGCTCGAT GGCACGAGCA GCGTTCTCTG AGGATGGGGC CCTGATGGAT	360
20	GGTGGCATGG ACCTCAACAT GGAGCAGGGC ATGGCAGAGC ACCTTAAGGA TGTGATCCTA	420
	CTGACAGCCA TCGTGCAGGT GCTCAGCTGC TTCTCTCTCT ATGTCTGGTC CTCTGGCTT	480
25	CTGGCTCCAG GCCGGGCCCT TTACCTCCTG TGGGTGAATG TGCTGGGCCC CTGGTTCACT	540
	GCAGACAGTG GCACCCCAGC ACCAGAGCAC AATGAGAAAC GGCAGCGCCG ACAGGAGCGG	600
	CGGCAGATGA AGCGGTTATA GCCATTGACA TTGTGGCCAC AGGCCACTGG CCCTGGGTGG	660
30	CTCTGTCAGG GTGCACAGCC CCTCATGCCT GGAGCAATGA GGGTCTAGTC CAGGGGCCAA	720
	AAGCAGTCTG AGGTATTGGG TATACTTATA CTCTATAGGG TCGTTGAATA AATGGCTTAG	780
35	AATGTGAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCC GGTACCCAAT TTCNCCTANA	840
	AT	842

40

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

50

	GGCAGCAGGC GCGGCGAGCG GTGGCGGCGG CGCCCCCGG CGGGAGCCGT TCCCTTTCCC	60
	GTCGGGGAGC GCGGGGYCGG GGCCAGGGG ACCCGGGCC ACGGAGAGCG GGAAGAGGAT	120
55	GGATTGCCCC GCCCTCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAAGAAGT TCAGAAGCAA	240
60	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTTGATCTC AGCAGTTTTG ACTTCAGAAC	300

TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT 360
 CAATCAAAAT AAGGGTAAAC CAGACTTGAA ATACAACATT GCCAATTAGA CAAACAGCAT 420
 - 5 CAATTTTCAA ACAACCGGTA ACCCAAAGTC ACAAATCATC CTAGTAATAA AGTGAAATCA 480
 GACCCACAAC GAATGAATGA ACAGCCACGT CAGCTTTTCT GGGAGAAGAG GCTACAAGGA 540
 10 CTTTAGTGCA TCAGATGTAA CAGAACAAAT TATAAAACC ATGGAACACTAC CCAAAGGTCT 600
 TCAAGGAGTT GGTCCAGTAG CAATGATGAG ACCCTTTTAT CTGCTGTTGC CAGTGCTTTG 660
 CACACAAGCT CTGCGCCAAT CACAGGGCAA GTCTCCGCTG CTGTGGAAAA GAACCTGCTG 720
 15 TTTGGCTTAA CACATCTCAA CCCCTCTGCA AAGCTTTTAT TGTACAGAT GAAGACTCAG 780
 GAAACAGAAG AGCGAGTACA GCAAGTACGC AAGAAATTGG AAGAAGCACT GATGGCAGAC 840
 ATCTTGTCGC GAGCTGCTGA TACAGAAGAG ATGGATATTG AAATGGACAG TGGAGATGAA 900
 20 GCCTAAGAAT ATGATCAGGT AACTTTTCGAC CGACTTTCCC CAAGAGAAAA TTCCTAGGAA 960
 ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA 1020
 25 TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGATG TATTTTIGAT GTATATATCT 1080
 ATTATFCAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA 1140
 TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG 1200
 30 TAGCACTTAC GTAAAACATT TGTTTCCCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC 1260
 TAAATAAATT TCCCAGTTAA AGATTATGT GACTTCACTG TATATAACA TATTTTATA 1320
 35 CTTTATGAA AGGGGACACC TGTACATTCT TCCATCGTCA CTGTAAAGAC AAATAAATGA 1380
 TTATATCCA CAGAAAAAA AAAAAAAAW MWSTYGARRR GSRGCMCRSW AYMMARWCC 1440
 CCWMRTWRGS MKTCSTMTKA YTTACATTCA ACTCTGATCC CGGGGCCTTA GGTTTGACAT 1500
 40 GGGAGGTGGG AGGAAGATAG CGCATATATT TGCAGTATGA ACTATTGCCT CTGGGACGTT 1560
 GTGAGGAATT GTGCTTTCAC CAGAATTCT AAGGATTCT GGCTTAAATA TCACCTAGCC 1620
 45 TGTGGTAATT TTTTTCCT 1640

50 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

60 TGAATTTAGN AAACACTTTG GAAAACTCAT AACCTCATCA GAACTGCCT TTAGCCACAC 60

TCCTGACCTT CTAGATGAGT AACAAAAAAA TGAAATAAGT TCTTGAAAT TAAGCCATTT 120
 ATTTTAATTT GCTATTTTTT TCAATGTTCT AGGTATCTTT AAATTTGTTA TTGTGGAATC 180
 -5 ATTTTCCTGC CAGATACCTT TATCAAAAT ATTGGCCTCA TGAGAGCTGA AGTAAGTCAG 240
 CTTTTTGGTG AACTTTAGTG GACTTCTGTG AGATTGTAGT TGTACTTTGT ATCTCTAAAT 300
 10 CTAAAGATAG TTTTATAAAA CTCCCAAAGA AAATCTGCTC TCCTTTCTGA TCTAAAAACT 360
 CATCTTTGGG GTAAAGAGTT AAGTGTCCAA AGGTTGTCAC AGTTCATGAG GTCAGAGGGA 420
 GCTAGCCTGG CACCTGGACT CTGCCATCC ACAGCTGACA GATTCCAACA GAAGTGTATT 480
 15 TAAATTCTCC AGTAGACAAT GCTGGGTAAG GGAGGGGTA GGGCTGGGTT ATTAAGATAC 540
 AGGCTGCTGT ATTTTACATT GGTGTGGGG GAAGGGGAGC CTGGAGAAAA CAAAGTCACT 600
 20 ATTCCTTTT TTGAAACAGG AAAAAAATT ATTTTGTGT CAGTAAAAAT GGTAGAGAAT 660
 TCCAATGTCC CTAGCCACAA GGGACCAGTT CCACTGAGAA GTGAACAGTG GGAAGTCAAA 720
 ATTTTCAGAAA CATTTGGGGA AGGGAAAAAT GGCTTTCTCT TAATTGGCAG ATGTTCCAGT 780
 25 GGGGSGGGGG GGCTCTGTTT TTGTTGGGAT GTGTTATGTT GTATGTACGC ATATATGGAC 840
 CGGAGTCTGC TGAGTTTATA AGGTTCCAAA AATATGGTAA AATCTGGTT TTTGTTAATT 900
 30 TATCTCAATA AAAGCCCACT GGRACCTCAA AAAAAAAAAA AAAAAAAGA NN 952

35 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

45 GACGTCATAG GTAAACAGGC TCTGTATCCG TGGCAGCGC CGTGGCAGGC TGGCTGGGTA 60
 CCGGCTGTGC CTGACCCAGG AGAAGCTGCC TGTCTACATC AGCCTGGGCT GCAGCGCGCT 120
 GCCGCCGCGG GGCCGGCAGC TGAAGTATGT GCTCTTCAGG GCGGGCACCG TGTTCATTC 180
 50 ATCTTTGTAC CCCCAGCATC TAGCAGTGTT GGCATGTAGT AGGCACTCAA GAAATGTGTG 240
 TTGAATGAAC GATGCCTGTG ACAAGCAAGC GGACTTTATT CTTTCCTGAC CCTTGCTCCT 300
 55 ATGACACACC TCCTCCTGAC TGCCACTGTC ACTCCTTCAG AGCAGAACTC CTCTAGGGAA 360
 CCTGGATGGG AAACAGCCAT GGCCAAGGAC ATCCTGGGTG AAGCAGGGCT ACACCTTGAT 420
 60 GAACTGAACA AGCTGAGGGT GTTGGACCCA GAGGTTACCC AGCAGACCAT AGAGCTGAAG 480

GAAGAGTGCA AAGACTTTGT GGACAAAATT GGCCAGTTTC AGAAAATAGT TGGTGGTTTA 540
 ATTGAGCTTG TTGATCAACT TGCAAAAGAA GCAGAAAATG AAAAGATGAA GGCCATCGGT 600
 5 GCTCGGAAC T GCTCAAATC TATAGCAAAG CAGAGAGAAG CTCAACAGCA GCAACTTCAA 660
 GCCCTAATAG CAGAAAAGAA AATGCAGCTA GAAAGGTATC GGGTTGAATA TGAAGCTTTG 720
 10 TGTAAAGTAG AAGCAGAACA AAATGAATTT ATTGACCAAT TTATTTTTC AAAATGAACT 780
 GAAAATTTTCG CTTTTATAGT AGGAAGGCAA AACAAAAAAA AGCCTCTCAA AACCAAAAAA 840
 ACCTCTGTAG CATTCCAGCG GCTTGACCAA TGACCTATGT CACAAGAGGT GGCGTGTAAG 900
 15 GAATGCAGCC CCCTGAAGAC AGCACTACAA GTCTGGGGGA GCCAGTTTTA ACATCAGTGC 960
 ACAGCTGCTG CTGGTGGCCC TGCAGTGAC GTTCTCACCT CTTATGCTTA GTTGGAAC TA 1020
 AGCAGTTTGT AAACCTTTCAT CCTTTT TTTT GTAAATTCAC AAAGCTTTGG AAGGAGAAGC 1080
 20 AATAAATTTT TGT TTTTCAA TGGCTTGATG TACCTTTT TTTT CCTGTTGCTC TTGAAATATG 1140
 TTTAACTCCT CATGAGAGAA CCCTGGATTC TCTATCCCCT AGTCCACAAA ACAAAACCAGG 1200
 25 CAGTGGTCAG CAGCTACCTT TNATTTGGAT CACACACGTG AGTCAGACAG TACCAC 1256

30 (2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1143 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

40 GGCCGTAGCA GCCGGGCTGG TCCTGCTGCG AGCCGGCGGC CCGGAGTGGG GCGGCGGCAT 60
 GTACCTTCCA CATTGAGTAT TCAGAAAGAA GTGATCTGAA CTCTGACCAT TCTTTATGGA 120
 45 TACATTAAGT CAAATATAAG AGTCTGACTA CTTGACACAC TGGCTCGAGC AAACATGAAC 180
 GTTGAGTTG CCCACAGTGA AGTGAATCCA AATACCOGTG TCATGAACAG CCGGGGTATG 240
 TGGCTGACAT ATGCATTGGG AGTTGGCTTG CTTTATATTG TCTTACTCAG CATTCCCTTC 300
 50 TTCAGTGTTT CTGTTGCTTG GACTTTAACA AATATTATAC ATAATCTGGG GATGTACGTA 360
 TTTTTCATG CAGTGAAAGG AACACCTTTC GAAACTCCTG ACCAGGGTAA AGCAAGGCTC 420
 55 CTAACCTCAT GGGAACTTTC GGACTATGGA GTACAGTTTA CATCTTCACG GAAGTTTTC 480
 ACAATTTCTC CAATAATTCT ATATTTTCTG GCAAGTTTCT ATACGAAGTA TGATCCAAC 540
 CACTTCATCC TAAACACAGC TTCTCTCCTG AGTGTACTAA TTCCCAAAAT GCCACAACTA 600
 60 CATGGTGTTC GGATCTTTGG AATTAATAAG TATTGAAATG TTTTGAACT GAAAAAAAT 660

TTTACAGCTA CTGAATTCTT TATAAGGAAG GAGTGGTTAG TAAACTGCAC TGTTCCTSTG 720
 ATAATGTGAA ATGAGAAGTA TTTACATTGG AGGGCCAATG GCTGGTCCTT CAAGTGCTGT 780
 -5 TTTGAAGTGC AGATTTCCTT TAAATGATGC CTCTGTTTAA TACACCTGGT ACATTCTGA 840
 AGAGGGGCTT TATAAGCAGG CTGGGCAGGC CCAGCTTATA AGTTAAAGGG CATCACAGTG 900
 10 AGGGTG TAGT AGATAAATTC AAGGAAATAA GAGATTTGTA AGAAACTAGG ACCAGCTTAA 960
 CTTATAATGA ATGGGCATTG TGTTAAGAAA AGAACATTTT CAGTCATTCA GCTGTGGTTA 1020
 TTTAAAGCAG ACTTACATGT AAACCGAAT CCTCTCTATA CAAGTTTATT AAAGATTATT 1080
 15 TTTATTACCG TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
 GAN 1143

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(2) INFORMATION FOR SEQ ID NO: 120:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCCCGG CCCCCACCC ACGTCTGCGT TGCTGCCCGG CCTGGGCCRG GCCCAAAGG 60
 35 CAAGGACAAA GCAGCTGTCA GGAACCTCC GCCGAGTCG AATTTACGTG CAGCTGCCGG 120
 CAACCACAGG TTCCAAGATG GTTTGCGGGG GCTTCGCGTG TTCCAAGAAC TGCCTGTGCG 180
 CCCTCAACCT GCTTTACACC TTGGTTAGTC TGCTGCTAAT TGAATTGCT GCGTGGGGCA 240
 40 TTGGCTTCGG GCTGATTTCC AGTCTCCGAG TGGTCGGCGT GGTCAATGCA GTGGGCATCT 300
 TCTTGTTCTT GATTGCTTTA GTGGGTCTGA TTGGAGCTGT AAAACATCAT CAGGTGTTGC 360
 45 TATTTTTTTA TATGATTATT CTGTTACTTG TATTTATTGT TCAGTTTCTT GTATCTTGCG 420
 CTTGTTTAGC CCTGAACCAG GAGCAACAGG GTCAGCTTCT GGAGGTGGT TGGAACAATA 480
 CGGCAAGTGC TCGAAATGAC ATCCAGAGAA ATCTAAACTG CTGTGGGTTT CGAAGTGTTA 540
 50 ACCCAAATGA CACCTGTCTG GCTAGCTGTG TTAAAAGTGA CCACTCGTGC TCGCCATGTG 600
 CTCCAATCAT AGGAGAATAT GCTGGAGAGG TTTTGAGATT TGTGGTGGC ATTGGCCTGT 660
 55 TCTTCAGTTT TACAGAGATC CTGGGTGTTT GGCTGACCTA CAGATACAGG AACCAGAAAG 720
 ACCCCGCGC RAATCCTAGT GCATTCCTTT GATGAGAAAA CAAGGAAGAT TTCCTTTCGT 780
 ATTATGATCT TGTCACTTT CTGTAATTTT CTGTTAAGCT CCATTGCCA GTTTAAGGAA 840
 60

GGAAACACTA TCTGGAAAAG TACCTTATTG ATAGTGGAAT TATATATTTT TACTCTATGT 900
 TTCTCTACAT GTTTTTTCTT TTCCGTGCT GAAAAATATT TGAAACTTGT GGTCTCTGAA 960
 -5 GCTCGGTGGC ACCTGGGAAT TTACTGTATT CATTGTCGGG CACTGTCCAC TGTGGCCTTT 1020
 CTTAGCATT TACCTGCAG AAAAAGTTT TATGGTACCA CTGTGTGGT TATATGGTGA 1080
 10 ATCTGAACGT ACATCTCACT GGTATAATTA TATGTAGCAC TGTGCTGTGT AGATAGTTCC 1140
 TACTGGAAAA AGAGTGGRAA TTTATTAAAA TCAGAAAGTA TGAGATCCTG TTATGTAAAG 1200
 GGAAATCCAA ATTCCCAATT TTTTGTGGT TTTTAGGAA AGATGTGTG TGGTAAAAAG 1260
 15 TGTTAGTATA AAAATGATAA TTWACTKGTA GTCCTTTATG ATWACACCAA TGTATTCTAG 1320
 AAATAGTTAT GYCYTAGGAA ATTGTGGTTT AATTTTGTAC TTTTACAGGT AAGTGCAAAG 1380
 GAGAAGTGGT TTCATGAAAT GTTCTAATGT ATAATAACAT TTACCTTCAG CCTCCATCAG 1440
 20 AATGGAACGA GTTTTGAGTA ATCAGGAAGT ATATCTATAT GATCTTGATA TTGTTTTATA 1500
 ATAATTGAA GTCTAAAAGA CTGCATTTT AAACAAGTTA GTATTAAATGC GTTGGCCAC 1560
 25 GTAGCAAAAA GATATTTGAT TATCTTAAAA ATTGTTAAAT ACCGTTTCA TGAAAGTTCT 1620
 CAGTATTGTA ACAGCAACTT GTYAAACCTA AGCATATTTG AATATGATCT CCCATAATTT 1680
 GAAATGAAA TCGTATTGTG TGGCTCTGTA TATCTGTGA AAAAATTAAA GGACAGAAAC 1740
 30 CTTTCTTTGT GTATGCATGT TTGAATTAAA AGAAAGTAAT GG 1782

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(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

45 GTTGGCTGCA GATTGTGGT GCGTCTGAG CCGTCTGTCC TGCGCCAAGA TGCTTCAAAG 60
 TATTATTAAA AACATATGGA TCCCATGAA GCCCTACTAC ACCAAAGTTT ACCAGGAGAT 120
 50 TTGGATAGGA ATGGGGCTGA TGGGCTTCAT CGTTTATAAA ATCCGGGCTG CTGATAAAAG 180
 AAGTAAGGCT TTGAAAGCTT CAGCGCCTGC TCCTGGTCAT CACAACCAGA TTTACTTGGA 240
 GTACATGTGA AAGAAAACGT CAGTCTGCCT GTAAATTTCA GCAAGCCGTG TTAGATGGGG 300
 55 AGCGTGGAAC GTCACGTGAC ACTGTATATA GTACCGTTTA CTTCATGGCA TGAATAAATG 360
 GATCTGTGAG ATGCACTGCT ACCTGGTACT GCTTTCAGTG TGTCCCCCT CAGCCCTCCG 420
 60 GCGTGTGAG CATACTCTGA GTAGATAATT TGTCATGCAG CGCATGCAAT CAGAATCTCA 480

CTGAGCCACC CATCATTTGTG AAATAATTAC CTCAGTTGTA CAGGACTTGG TGATCAGGAT 540
CCAGGCACCTC ACTTGTATTTC TACTGCTCAA TAAACGTTTA TTAAACTTGA AAAAAAAAAA 600
AAAAAAAAAA 610

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GGTACGCCTG CAGGTACCGG TCCGGAATTC CGGGTCGCCC ACGCGTCNGG CCACGCGTCC 60
ACCCACGCGT CCGSCCAGCG GTCGGAGCCG AGCCGGACTG GTCAGGATGA TCACGGACGT 120
GCAGCTCGCC ATCTTCGCCA ACATGCTGGG CGTGTGCTC TTCTTGCTTG TCGTTCTCTA 180
TCACTACGTG GCCGTCAACA ATCCCAAGAA GCAGGAATGA AAGTGGCGCT TTCTCCGCCC 240
CAGGGTTCCA GGACATAGTC TGAGGCAAGA TGGAGGGTAT GAGGGGCCTT CACACTTCAC 300
TTCATCCCTT CTACCCATCA CAACATACAA AGCAACTACA CCTGGATTTT TCCAAACAAC 360
TTTTATTTC TCAGAGTCTT CCTTAATCCT ATGGAACAAG AAGCTGCCAC TGAATAGGGC 420
CCAGTATAGG GGCTTGCTTT TCTACTCCCT CCCCCAATA TAAAAATATA GACTTTTAA 480
AAAAAAAAA AAAAANTTCG NGGGGGGSCC GGTACCCATC CCCCTA 526

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGTACCGGTC CGGAAATTCC CGGGTCGACC CACGTCGTCS GGGGAACATG GCGGCTKCGG 60
AGCCGGCGGT CCTTGCCTC CCCAACAGCG GCGCCGGGGG CGCGGGGGCG CCGTCGGGCA 120
CAGTCCCGGT GCTCTTCTGT TTCTCAGTCT TCGCGCGACC CTCGTCGGTG CCACACGGGG 180
CGGGCTACGA GCTGCTCATC CAGAAGTTC TCAGCCTGTA CGGCGACCAG ATCGACATGC 240
ACCGCAAATT CGTGGTGAG CTGTTCCCG AGGAGTGGGG CCAGTACGTG GACTTGCCCA 300

	AGGGCTTCGC GGTRAGCGAG CGCTGCAAGG TGCGCCTCGT GCCGYTGCAG ATCCAGCTCA	360
5	CTACCCTGGG AAATCTTACA CCTTCAAGCA CTGTGTTTTT CTGCTGTGAT ATGCAGGAAA	420
	GGTTCAGACC AGCCATCAAG TATTTTGGGG ATATTATTAG CGTGGGACAG AGATTGTTGC	480
	AAGGGGCCCC GATTTTAGGA ATTCTGTGTA TTGTAACAGA ACAATACCCT AAAGGTCTTG	540
10	GGAGCACGGT TCAAGAAATT GATTTAACAG GTGTAAACT GGTACTTCCA AAGACCAAGT	600
	TTTCAATGGT ATTACCAGAA GTAGAAGCGG CATTAGCAGA GATTCCCGGA GTCAGGAGTG	660
15	TTGTATTATT TGGAGTAGAA ACTCATGTGT GCATCCAACA AACTGCCCTG GAGCTAGTTG	720
	GCCGAGGAGT CGAGGTTTAC ATTGTTGCTG ATGCCACCTC ATCAAGAAGC ATGATGGACA	780
	GGATGTTTGC CCTCGAGCGT CTCGCTCRAR CCGGGATCAT AGTGACCACG AGTGAGGCTG	840
20	TTCTGCTTCA GCTGGTAGCT GATAAGGACC ATCCAAAATT CAAGGAAATT CAGAATCTAA	900
	TTAAGCGGAG TGCTCCAGAG TCGGGTCTGC TTTCCAAAGT ATAGGACATT TGAAGAACTG	960
25	GTATGCTACT CACTGGTGAA GGACAGTCAG GTGAAGGACT GTAAGCCAC ACAAGCTCTT	1020
	CTTATCTCTA CTAGAATTAA AATGTTAAGT CAAAAACGGC TCCTTTTTTG CGCCTCCTAG	1080
	TGAAACTTAA CCAGCTAGAC CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT	1140
30	CCGGTGCTGC TTACCTTCCT TTTTGTGTTAA TGTGCTTTTA TTTATTAAAA AAAATTACAA	1200
	TGAAGATGCC TGTMTTGTCT CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT	1260
35	CTTGTGAAGT TTTCTTAAAT TGTTCACTTT AAAGAAAATG ACGTACCAAC AATGATTGG	1320
	CTTTTATATT ACTGTAAGAT GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG	1380
	ATTGATTGGA ATAAGATTAT TGCATATGAA TTTACCCACA GGACTCTGAA TCATGTTACC	1440
40	CACTCCCCTC ACAATGTTGT CCACTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT	1500
	GTTGAATAAT TACATATCTT TCTTGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA	1560
45	AATCTCTGTT AATATTCTCT CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG	1620
	CCATATTATT GGTGGAGGGC TGTTTTAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT	1680
	ACCAACATCT TGAATATATA TTCTAGTGTC CACAAGATT AGCAAAAAGA TAAAGCTTGG	1740
50	GTGGAATATC ATTTTAAAAT GTTCATGTTT TGTTCATAT TTTCTTCACC TACTCTCCAA	1800
	ATATGTAAAT GCAAAAAGTC TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATTGT	1860
55	TCTCTTCGAT AAATTTATTT TCATTAAATA CTTRTTAGAG GGTTTTGAAA TGTTTTTCAA	1920
	ATATGTGAAA TGTGAAACTG CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG	1980
	ATTGAAATTA TTTTGNCCCT CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT	2040
60	ATTTATTTAA GGTNATAAAA TCTTGACATT TATAATCTTT C	2081

-5 (2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1717 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

15	CCCCGGCGGA GCTGGACCCG CGGTGGGCTA GGGGCAGGGC CGGAGCCGCG GCGGCGGAGC	60
	TGTGGATCCT TCATGATGAG AGATTTGGGG ACACTTCTCT CTCCTGTGTG TAGTTGATAG	120
	TTTGGTGGTG AAGAGATGGC TGACAGTGTC AAAACCTTTC TCCAGGACCT TGCCAGAGGA	180
20	ATCAAAGACT CCATCTGGGG TATTTGTACC ATCTCAAAGC TAGATGCTCG AATCCAGCAA	240
	AAGAGAGAGG AGCAGCGTCG AAGAAGGGCA AGTAGTGTCT TGGCACAGAG AAGAGCCCAG	300
25	AGTATAGAGC GGAAGCAAGA GAGTGAGCCA CGTATTGTTA GTAGAATTTT CCAGTGTTGT	360
	GCTTGGAATG GTGGAGTGTT CTGGTTCAGT CTCCTCTGT TTTATCGAGT ATTTATTCCT	420
	GTGCTTCAGT CGGTAACAGC CCGAATTATC GGTGACCCAT CACTACATGG AGATGTTTGG	480
30	TCGTGGCTGG AATTCTTCCT CACGTCAATT TTCAGTGCTC TTTGGGTGCT CCCCTTGTTT	540
	GTGCTTAGCA AAGTGGTGAA TGCCATTTGG TTTCAGGATA TAGCTGACCT GGCATTTGAG	600
35	GTATCAGGGA GGAAGCCTCA CCCATTCCCT AGTGTGAGCA AAATAATTGC TGACATGCTC	660
	TTCAACCTTT TGCTGCAGGC TCTTTCCTC ATTCAGGGA TGTTTGTGAG TCTCTTCC	720
	ATCCATCTTG TCGGTGAGCT GGTAGTCTC CTGCATATGT CCCTTCTCTA CTCACTGTAC	780
40	TGCTTTGAAT ATCGTTGGTT CAATAAAGGA ATTGAAATGC ACCAGCGGTT GTCTAACATA	840
	GAAAGGAATT GGCCTTACTA CTTTGGGTTT GGTTTGCCCT TGGCTTTTCT CACAGCAATG	900
45	CAGTCCTCAT ATATTATCAG TGGCTGCCTT TTCTCTATCC TCTTTCCTT ATTCATTATC	960
	AGCGCCAATG AAGCAAAGAC CCCTGGCAAA GCRTATCTCT TCCAGTTGCG CCTCTTCTCC	1020
	TTGGTGGTCT TCTTAAGCAA CAGACTCTTC CACAAGACAG TCTACCTGCA GTCGGCCCTG	1080
50	AGCAGCTCTA CTTCTGCAGA GAAGTTCCCT TCACCGCATC CGTCGCCTGC CAAACTGAAG	1140
	GCTACTGCAG GTCAGTGTG TGCCTGCCAT CCAAAGGGGA TGGGCGGGAT TGGAAGAAGC	1200
55	TGTGGCAGCT CTTTTCCTG TTCACCTCCC GCCTGCCAGG GAAGGCAGGA CCCGCTCTGC	1260
	CAAGGGCCCT CTGCGTATTC CCTTCTCTCT GAGGAATTGA AATTTTGTG TCTGGTGCAC	1320
60	GTAAGGCAGA ATGTTCCCTG ACACCAGTGT GTGGATTTTT AACATCACCG TGAGTCTGAA	1380

AGGACCACAG GTTTTTCTGC AGCTATTTTC TAGCATTTGC CAGTCCCTGT GCCTGGACTG 1440
ATTGGAACAC TTGTTTTTC TCCCTGTGCC ATTTACCCCT CCACCTTCC ATCCTGCCTT 1500
-5 CTACCACCCT TGGATGAATG GATTTTGTA TTTCTAGCTGT TGTATTTGT GAATTTGTTA 1560
ATTTGTGTGT TTTTCTGTGA AACACATACA TTGGATATGG GAGGTAAAGG AGTGTCCAG 1620
TTGCTCCTGG TCACTCCCTT TATAGCCATT ACTGTCTTGT TTCTTGTAAC TCAGGTTAGG 1680
10 TTTTGGTCTC TCTTGCTCCA CTGCAAAAAA AAAAAA 1717

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(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

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CCACGCGTCC GGTCACTATG TAGTGGAGGG GCAGACACCC TCCCGCAAAT TCTGGAAGGT 60

TCTTAGTCTC GACTAGGGCA GTAGCCCCAG GACTCCTAGT CGCCGGCTTC AGGTCACTGC 120

30

CGGCTGAACG GAGCTGCCGT CGCCATGTTT GGCTGCTTGG TGGCGGGGAG GCTGGTGCAA 180

ACAGCTGCAC AGCAAGTGGC AGAGGATAAA TTTGTTTTTG ACTTACCTGA TTATGAAAGT 240

35

ATCAACCATG TTGTGGTTTT TATGCTGGGA ACAATCCCAT TTCCTGAGGG AATGGGAGGA 300

TCTGTCTACT TTTCTTATCC TGATTCAAAT GGAATGCCAG TATGGCAACT CCTAGGATTT 360

GTCACGAATG GGAAGCCAAG TGCCATCTTC AAAATTTCAG GTCTTAAATC TGGAGAAGGA 420

40

AGCCAACATC CTTTGGAGC CATGAATATT GTCCGAACTC CATCTGTTGC TCAGATTGGA 480

ATTTCACTGG AATTATTAGA CAGTATGGCT CAGCAGACTC CTGTAGGTAA TGCTGCTGTA 540

TCCTCAGTTG ACTCATTCAC TCAGTTCACA CAAAAGATGT TGGACAATTT CTACAATTTT 600

45

GCTTCATCAT TTGCTGTCTC TCAGGCCAG ATGACACCAA GCCCATCTGA AATGTTCAAT 660

CCGGCAAATG TGGTTCTGAA ATGGTATGAA AACTTTCAA GACGACTAGC ACAGAACCCT 720

50

NTNTTTTGGN AACATAATT TGAATAAAAT AATTTTAAAT GGATTTGNA AAAAAAAAAA 780

AAAAAAAAA AAAAAAAAAA AAAA 804

55

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

-5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

	GGCACAGCCC AGGGCCTTGA AGCCAGCTGG CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG	60
	GGAGGGTCTG GGATGGGGCT GCCCCTGATG GCCCTGATGT GGAGTACCTT GCCAGCATCT	120
10	GCTGGGGTGA ACTTTATTTT AGCCCTTCCC TTGTTGCTCT TATGGAAGAA CAGAGGAGGG	180
	GTGGGCAGGT CAGTGATGTC AGCAGTGGAG TGATTCCCAG CACAGCGGCT TCTGGGAAGA	240
15	GGGCATGGAG GCATTCTTTT CAGGGAATG GTCCATNATT TCAGCCAGAA GGCATTGCAT	300
	TAAGTTAAGT CCNGGACTTT TGTGGCCCAG CTCTGTGTTA TTAAGGGCCC TTGGCGAAGA	360
	CTTCAAGGAG GGGGCAAAAN GACCTTTAAG TTTTtaggTT TAACACAGGG AACCCNCAA	420
20	GGGTTATTTT G	431

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(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 3752 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35	NGGCACGAGG AGAGTCACCT GGACTCAGAA CTAGAGATAT CCAATGACCC AGACAAAATT	60
	AAACTTCAGC TTTCTAAGCA TAAGGAGTTT CAGAAGACTC TTGGTGGCAA GCAGCCTGTG	120
40	TATGATACCA CAATTAGAAC TGGCAGAGCA CTGAAAGAAA AGACTTTGCT TCCCGAAGAT	180
	ASTCAGAAAC TTGACAATTT CCTAGGAGAA GTCAGAGACA AATGGGATAC TGTTTGTGGC	240
45	AAGTCTGTGG AGCGGCAGCA CAAGTTGGAG GAAGCCCTGC TCTTTTCGGG TCAGTTCATG	300
	GATGCTTTGC AGGCATTGGT TGA CTGGTTA TACAAGGTGG AGCCACAGCT GGCTGAGGAC	360
	CAGCCCGTGC ACGGGGGACC TTGACCTCGT CATGAACCTC ATGGATGCAC ACAAGGTTTT	420
50	CCAGAAGGAA CTGGNGAAAG CGAACAGGAA CCGTTCAGGT CCTGAAGCGG TCAGGCCGAG	480
	AGCTGATTGA GAATAGTCGA GATGACACCA CTTGGGTAAA AGGACAGCTC CAGGAACTGA	540
55	GCACTCGCTG GGACACTGTC TGTAACTCT CTGTTTCCAA ACAAAGCCGG CTTGAGCAGG	600
	CCTTAAACA AGCGGAAGTG TTTCGAGACA CAGTCCACAT GCTGTTGGAG TGGCTTTCTG	660
	AAGCAGAGCA AACGCTTCGC TTTCGGGGAG CACTTCCTGG ATGACACAGA GGGCCTGCAG	720
60	TCTCTCATTG ACACCCATAA GGAATTCATG AAGAAAGTAG AAGAAAAGCG AGTGGACGTT	780

	AACTCAGCAG TAGCCATGGG AGAAGTCATC CTGGCTGTCT GCCACCCCGA TTGCATCACA	840
5	ACCATCAAAC ACTGGATCAC CATCATCCGA GCTCGCTTCG AGGAGGTCCT GACATGGGCT	900
	AAGCAGCACC AGCAGCGTCT TGAACCGCC TTGTCAGAAC TGGTGGCTAA TGCTGAGCTC	960
	CTGGAAGAAC TTCTGGCATG GATCCAGTGG GCTGAGACCA CCCTCATTCA GCGGGATCAG	1020
10	GAGCCAATCC CGCAGAACAT TGACCGAGTT AAAGCCCTTA TCGCTGAGCA TCAGACATTT	1080
	ATGGAGGAGA TGAATCGCAA ACAGCCTGAC GTGGACCGGG TCACCAAGAC ATACAAAAGG	1140
15	AAAAACATAG AGCCTACTCA CGCGCCTTTC ATAGAGAAAT CCCGCAGCGG AGGCAGGAAA	1200
	TCCCTAAGTC AGCCAACCCC TCCTCCCATG CCAATCCTTT CACAGTCTGA AGCAAAAAC	1260
	CCACGGATCA ACCAGCTTTC TGCCCGCTGG CAGCAGGTGT GGCTGTTAGC ACTGGAGCGG	1320
20	CAAAGGAAAC TGAATGATGC CTTGGATCGG CTGGAGGAGT TGAAAGAATT TGCCAACTTT	1380
	GACTTTGATG TCTGGAGGAA AAAGTATATG CGTTGGATGA ATCACAAAAA GTCTCGAGTG	1440
25	ATGGATTTCT TCCGGCGCAT TGATAAGGAC CAGGATGGGA AGATAACACG TCAGGAGTTT	1500
	ATCGATGGCA TTTTAGCATC CAAGTTCCCC ACCACCAAGT TAGAGATGAC TGCTGTGGCT	1560
	GACATTTTCG ACCGAGATGG GGATGGTTAC ATTGATTATT ATGAATTTGT GGCTGCTCTT	1620
30	CATCCCAACA AGGATGCGTA TCGACCAACA ACCGATGCAG ATAAAATCGA AGATGAGGTT	1680
	ACAAGACAAG TGGCTCAGTG CAAATGTGCA AAAAGGTTTC AGGTGGAGCA GATCGGAGAG	1740
35	AATAAATACC GGTTCCTCCT CGGCAATCAG TTTGGGGATT CTCAGCAGTT GCGGCTGGTC	1800
	CGTATTCTGC GCAACCGTGA TGGTTCGCGT TGGTGGAGGA TGGATGGCCT TGGATGAATT	1860
	TTTAGTGAAA AATGATCCCT GCCGAGCAG AGGTAGAACT AACATTGAAC TTAGAGAGAA	1920
40	ATTCATCCTA CCAGAGGGAG CATCCAGGG AATGACCCCC TTCCGCTCAC GGGGTCGAAG	1980
	GTCCAAACCA TCTTCCCGG CAGCTTCCCC TACTCGTTCC AGCTCCAGTG CTAGTCAGAG	2040
45	TAACCACAGC TGTACATCCA TGCCATCTTC TCCAGCCACC CCAGCCAGTG GAACCAAGGT	2100
	TATCCCATCA TCAGGTAGCA AGTTGAAACG ACCAACACCA ACTTTTCATT CTAGTCGGAC	2160
	ATCCCTTGCT GGTGATACCA GCAATNAGTT CTTCCCCGGC CTCCACAGGT GCCAAACTA	2220
50	ATCGGGCAGA CCCTAAAAAG TCTGCCAGTC GCCCTGGGAG TCGGGCTGGG AGTCGAGCCG	2280
	GGAGTCGAGC CAGCAGCCGG CGAGGAAGTG ACGCTTCTGA CTTTGACCTC TTAGAGACGC	2340
55	ATTGCTTGTT CCGACACTTC AGAAAGCAGC GCTGCAGGGG GCCAAGGCAA CTCCAGGAGA	2400
	GGGCTAAACA AACCTTCCAA AATCCCAACC ATGTCTAAGA AGACCACCAC TGCTTCCCC	2460
	AGGACTCCAG GTCCCAAGCG ATAACACTGT CTAAGCACCC CCAAGCCACT ATCCACTTTG	2520
60	AATCCTGCTC CATAATTGG GTGTATATTT ATTCTGAACG GGAGAAGTTA TATTGTTAAA	2580

AGTGTAAG AATAATTGTG TTATGAAGCT GCCTTATTTT TTTTCTTTTT GTAAGTTACT 2640
 ATTTTCATGT GAATATTTAT GTAGATAAAA TTGCTCCTT GGTAACCCTG TAATGGATGG 2700
 -5 GGGCCAGAAA TGAAATATTT GAGAAAAACA AGTGAAAAGG TCAAGATACA AATGTGTATT 2760
 AAAAAAAAAA AAGCCTATTA ATAGGGTTTC TCGCGGTGC AGGGTTGTAA ACCTGCTTTA 2820
 10 TCTTTTAGGA TTATTCCTAA ATGCATCTTC TTTATAAACT TGACTTGCTA TCTCAGCAAG 2880
 ATAAATTATA TTAAAAAAT AAGAATCCTG CAGTGTTTAA GGAATCTTT TTTGTAAAT 2940
 CACGGACACC TCAATTAGCA AGAACTGAGG GGAGGGCTTT TTCCATTGTT TAATGTTTTG 3000
 15 TGATTTTTAG CTAAAGAGAG GGAACCTCAT CTAAGTAACA TTTGCACATG ATACAGCAAA 3060
 AGGAGTTCAT TGCAATACTG TCTTTGGATA TTGTTTCAGT ACTGGGTGTT TAAAGGACAA 3120
 20 ATAGCTGCTA GAATTCAGGG GTAAATGTAA GTGTTTCAGAA AACGTCAGAA CATTTGGGGT 3180
 TTTAACTGA TTTGTTGCTC CCTATCCAGC CTAGACACCA GTAACCTTG TGTTCACCAG 3240
 GACCCAGACC CTTGGCAAGG GATAGGCTCG TTGGTGACAT TGTGAATTT AGATTGTTT 3300
 25 TATCCACTTT TTTTGCTATT TATTTAAATG GTCGATCAAC TTCCACAAA CTGAGGAATG 3360
 AATTCACGA GCCTGTTCTG AAAATGTGGA CGTAAGACAA ACACGTGCTC GTCCTTTAAT 3420
 30 GGAGTTCACC AGCACACTTG TTAACCACTG CTGTTTGCTT TCGTCTTTT TTGTGCGTAA 3480
 TAAAGTCAAC TGACCAAGTG ACCATGAAAA GGGGCTGTCT GGGGCTCCTG TTTTTTAGCT 3540
 GCTGTTCTTC AGCTCCGACC ATGTTGCTGT GTGATTATCT CAATTGGTTT TAATTGAGGC 3600
 35 AGAACTGAA GCTCTACCAA TGAAGTGTG AGAAACAAGA CACACTTTG TATTAAATT 3660
 GCTTGCACTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGG GGGGCGCGT 3720
 40 ACCCAATTCG CCGTATATGA TCGTAAACAA TC 3752

45 (2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55 TGACCTCTG CCTGCCGGGC TCAGTGCTGG ACGCTTCTG TTTGTGCGA GTCGGTCTC 60
 GGTAACACCA GCGGCTGTG GTCCACCACT CCATTCAGCA GCTCCATTG GTCCAGCAAC 120
 60 CTTAGCAGCG CCTTCCCTC ACCACTCCAG CAAACACGT GGCAAGCATC GGCCTCATG 180

GCACAGAAAA CTCCCCTGCT CCTCACGCTC CCTCCACCTC CAGTCCAGCT GACGACTTGG 240
 GACAGACCTA CAACCCGTGG CGGATATGGA GCCCCACGAT TGGAGAAGA AGCTCGGACC 300
 -5 CTGGGTCTAA TTCGCACTTT CCTCACGAGA ATTAAATTAA GCAAAAAACA AACAAACATA 360
 GTGGGCCCTC GTCTAGATCA TGATGTGCCA GTTCTGAGA CATCTTTTAA AGGCTCTTAC 420
 10 TGCAGCTCCC CTCCCCACCC TCCTCTTCTT TGCAAAACAG ACCCAAGCAG GGCAGGCTCA 480
 GACCACTCGC TTCTTTCAGA TCTTCTTGC AATTATGATA ACATGAGATT TGCTGTTGTG 540
 CTTTTAGAGA AAAGCTGGA CTCAGCCACA AACTCTAATA AGACCTGTAC ATCTGAGAAC 600
 15 CTTTCCCGTT ACTGCGTTTT CACCACCTGT CTTCCCATG CTTTATTTAT CTGTATGAAC 660
 ACAGATTTGA CATTACAGCT AAGGAAATAA TTTGAGTTGA TTCAGAAATC CTGGCATGTG 720
 20 ACAATTTTGT TAAATTACCA AGTTTGGTTT TTAATAATTT CTCAATATTA TGCGCCAAGA 780
 TCTAATTTTA AAAGTGTATG AGGACTTTGT GCTGAAAATA GAGTATTTTT TTAAAGTAAG 840
 GCTGTCTTGG TTTAAAGCA GATTACAGAA ATGTAAGTCA ACTTAAGAAC RGTGAATGAA 900
 25 TGTAAAAACA TTCAGTYGAG ACCATATGCA TTTTCTGTGC TGTTGTACT TGAGGTATGT 960
 AACATTTGTA TACCTGAAC TATTTTAAAG ATGAACTGAA ATGCACATAG CCAAGTCTTG 1020
 30 AGATACAAGA TTGAATGTGT ATTTCTTAAA AATACAACCT TGTGTTGTAC TTTGAAATAA 1080
 ATGATGCTTT TTTCAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG GCCCGGTACC 1140
 CAAT 1144

35

(2) INFORMATION FOR SEQ ID NO: 129:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1830 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GCATGCAGAG GAGCACCTG AGCGTGTGCC TGAGCAGGC GGCCATSTTG GCACGGAGCC 60
 50 ACGGGTGTCT GCCCAAGTGC ATCATGCAGG CCACGGACAT CATGCCGAAC AGGGCCCAAG 120
 GGTGGAGATT CTGGCCAAAA ACCTGCGAGT CAAGGACCAG ATGCCCCAGG GTGCTCCGCG 180
 CCTCTACCGC CTCTGCCAGC CGCCGGTGA TGGGACCTC TGAACACCCA AATGCCCCAC 240
 55 GCTGGGCCGC GGCCTCTGGA GCTGGGATTT GGGAGGACAC AGCAGGCAGC GCTGGCCTTC 300
 TCCAGGGATG GCCCAANGCT TCCGCARCCG CCCGTTCCGG GACCTGCCCA GCGTCCTCCC 360
 60 TGCCTCCTTC CGGGACAAGC CTGGCCACCC TCGCTGTGAT GACGAGCTGG CTGATTGGCC 420

	CTGGGCCGGC CCATTCTTCA CACGCCTGCC AGAAGCTGGA GGGGTGCTGG AGACCCATAG	480
- 5	AGCTGATGGG AGCAGCTGGT GCCTGGCCTT CGGCTCCTGC GTCCCCAGAA CCCAAGGGAA	540
	CGTCATGGAG GCCACATGGG GCCACCCGGC TCCCTCGGGA TGGCTCCGCT GCACTTTGA	600
	AACCCCGGTT TCCTTCAACG TCCACATTCC AGGTGACCAC ACGTGTCTCC TCCTCCTCAT	660
10	CTTAGCTTCC AGGTCACCC TAACCCTGTA CTAACCTGCT TGGTGGACTT GGAAAAGACT	720
	TGGCTCTGTC GGGAAAGGAG AGACGGGGCC TCCATCACGC CTGTTACCAG AGGATCCCCG	780
15	AGAGCCACAC CAGCTCTGGA CATCACCGCC CCTGGAAC TG GCCACCAG CCCTGGGCAC	840
	GAGATTTGCT CTGACTTTAT TTATATGGCA TGAAATCTCT GGTTTATTTT GGGATTTTTT	900
	GTGTTGGTG TTGTCAAAGT TTGTTTTTC TAAAGTTGTG TGATTATATA TTTGACATTT	960
20	TACATTTCAA AGAAAGGTAT GTTGTCTAAC AGGGGACCAA CAGAAGGTAG TATTGACAAC	1020
	TGTTCTTGCT TCTACTAAAA AAAAAAGAGC ACAAAGAAA AACTAAATTA TTGAAAAATT	1080
25	AAAAATGTC ATTGTTTCCT GTTGTTAAT ATTAGGTTG TAAGGTGTCG TTTTGAGGTA	1140
	TCGACTGTGA TTCCTTCCCC CACCCTCCAT TCTCCAGCGG TTGGCCGGTG TTAGAACTCG	1200
	CTCTCTTTGA GTGACTGGCT ACAAGGGCCT GAGAGGTGGC CAGCCAGGGT TGGAGCTGGA	1260
30	GGGGATGGAG CCCACCTGA GGTGCCGTGT CACACGGGTT AGAGGGTCAC TGGGAAACAC	1320
	CGGGCGGTGG CTTCTGTGAT TTATTTTCTT GATGGTAACT TCTCAGAGCA GGGCRATTGG	1380
35	GACATACCA GCCAGAGCAC AGGAAGCCAC CCTGCCTGCT GGGGAGGAGG GACCCACACA	1440
	AGCCCCCTCG GCAGTTTGTC CCCCCAGCTT CGGTATGCCT TCAGGGAAAG GTCACAGCTG	1500
	GGGAGGAAGC GGGGGGACGC CTGTCACCCC TGGCAGGTGG TGAGTTCAGG TGGGGGCTCC	1560
40	CTGCTKCCC CAGGCCTGGG AGCTTGAAGC CCTCCCGCA TCTGGCATCC GAGCCTCCCG	1620
	CCCTCCAGG TCGCCTTCCC TCTCTTGCCG CAGCATAAC GAGGGCAGGC AGTGGCCTTG	1680
45	TCACTGTATC TTGCATCAGA GACAAAGGAG GACCCGCTTT AGCCCTGCTG CGGGAAATGG	1740
	GGGATGGCCC AGGGCCAGCG CATGTGCAC TGGTTTACTT TAAATGTAC AGATTCTTCT	1800
	CGTTAAATTC TTGATAGATT TTTTATTATT	1830
50		

(2) INFORMATION FOR SEQ ID NO: 130:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	GGCCGCCCGG ATGGCGACCC CAGCCTCGGC CCCAGACACA CGGGCTCTGG TGGCAGACTT	60
-5	TGTAGGTTAT AAGCTGAGGC AGAAGGGTTA TGTCTGTGGA GCTGGCCCCG GGGAGGGCCC	120
	AGCAGCTGAC CCGCTGCACC AAGCCATGCG GGCAGCKGGA GATGAGTTCG AGACCCGCTT	180
10	CCGGCGCACC TTCTCTGATC TGGCGGCTCA GCTGCATGTG ACCCCAGGCT CAGCCCAACA	240
	ACGCTTCACC CAGGTCTCCG ATGAACTTTT TCAAGGGGGC CCCAACTGGG GCCGCCTTGT	300
	AGCCTTCTTT GTCTTTGGGG CTGCACTGTG TGCTGAGAGT GTCAACAAGG AGATGGAACC	360
15	ACTGGTGGGA CAAGTGCAGG AGTGGATGGT GGCTTACCTG GAGACGCGGC TGGCTGACTG	420
	GATCCACAGC AGTGGGGGCT GGTATATCCA GATCACTGAA GCTGAGATGG CTGATGAAGT	480
20	AATTTCAGT GAAATTTTAA GCGACTGTGA CTCTGCTGCA AGTTCCCCAG ATCTTGAGGA	540
	GCTGGAAGCT ATCAAAGCTC GAGTCAGGGA GATGGAGGAA GAAGCTGAGA AGCTAAAGGA	600
	GCTACAGAAC GAGGTAGAGA AGCAGATGAA TATGAGTCCA CCTCCAGGCA ATGCTGGCCC	660
25	GGTGATCATG TCCATTGAGG AGAAGATGGA GGCTGATGCC CGTTCCATCT ATGTTGGCAA	720
	TGTGGACTAT GGTGCAACAG CAGAAGAGCT GGAAGCTCAC TTTTCATGGCT GTGGTTCAGT	780
30	CAACCGTGTT ACCATACTGT GTGACAAATT TAGTGGCCAT CCCAAAGGGT TTGCGTATAT	840
	AGAGTTCTCA GACAAAGAGT CAGTGAGGAC TTCTTTGGCC TTAGATGAGT CCCTATTTAG	900
	AGGAAGGCAA ATCAAGGTGA TCCCAAAACG AACCAACAGA CCAGGCATCA GCACAACAGA	960
35	CCGGGGTTTT CCACGAGCCC GCTACCGCGC CCGGACCACC AACTACAACA GCTCCCGCTC	1020
	TCGATTCTAC AGTGGTTTTA ACAGCAGGCC CCGGGTCCG GTCTACAGG GCGGGCTAG	1080
40	AGCGACATCA TGGTATTCCC CTTACTAAAA AAAGTGTGTA TTAGGAGGAG AGAGAGGAAA	1140
	AAAAGAGGAA AGAAGGAAAA AAAAAAGAAT TAAAAA AAAA AAAA ACAGAAGWTG	1200
	MCCTTGATGG AAAAAAATA TTTTTTAAAA AAAAGATATA CTGTGGAAGG GGGGAGAATC	1260
45	CCATAACTAA CTGCTGAGGA GGGACCTGCT TTGGGGAGTA GGGGAAGGCC CAGGGARTGG	1320
	GGCAGGGGGC TGCTTATTCA CTCTGGGGAT TCGCCATGGA CACGTCTCAA CTGCGCAACT	1380
50	GCTTGCCCAT GTTCCCTGC CCCACCCAC CCCTCTCTC CGGCTCCCTG CCCCTCCAGA	1440
	TGCTCTGGTG ATCTATTTTG TTCTCTTTTG TGTTCCTTTT TCTGTTTTGA GTGTCTTTCT	1500
	TGTCAGGTTT CTGTAGCCGG AAGATCTCCG TTCCGCTCCC AGCGGCTCCA GTGTAAATTC	1560
55	CCCTTCCCCC TGGGGAAATG CACTACCTTG TTTTGGGGGG TTTAGGGGTG TTTTGTMTT	1620
	TCAGTTGTTT TGTTTTTTTG TTTTTTINTT TTCTCTTTGC CTTTTTTCCC TTTTATTTGG	1680
60	AGGGAATGGG AGGAAGTGGG AACAGGGAGG TGGGAGGTGG ATTTTGTTTA TTTTTTTAGC	1740

TCATTTCCAG GGGTGGGAAT TTTTPTTTAA TATGTGTCAT GAATAAAGTT GTTTTGTAAA 1800
 AKAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
 5 AAAA 1864

10 (2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2041 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

20 GGCACGAGCG CGCGGCAGGG CCCTGGACCC GCGCGGCTCC CGGGGATGGT GAGCAAGGCG 60
 CTGCTGCGCC TCGTGTCTGC CGTCAACCGC AGGAGGATGA AGCTGCTGCT GGGCATCGCC 120
 25 TTGCTGGCCT ACGTCGCCTC TGTITGGGGC AACTTCGTTA ATATGAGGTC TATCCAGGAA 180
 AATGGTGAAC TAAAAATTGA AAGCAAGATT GAAGAGATGG TTGAACCACT AAGAGAGAAA 240
 ATCAGAGATT TAGAAAAAAG CTTTACCCAG AAATACCCAC CAGTAAAGTT TTTATCAGAA 300
 30 AAGGATCGGA AAAGAATTTT GATAACAGGA GCGCGAGGGT TCGTGGGCTC CCATCTAACT 360
 GACAAACTCA TGATGGACGG CCACGAGGTG ACCGTGGTGG ACAATTTCTT CACGGGCAGG 420
 AAGAGAAACG TGGAGCACTG GATCGGACAT GAGAACTTCG AGTTGATTAA CCACGACGTG 480
 35 TGGAGCCCCT CTACATCGAG GTTGACCAGA TATACCATCT GGCATCTCCA GCCTCCCCCTC 540
 CAAACTACAT GTATAATCCT ATCAAGACAT TAAAGACCAA TACGATTGGG ACATTAAACA 600
 40 TGTTGGGGCT GGCAAAACGA GTCGGTGCCC GTCTGCTCCT GGCTCCACA TCGGAGGTGT 660
 ATGGAGATCC TGAAGTCCAC CCTCAAAGTG AGGATTACTG GGGCCACGTG AATCCAATAG 720
 45 GACCTCGGGC CTGCTACGAT GAAGGCAAAC GTGTTGCAGA GACCATGTGC TATGCCTACA 780
 TGAAGCAGGA AGGCGTGGAA GTGCGAGTGG CCAGAATCTT CAACACCTTT GGGCCACGCA 840
 TGCACATGAA CGATGGGCGA GTAGTCAGCA ACTTCATCCT GCAGGCGCTC CAGGGGGAGC 900
 50 CACTCACGGT ATACGGATCC GGGTCTCAGA CAAGGGCGTT CCAGTACGTC AGCGATCTAG 960
 TGAATGGCCT CGTGGCTCTC ATGAACAGCA ACGTCAGCAG CCCGGTCAAC CTGGGGAACC 1020
 55 CAGAAGAACA CACAATCCTA GAATTTGCTC AGTTAATTAA AAACCTTGTT GGTAGCGGAA 1080
 GTGAAATTCA GTTTCTCTCC GAAGCCCAGG ATGACCCACA GAAAAGAAAA CCAGACATCA 1140
 AAAAGCAAAA GCTGATGCTG GGGTGGGAGC CCGTGGTCCC GCTGGAGGAA GGTTTAAACA 1200
 60 AAGCAATTCA CTACTTCCGT AAAGAACTCG AGTACCAGGC AAATAATCAG TACATCCCCA 1260

	AACCAAAGCC TGCCAGAATA AAGAAAGGAC GGACTCGCCA CAGCTGAACT CCTCACTTTT	1320
5	AGGACACAAG ACTACCAITG TACACTTGAT GGGATGTATT TTTGGCTTTT TTTTGTGTGTC	1380
	GTTTAAAGAA AGACTTTAAC AGGTGTCATG AAGAACAAAC TGGAATTTCA TTCTGAAGCT	1440
	TGCTTTAATG AAATGGATGT GCCTAAAAGC TCCCTCAAA AAAGTGCAGA TTTTGCCTTG	1500
10	CACCTTTTGA ATCTCTCTTT TTATGTAAAA TAGCGTAGAT GCATCTCTGC GTATTTTCAA	1560
	GTTTTTTTAT CTGCTGTGA GAGCATATGT TGTGACTGTC GTTGACAGTT TTATTTACTG	1620
15	GTTCCTTGT GAAGCTGAAA AGGAACATTA AGCGGACAA AAAATGCCGA TTTTATTTAT	1680
	AAAAGTGGGT ACTTAATAAA TGAGTCGTTA TACTATGCAT AAAGAAAAAT CCTAGCAGTA	1740
	TTGTCAGGTG GTGGTGCGCC GGCATGATT TTAGGCAGA TAAAGAATT CTGTGTGAGA	1800
20	GCTTTATGTT TCTCTTTTAA TTCAGAGTTT TTCCAAGGTC TACTTTTGAG TTGCAAACCT	1860
	GACTTTGAAA TATTCCTGTT GGTCAATGATC AAGGATATTT GAAATCACTA CTGTGTTTTG	1920
25	CTGCGTATCT GGGCGGGGG CAGGTGGGG GGCACAAAGT TAACATATTC TTGGTTAACC	1980
	ATGGTTAAAT ATGCTATTTT AATAAAATAT TGAACTCAC CAAAAAAAAA AAAAAAAAAA	2040
	A	2041
30		

(2) INFORMATION FOR SEQ ID NO: 132:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2012 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

	TACCAAGCTG CAAGAATCTA CTATATCATG GCAGAAGAAG TAGAGTGGGA CTATTGCCCT	60
45	GACCGGAGCT GGGACGGGA ATGGCACAAC CAGTCTGAGA AGGACAGTTA TGGTTACATT	120
	TTCTGAGCA ACAAGGATGG GTCCTGGGT TCCAGATACA AGAAAGCTGT ATTCAGGGAA	180
50	TACACTGATG GTACATTCAG GNTCCCTCGG CCAAGGACTG GACCAGAAGA ACACTTGGGA	240
	ATCTTGGGTC CACTTATCAA AGGTGAAGTT GGTGATATCC TGACTGTGGT ATTCAAGAAT	300
	AATGCCAGCC GCCCCTACTC TGTGCATGCT CATGGAGTGC TAGAATCTAC TACTGTCTGG	360
55	CCACTGGCTG CTGAGCCTGG TGAGGTGGTC ACTTATCAGT GGAACATCCC AGAGAGGTCT	420
	GGCCCTGGGC CAATGACTCT GCTTGTGTTT CCTGGATCTA TTATCTGCA GTGGATCCCA	480
60	TCAAGGACAT GTATAGTGGC CTGGTGGGGC CCTTGGCTAT CTGCCAAAAG GGCATCCTGG	540

	NAGCCCCATG GAGGACGGAN TGACATGGAT CGGGAATTG CATTGTTGTT CTGATTTTT	600
	GATGAAAATA AGTCTTGGTA TTTGGAGGAA AATGTGGCAA CCCATGGGTC CCAGGATCCA	660
-5	GGCAGTATTA ACCTACAGGA TGAAACTTTC TTGGAGAGCA ATAAAATGCA TGCAATCAAT	720
	GGGAAACTCT ATGCCAACCT TAGGGGTCTT ACCATGTACC AAGGAGAACG AGTGGCCTGG	780
10	TACATGCTGG CCATGGGCCA AGATGTGGAT CTACACACCA TCCACTTTCA TGCAGAGAGC	840
	TTCTCTATC GGAATGGCGA GAACTACCGG GCAGATGTGG TGGATCTGTT CCCAGGGACT	900
	TTTGAGGTTG TGGAGATGGT GGCCAGCAAC CCTGGGACAT GGCTGATGCA CTGCCATGTG	960
15	ACTGACCATG TCCATGCTGG CATGGAGACC CTCTTCACTG TTTTTCCTCG AACAGAACAC	1020
	TTAAGCCCTC TCACCGTCAT CACCAAAGAG ACTGAAAAG CAGTGCCCCC CAGAGACATT	1080
20	GAAGAAGGCA ATGTGAAGAT GCTGGGCATG CAGATCCCCA TAAAGAATGT TGAGATGCTG	1140
	GCCTCTGTTT TGGTTGCCAT TAGTGTCAAC CTCTGCTCG TTGTTCTGGC TCTTGGTGGA	1200
	GTGGTTTGGT ACCAACATCG ACAGAGAAAG CTACGACGCA ATAGGAGGTC CATCTGGAT	1260
25	GACAGCTTCA AGCTTCTGTC TTTCAAACAG TAACATCTGG AGCCTGGAGA TATCTCAGG	1320
	AAGCACATCT GTAGTGCCT CCCAGCAGGC CATGGACTAG TCACTAACC CACACTCAA	1380
30	GGGGCATGGG TGGTGGAGAA GCAGAAGGAG CAATCAAGCT TATCTGGATA TTTCTTTCTT	1440
	TATTTATTTT ACATGGAAAT AATATGATTT CACTTTTTCT TTAGTTTCTT TGCTCTACGT	1500
	GGGCACCTGG CACTAAGGGA GTACCTTATT ATCCTACATC GCAAATTTCA ACAGCTACAT	1560
35	TATATTTCTT TCTGACACTT GGAAGGTATT GAAATTTCTA GAAATGTATC CTCTCACAA	1620
	AGTAGAGACC AAGAGAAAAA CTCATTGATT GGGTTTCTAC TTCTTTCAAG GACTCAGGAA	1680
40	ATTTCACTTT GAACTGAGGC CAAGTGAGCT GTTAAGATAA CCCACACTTA AACTAAAGGC	1740
	TAAGAATATA GGCTTGATGG GAAATGAAG GTAGGCTGAG TATTGGGAAT CCAAATGAA	1800
	TTTTGATTCT CCTTGGCAGT GAACTACTTT GAAGAAGTGG TCAATGGGTT GTTGCTGCCA	1860
45	TGAGCATGTA CAACCTCTGG AGCTAGAAGC TCCTCAGGAA AGCCAGTTCT CCAAGTTCTT	1920
	AACCTGTGGC ACTGAAAGGA ATGTTGAGTT ACCTCTTCAT GTTTTAGACA GCAAACCCTA	1980
50	TCCATTAAAG TACTTGTTAG AACACTGAAA AA	2012

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

-5	GAGCAGTATT TTAACCAACT TGTATTACAG ATGTTACAGT TCATGTTAGG AAGTCAGAAA	60
	AGACTTTGTT TGTCTTTGTT CTGCTGATGT GAGTCATGTT TTGTGGGGTC TTCCATGGCA	120
	CATTTACCTG TTGCTCCGTC CAGATGTTGA GGGCCAGTCT AGGCTGACAC ATCCTACCCG	180
10	AGGACAAGCC TGTTCCTCCAT TTCTTCACTC TCCCCTCCCC ATATAGCAAC TCTCCCAGGT	240
	TTAGATTACC GTTTTCGACG ACAGATTAAC CAAAAATGCC CCACACAGGT TTTATTACTG	300
15	TTATATACTA TACTTTTAAC AGTACAGACC CTAAATTTTA TTATTTGTTG CTCCCCCAAT	360
	CTGATACCAA ATGTTTAAAG TTGTTTGAAA TCCAAACATG GTAGTGTTCA TGGGTAAATA	420
	TTTTCTAGGC TATGTAAGAG TTAGCAGCCC ATAGCATAGA AGTAATCAAG TAGCATCTGA	480
20	GACTGTTGGA GGCAC TAGGG CCTCTCTGGG CCTAACAGCC TCACTTCCCC AGCCTCACCT	540
	TGCTGTCTC TGACACTGCC ATCAGGGCTG TTAGTGGCAC CTGTATGAGG CCAAGTGTGC	600
25	GTCCAGGGGA ACAGCACAGG TTAATGCGTC TCCCTAGAAC TCATGAAGTC AGTTTAATTC	660
	ATGCATGAAC ATGAGTTCAT TTTATGTTTT ATATAGCTTT CTTAGACATA CCAAACCATC	720
	ATTCATAAAT CAGATAAATT ATTCACTTTT TGTGTTTAGA AAGCTAAGTA TGTGTAGCTG	780
30	GAAACAAAAA TGAGCGTGT TTCTCTCCTG TTAATCTAGA GTGTGCAGTT ACACATGTGT	840
	GGATAATTTC ATGTTCCAGG GGCCTTGGC ATCTCCCATG GACTGATTCC CAGGAAGAAA	900
35	AGCCCAAAGG GAAACCCACG ATTCTTTTCG AGTAGATGTG GGAAAGAGCC CATTGGAGGA	960
	TATGAGGTCC TGTGAAATTC AGTTGTGTGT GTGGCTCCTT GTTAGCAGTC ATGTTGACAT	1020
	GGTGTTAGGA GGCTCCCCAT CCACCTTTTA CATGATGTAG GGACCAAGTGT CTTGTGAGAT	1080
40	TAACCTTGGG ACACAGTGGG TTAGCCTGGA GAAAATGAGA GGCCCTGCCT GGACCCAGGG	1140
	AGAGGAGCCA GTGACACAGG CAGAGCGGTG CAGCCCTCCT TCCCTTCCAT TTGGAGGAGG	1200
45	TGGTGCCAGG AGCCTGCCCC CTTACCTCTG CTGAAGCATA AGTGGACTTT GCTTTTGGGG	1260
	CTTATCTCTG ATACATGCTG GAGCCCTGCC TCTCCACTGC TAGATGGAAC CTGGAATCTC	1320
	TCATCTACCT CTTAGTCTGT CAGTTTCTAC GTGTGAGAAG CAAGCTTGTG GGCCAGTGTG	1380
50	CTTGATCATG CTGTAGCACT TAAAAAATAA TTCCAGGGTT CCCTGGAAAA CCAGTCCCAG	1440
	GGTTCCATG ATCTGTAGTT TCTACCTGGA TTATAACTGG TTTTGGGTAC CTGAATTTTG	1500
55	ATTGGTTAGC CTTAATTATA GTCTGGCGTG ATCATGTAGA ATCTTTTCTG GTGAACAGAT	1560
	CATAAAGTTC TATCAAGGAG TTCTATCAAG GCATCCATGT CAGTGGTGCT ATGCTGGTTA	1620
60	CAACTTGAGA TTTTGAAT AAAAAATTTG TCATAAAAAA AAAAAAAA	1669

(2) INFORMATION FOR SEQ ID NO: 134:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1565 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

	CACTTTTGCT ATATAACCTA AGTGATAACC CTCTTTTAGT TACCTGCCAA ACTCTGGNCT	60
15	TGGTTTATAT TGCAGTTAAC ACAGTTACAA AGCTGTAATG GTGTCTTTTT TTCCTTTGTA	120
	ACGGAATGTG TAAATCAAAG TATATACATT GTGTGGTGTT CCTGTTTCTG GAGTTTCATG	180
20	AGGATTTACA CATGGCATTG AGTGTTCTGT ATAGATCTGC CTACCTTTGT GAATTCATCT	240
	GTTAACCCTT CTTCCTTTGA GAGAGCACCG GCGATGGTGG TTAACCTCCT GTGTTTTCTC	300
	TCTCTCTAC TGGTTATTCT TGAATTAAGC ACAGACTCGT CAGCTCGGTT GCTTTATCAT	360
25	GAATAATGTG TGTGACCTTG CAGTTCTTCC ACAGTTCAGC AAACAAGTGC TAGCTTCACT	420
	GACCAAAAAT TAAGGAAGGA AAACACAGTT TTTAAAACGA TCCATCTTTT AACAGCCGAA	480
30	ACCGATGTGT CTATGGTGCT GCACCTTGCT GTTGTACTTC TGAAATCAGA CGTGTGTGAA	540
	CGATCATTTT TGACTTAACC GTGAGATGCT CACGAGTACC CTTCTGTGTG TTTTGTTPAGC	600
	ATTGAAATCG AGACTATTTA TTTGGAATAT ATACAACAGT GTTTTTCCAC TGTATTTTCA	660
35	TTGCAAAAGT TGAGAACTGC TTTCTCTACC TTTTGCAAAA TAATTGATAT TCCATATTGG	720
	ATTCTCAAAG ACTTCGATAT GGTGAACCTA TTAAACCTAG AAATTGTATT CATCCTTTCA	780
40	TGACTGTGGC CTGAGTTCCC CAGCCCCTCT CCTCCTTTTT TTTAGATGAG ATTTAGCACA	840
	CTCTCAGTTA TTTAAACATG CAACATTTCT TGAGTATGTA TGTGAGGCC ATCTGAGCTC	900
	ATAGCTGATT CAGTAACCAG TTTCATGCTG TGTCAATCAC ACTCACTACT TAATACTGCC	960
45	ATGGTGAAAA TGTGGAGGAA AAATGTATCC ATGTGTGTCT GGAAGCATA TACACTTGTA	1020
	CATTTTTTAA TACTCTGATT CTGTAACATT TCTGAGTTTT GTTTGTGTTT ACAGNAAAAA	1080
50	AAAAAAAAGT GATAAAGCAA TCAGAAGACC AAGAGGTTTA CTATTGATGC TTAGGGTCGT	1140
	CTGACCTTGG CTGGCCAATA GACCTACACG GCCAAATTAA TTTACGAGAG TAATAATTTT	1200
	TCAAAGCCA ATTTTTTTTC TGTATTTTCT GTATGAAACT GCCAATATCA TGAATAGAAA	1260
55	GGGAGAACCA TAAAGGAGAA AGAACGTGAT GTTCTGTTAT GTTCATGTAA ACCTAAAGAA	1320
	ACAGTGTGGA GGCAGGCGCG ATCAGCCGAA CTCTAGGGAC TTGGTGTGTC TTGGAAGGCA	1380
60	TCCATACCTG CATTTTGCAT TCTTCGTATG TAATCATATT GCCAAAGACA AACTATTTCA	1440

TCATTTATTG TAAATAACAC TTTTCCCCAG ACCTACCATA AAGTTTCTGT GATGTATTGT 1500
CTTCCAGTTG CAATAAAAT TACTGAGTTG CATCAATTGA AGAAAAAAAA AAAAAAAAAA 1560
-5 CTCGA 1565

10 (2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 2007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

20 TCTAAAAGCC CCCTTATACC CCACTTGTG CAGCAAAGAT CCCCCTGCAG GTCACAGCCT 60
GATTGTGGC CAGGCTGGAC AAATTCCTGA GGCACAACCT GGCTTCAGTT CAGATTTCAA 120
25 GCTGTGTGG TGTGGGACC AGCAGAAGGC AAACGTCCAG CCAACACACA GGACTGTAAG 180
AGGACTCTGA GCTACGTGCC CTGTGAAGAC CCCCAGGCTT TGTCATAGGA GGTCGTTTCAG 240
CTTCCCCAAA GTCAGAGGTG ATTTGATTG GGAAGACTG AATATCACA CCTAAGTCGT 300
30 GAGCATATCC TGAGTTTTAC TTCCTATGG CTGCCCCTCC AAGTTCTCTC TCTCATACAC 360
ACACACACCC TTGCTCCAGA ATCACCAGAC ACCTCCATGG CTCCAGCTAT GGAACAGCT 420
35 GCATGGGGC TGCCTTTCTG TTTGGCTTAG GAACTTCTGT GCTTCTGTG GCTCCACTCG 480
CGAGGCAGCT CGAGGTGTG GACTCCGATT GGGCTGCAGG CAGCTCTGGG ACGGCACAGG 540
GCGGGCGCTC TGATCAGCTC GTGTAAACA CACGCTCTTC TTGGCTCCTT GGCAGTTCTT 600
40 TCTGCGAATA GTCCTCTCCC TGGCCAGTTG AATGGGGGAA GCTGCTGGCA CAGGAAGGAG 660
AGGCATCCC GGCTGAGGCT TAGGAAATTG CTGGAGCCGG CTCCAAGCAG ATAATTCACT 720
45 GGGGAGGTTT TCAGAGTCAA ACATCATTTCT GCCTGTKTTG GGGGCCAGGT GTGTCACACA 780
AGCATCTCAA AGTCAAAGC CATCTGGGGC TGCTGCTTCT CTTTCTCAGG CTCTGGGGAA 840
AGGAATCTCC CTCTCTCTC ACTTGATTCC AAGTGTGGTT GAATTGTCTG GAGCACTGGG 900
50 ACTTTTTTTC TCTTTTCCTT GATGGACCAA CAGTGCAAAT GCAATCTCGC CATTTAACTT 960
TCAGGTCGAT TTCCTTTCCT GATCAGACAT CTTTGTGCCC CCTTTAGGAA GGAAAAGAAT 1020
55 ACACCTACGA TGTGCCAGGC ACTGTGTTAG GCGCTTTTAT ATAGATCTC GTTAGGATGA 1080
GACTAAGGGA TGAGGACATC TCTTTATAAA AGGCCCTTAA GTAATGGATA AACAGAAACA 1140
CTTAGAGGTG AGAAGGTCTG TCTTCAAGAT CCAAGGTAAG ATTGCCTTCA GTCTGATGTT 1200
60 TGTCTCAAG GACTTATCCC CTACAATATT CTCCCACTCC ATACTTCTCC TTCTACCCCA 1260

5 CCATGTGCTC CCGTGCACTC CTCAGATGGT CAGAGGGGTA ACCCAAGTCC TTAGAGAATT 1320
 TGGGGACCAA TAGAATATGT GATGTGTGAA TTTTCTTTAA AAAACTTAAG GAGTCTTTGC 1380
 TACCTTCTGC TTGTTGAGTT GTTTTGGCAT TCATATTAAA AGCCAGCATC TCACTATTTA 1440
 TTGACAGGTT GGGCTGTGTG TGTGCGCATG TGTGTATACA TTTCCAGGCG TGCCTGTGTC 1500
 10 CTGTAGCTTT TTAAGAGGAA ACCCAGTCAT CCCACTATGA ATCTGGCATC TTCTTATGCT 1560
 TCTAGTGTTC TGGCCATACA TCAACCAAGG GGTTTAATTT ATCCAATGCT TGACGACATG 1620
 TTCAGGAGGG GCTGGATCAA ATTTTGAGAG GGTATGGA AAGGGAGGGG GAGAAGAAAT 1680
 15 TGACATTTAT TTTATTATTT ATTTTAAATG TTTACATCTT CTTTATGTTG TATCAAGCCT 1740
 GAATAGAAAC TGATAGCATT AAAATACTCC GTTCCTCTCT CTCTTCTCGC TTCCTTTTTT 1800
 20 TTTTTTTTTA AATTTAGGAT AACACATTTT TGTTCCTAAA GTGATTTGTG ATTTGTGCTG 1860
 TATAAACTGT ATAAAAGGTT CTGTTTAA AGGTGGATT TCATTCCTCT GGGGACAGTG 1920
 GTCGCCAAGA CATCTACATT GTAAGAGAAC ACAGTGAAG ATCCTGTCCT GATTCTCAAA 1980
 25 AATTATTTTC TCTGTATGAT TAAAAGT 2007

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(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1291 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

40

CTTTTAACCC TCCCCCTTCA CACACATACA TATCAGGTG TTTCTAGTT AAAAACCCAA 60

GTAGCTCAGA TTCTACTTTA ATGTCAGTGC AGATTGTCAT TGAATCATGC CATTATGTTT 120

45

TTTCTCATT TTAGCTGTT GGGTCTTAGT TTTTAAATG ATATAAGAA CTCAGCAATG 180

GTTTTATTTT CTACTCATAC TTAGGGTTTA GGAAACACTA CCACTAGTTA TCATTTAATC 240

50

AACTTCAATG GTCTACTGAA ACAAAAATGG TAACTTTCA TTAGTGGATT ATTTAGAGTT 300

ATAGTAGTTG TTTCCAGAAA ACACTTCCTC ACAATTGTAC TTCCCAATCA AATCATGTGA 360

TCATACAGTT ATTCCCATGA AAGGCAGAAT GTTTGTTTCA AAATTAATCT AGTTTTCTGT 420

55

ACATTTAAAT TTGAGAAGGT GACAACTGGC TCTTTCCAG TCTTCCTTCA TGTCAGTTT 480

CTGATAGACC ACTATTGGCA AACAGTATCT GTCAACTACC AAATGTGTAA AATTTTCTGT 540

60

ATTTCACTTT GTCTTATTTG TAAATAGTGA ACTAAACTT TTGGCAGATC AGCAACATTT 600

GCTGAGCCTG TTTTPTAAGC TAATGTGTAT TCTTACTAAT GTTCCTATCA AGAATGGATT 660
 TGTAATATAT GCTGTCTATT TCTAATGTTC ACATTCATAT TTTGAGGTTC TATCTTATTT 720
 5 TAATAGAGAA CAGACTTCTC AAAAAATCTT CAGAAGCAGC TTATTATTGA AATATCGAAA 780
 TATTGAAATA AACCCGGTGG GTTAGATTAC TCATCTGTCC ACCAAGTGGG ACATTTGCAT 840
 GGACTGGGGG CTTAAAGGAC TTAGAAGAGA CCTGTAAGTA AATCCTGAAA ATGAGCCAAT 900
 10 CCCCACTTGA ATGGTTACTG GAGTAAACCC ACCTTTACCA CCCCAATTAC AGCACCCGAG 960
 GCCGATAAAC CAACTTGGCT CTGGTTCATT TTTCTTTTCT TCATTTGTGA TGCTCAGATT 1020
 15 CAAAATGTGT GTTCTACACT GTTACAGGCT TCTCTTTTGT TTGATTAAAG ATTTTAGTCC 1080
 TACTTTTGTA TGGACACATT AGAATATTCA GAGACCAAAA TAGAAGAATT TGCTGTTAGA 1140
 TATTTTTCAG AAGTCAGCAG ATTGTGGCA AATCATTAT TGCCTTTTT AAAAATTCAT 1200
 20 TTAAGCAGTT CAGAGAGTAG ACTACTCAGA AAATTATTTC ACGTAATTGT CTAAGAGGTC 1260
 AATATTTTTT AATGCATATT GAATCAAATA A 1291

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(2) INFORMATION FOR SEQ ID NO: 137:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GGCACGAGGA CCTACTTTTG TAACAGACCA TGGTTGTGTC CAAGGTAAAA CCACAGTGAT 60
 40 ATTTTGGAT GCTTTGTCTG CAATCTTGAC TTGTTTTTGC AGTATCATT TTCAGACTTC 120
 AAATGTGAA TCTTTTAAAC ATCTTGATAA TTTGTTGTG AGAGCTGTTT ATTCTAAAAT 180
 GTAATGAAAT TCAGTCTAGT TCTGCTGATA AAGATCATCA GTTTTGAAAG GTTACTGATT 240
 45 TTCTCTTCC CTCTTAGTTT TTTACCCAAT ATATGGAGAA GAGTAATGGT CAATCTTAAC 300
 ATTTTGTTTT AATTGTTTAA TAAAGCTGCT GGCAGTGGT GCAGCATTCC TACCTAGTGT 360
 50 CATAAAAGCA AAATACTTAC ATAGCTTTCT TAAAATATAG GAATGACATT ACATTTTATAG 420
 GAGAAAGTAA GTTGCTTTGC ACCGCCTACT TAATTCCTTT CCATATATTG TGATACAAAC 480
 TTTTGAATAT GGAATCTTAC TATTTGAATA GAAATGTGTA TGTATAATAT ACATACATAC 540
 55 ATAAGCATAT ATGTGTGTGT GTGTGTGTAT ATATATATAT ATGCATGCTG TGAAACTTGA 600
 CTACACAACA TAAATCACTT TTTAAATTC AGGAACGGGT AGTCTGACAC GGTGATTATC 660
 60 CTTTIGAGGC TGAATCCGTT ATTAACCTGT TATTTAGGTT TTAATCCAG TAGCAAGGGA 720

	TTCTAAGTTA GTTGCACTTA CATGATTATT GTGATTTAAA ACTAAGAATA AAGGCTGCAT	780
5	TTTCAAAGAT AAATTGGAAT TGCTGTTGGT GAAATAACAA CCAAATACT GAATCTGATG	840
	TACATACAGG TTTCTACAGG AAGAGATGGT ATAATTTACA ATTTGGAGAT TTAATAACCA	900
	GGGCTACCCA GAAAAAGTGA CTTGATAACA TGGTACCAAT AAGTAAGGGA TGCTCTCTCG	960
10	GTTTGCTTTT GCCACTTTCA AGATTTTAAC TTCTCAGGTT ATTAATCAAA ATTATTGTAT	1020
	AAGTTAGCCA ATAGAATTTT TAGGTTAAAA CAACAGATGG GGGGTTTGTG GAGTGTTTAA	1080
15	TGTCATGGGC ATTTTTAGTA GCATAGACCC TTGTCTCTGC ATTTGAATGT TTCGTATATT	1140
	TTTGTTCAC AGTTAATCTT CCTCCCCAA GTTTGCTATT CAAATCAACT GCCTGAATGA	1200
	CATTTCTAGT AGTCTGATGT ATTTTCTGA GGAATAGTTT GTGATTCCAA TGCAGGTGTC	1260
20	TTCATTACCA TTACCTCTAC ACTGCAGAAG AAGCAAACT CCTTTATTAG AATTACTGCA	1320
	CATGTGTATG GGGAAATAG TTCTGAAAGG CTAGAATGAT ACAAGTGAGC AAAAGTTGGT	1380
25	CAGCTTGGCT ATGGAGTGGT GGCAATAATC TCTAAACATT CCAAAGACC ATGAGCTGAA	1440
	CCTAAACTCC CTTGGGAATC TGGACAAAG GAATATGAAA ATTGCCATTT GAAAACTGAC	1500
	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	1560
30	AATTATAGAG ACTACAGCTA AATAAATTTG AACATTAAAT ATAATTTTAC CACTTTTGT	1620
	CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	1680
35	GATACTGAGT TGACTGTTCC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	1740
	GTGCACAACT TAGGTTATTT TTGCTTCCGA ATTTGAATGA AAAACTTAAT GCCATGGATT	1800
	TTTTCTTTT GCAAGACACC TGTTTATCAT CTTGTTTAAA TGTAATGTC CCCTTATGCT	1860
40	TTTGAAATAA ATTTCTTTT GTAAAAAAA AAAAAAAA AAAAAA	1906

45 (2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1935 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

55	TCTGAATAA TGCTAACAGA TCCCCCTGAG GGATTCTTGA TGGGCTGAGC AGCTGGCTGG	60
	AGCTAGTACT GACTGACATT CATGTGATG AGGGCAGCTT TCTGGTACAG GATTCTAAGC	120
60	TCTATGTTTT ATATACATTT TCATCTGTAC TTGCACCTCA CTTTACACAA GAGGAACTA	180

	TGCAAAGTTA GCTGGATCGC TCAAGGTCAC TTAGGTAAGT TGGCAAGTCC ATGCTTCCCA	240
	CTCAGCTCCT CAGGTCAGCA AGTCTACTTC TCTGCCTATT TTGTATACTC TCTTTAATAT	300
5	GTGCCTAGCT TTGGAAAGTC TAGAATGGGT CCCTGGTGCY TTTTACTTTT GAAGAAATCA	360
	GTTTCTGCCT CTTTTTGGAA AAGAAAACAA AGTGCAATTG TTTTTTACTG GAAAGTTACC	420
10	CAATAGCATG AGGTGAACAG GACGTAGTTN AGGCCCTCCT GTAAACAGAA AATCATATCA	480
	AAACACTATC TTCCCATCTG TTTCTCAATG CCTGCTACTT CTGTAGATA TTTCAATTCA	540
	GGAGAGCAGC AGTTAAACCC GTGGATTTTG TAGTTAGGAA CCTGGGKTCA AACCCTCTTC	600
15	CACTAATTGG CTATGTCTCT GGACAAGTTT TTTTTTTTTT TTTTTTTTAA ACCCTTCTCG	660
	AACTTTCCTT TTCTATGTCT ACCTCAAAGA ATTGTGTGA GGCTTGAGAT AATGCATTTG	720
20	TAAAGGTCTT GCCAGATAGG AAGATGCTAG TTATGGATTT ACAAGGTGTG TAAGGCTGTA	780
	AGAGTCTAAA ACCTACAGTG AATCACAATG CATTTACCCC CACTGACTTG GACATAAGTG	840
	AAAAGTAGCC AGAAGTCTCT TTTTCAAATT ACTTACAGGT TATTCAATAT AAAATTTTGT	900
25	TAATGGATAA TCTTATTTAT CTAAACTAAA GCTTCCTGTT TATACACACT CCTGTTATTC	960
	TGGGATAAGA TAAATGACCA CAGTACCTTA ATTTCTAGGT GGGTGCCTGT GATGGTTCAT	1020
30	TGTAGGTAAG GACATTTTCT YTTTTTCAGC AGCTGTGTAG GTCCAGAGCC TCTGGGAGAG	1080
	GAGGGGGGTA GCATGCACCC AGCAGGGGAC TGAAGTGGGA AACTCAAGGT TCTTTTTTACT	1140
	GTGGGGTAGT GAGCTGCCTT TCTGTGATCG GTTCCCTAG GGATGTTGCT GTTCCCTCC	1200
35	TTGCTATTCG CAGCTACATA CAACGTGGCC AACCCAGTA GGCTGATCCT ATATATGATC	1260
	AGTGCTGGTG GTGAETETEA ATAGEEECAE CCAAGCTGGC TATAGGTTTA CAGATACATT	1320
40	AATTAGGCAA CCTAAAATAT TGATGCTGGT GTTGGTGTGA CATAATGCTA TGGCCAGAAC	1380
	TGAAACTTAG AGTTATAATT CATGTATTAG GGTCTCCAG AGGGACAGAA TTAGTAGGAT	1440
	ATATGTATAT ATGAAAGGGA GGTATTAGG GAGAACTGGC TCCCACAGTT AGAAGGCGAA	1500
45	GTGCGACAAT AGGCCGTCTG CAAGCTGGGT TAGAGAGAAG CCAGTAGTGG CTCAGCCTGA	1560
	GTTCAAAAAC CTCAAAACTG GGAAGCTGA CAGTGCAGCC AGCCTTCAGT CTGTGGCCAA	1620
50	AGGCCAAGAG CCCCTGGCAA CCAACCCACT GGTGCAAGTC CTAGATTCCA AAGGCTGAAG	1680
	AACCTGGAGT CTGATGTCCA AGAGCAGGAA GAGTGAAGA AAGCCAGAAG ACTCAGCAAA	1740
	CAAGGTAGAC AGTGTCTACC ACCAYAGTGG CCATACCAAA GAGGCTACCG ATTCCTTCCT	1800
55	GCTACCTGGA TCCCTGAAGT TGCCCTGGTC TCTGCACCTT CTAAACCTAG TTC'TTAAGAG	1860
	CTTTCCATTA CATGAGCTGT CTCAAAGCCC TCCAATWAAT TCTCAGTGTA AGYTTCAAAA	1920
60	AAAAAAAAA AAAAA	1935

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

5	NGCCCCCTTG GCACAAGTCA GATGAAGCAC GTTCTGCCGG GGAGGCCCTC AMCTTCCAGA	60
15	GAGGACAGAC ACAGATTTCC TGCTGGGGGA GGGAGGAGTC CACGCATCCT GATGCTGCCT	120
	GGAAGCTTAT TTTCCCGTGG CCAGGATGCA TTTCTCTGAG TGGAAACAGG TTCTTGTCATG	180
20	TGGATGTGTG TTTCCCCAGG CAGACGGCCC CTCTYTTCCC AGCACTTCCC TGCCTCCCCC	240
	AGGCCTCAGG CCAGCACCCA GTTCCTCCTC ACATGGCAGG TGAGCACAGA CTTCTAGTTG	300
25	GCAGGAGCTG AGGAGGGTGA ACAAAACCCG AGGGAGGCCG GGCCCTTGCT CCCGAGTTGG	360
	GGGGAGGGGG TGTGGCAACG TGCCCCCGCG AGAGGCCACG CATGTTTGAC CAAAGCCCTC	420
	ATTGTGGTCC GAGGACAGCC TTTTCCCCAG GCCTCARAGC ATTGCTCATC CGTGCCAAAC	480
30	TGGGTAGGTG GATTTGAGCG GAAAGACTCC CAAAATGTGC CAAGAATTTC CCRGTCCCAG	540
	GCAGGCAGG GGAAACTAAG GGCAAGCAGG ATACAGGGCG AGGGATGTGG CAGGTGAGGG	600
35	GGCTCCCGCC TGTGCCCCCT CTCTCACCA TGTCTCCCCC ACCCTGCCTC AGTTCTCCGT	660
	TCCCCCTCAT CTCCGTCCCC CTCTTTGAAG CTGTCCCCAT CTCAGTGTC AACCAGCCTT	720
	CTCTCAKCT GACCACCCTC CTCTGACCSA CGCCCCCTCC TTGTCTGAAA AAAGGAGCCT	780
40	TGAATGGTGG AGGGAGGCAG TGGGGAGAAA GGTCTCACC GACAGGTTGG GAGAATGAGG	840
	TCAGCGGTGC TGGGAACAG ATGGAGGGGG CAGTGGGGAC AGGGCTTGGG CAGACACCAG	900
45	CAGGAATAAT TTGAAATGTG TGAGGTGACT CCCCAGAGGC CTTGGGCTTG GGCATTTGGG	960
	AAAAGAATGA TGTCTGGAAG GGCTTAAGGG ACACAGTGGA CGAGGGGAGA GTCCTCATCT	1020
	GCTGGCATT TGTGGGGTGT TAGTGCCAAA CTTGAATAGG GGCTGGGGTG CTGTCTTCCA	1080
50	CTGACACCCA AATCCAGAAT CCCTGGTCTT GAGTCCCCAG AACTTTGCCT CTTGACTGTC	1140
	CCTTCTCTTC CTACCTCCAT CCATGGAAAA TTAGTTATTT TCTGATCCTT TCCCCGCTT	1200
55	GGTCTAGCTC CTCTCCAAAC AGCCATGCCC TCCAAATGCT AGAGACCTGG GCCCTGAACC	1260
	CTGTAGACAG ATGCCCTCAG AATTGGGGCA TGGGAGGGGG GSTGGGGGAC CCCATGATTC	1320
	AGCCACGGAC TCCAATGCCC AGCTCCTCTC CCAAAACAA TCCCGACAAT CCCTTATCCC	1380
60	TACCCCAACC CTTTGCGGCT CTGTACACAT TTTTAAACCT GGCAAAAGAT GAAGAGAATA	1440

TTGTAA

1446

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(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTTTTTTTTT TTTGATATGA AATTGTCTTT CTCCATTGCA GAAATAAGCT AGGGAAACAC 60
TAACCCAAAA ACTTCTGTGA GAGCTGTTC TTTGGAGGCA GCATCACTTA TTGGCAGTAA 120
20 AGACTCAGTA TAAAAGCACC AGCATCCCTA CTTGGGTGAT GGGGATTAAT TTTATAGCAT 180
TCCATTTTCC TAGTGCCACA TGTGAAATG GATTTTGATG ATCTTAATCT ATATTCTACC 240
25 CTTATAATAA AAGATCAAAA GATATATCTC CTATGAACAG ATTGGAGATA GGAGATGAAA 300
AGTTGGGAGG ATGTCTTTAT TCTAATGTGA GGGTAGGGAA AATGTGGATA ACATTACTGG 360
GGTGARGGAG GCATGTGTTCT TTAGTTGGAG TTCTCATTTT TATTCTCCAG TACTGACTTG 420
30 TGGGGAAAGC ATACTTTTTTC ACTGCCAGGT ACTGAATGCA GAGGCTCAGT GAAGTATATA 480
TGTGGGAAGT GCATGCATTT CGTTTATTAG CAAACATAGC TGGATTAAGA CAAAGTTGTT 540
35 GGTTTGAAAA GGGGTTAAAG CCTTAAGTGA ACAAATCTAG CTAACAGTGA ATGAACTAGG 600
TAATATAACT TGCATATTTT TAATTTCCCTT TGGTTAAAGG TCCCCCATAC TTCTCTGTTT 660
GGAGACATGA GAAGTATGAT TACTTCAGTG TTAGTTTCT TAATTTTTTT TTTCCCTAT 720
40 TTGTCCCTTG TCACTTTGTT GCAAGCTAGA AATCTGTGGG TTATACATAG GGCAGCTCTT 780
TGTGAAAGTG GTTTATTCCA CTGGAGAAAG GGGATTGAAA ATCAGTTAGA ACCAATGTAT 840
45 TTCTTGCCCC ACGGAACACT ATTCTATATA GATAGCTGAA AGAAGCTGCT GTGAGGAGCT 900
CAGCTCCAAA CACAGGATCA GCACCTTGTA TAGGAATTCC CATGAATTAT GACTTCTCAT 960
TCTGTTTTAT CAGAGTGCAT ATATGTCCTA CTTCAGGAAA AGTAAAACAG TCATTTACGA 1020
50 AAGAAAGTCA ATCTGTATCC TAAGCATTTT AATAAAAAGT TAAAACAAAA AATTAAAAGG 1080
GACACTCGAG GGGGGGCCCC AAACCAAT 1109

55

(2) INFORMATION FOR SEQ ID NO: 141:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TAGGACTAAC TTAAATTCCTT TTATTCATCT TTTATTTATT AAAAAATTTT ATTTCTTTGA 60
10 ATTTTCCTGT AATTTCCTTA RGCTCTTCTA TAAAATGTTA TATTCATGTG AACCATACCT 120
CATTATCCTT AACATTTACT CTCAAAAAGC TTTTATTTT TATTTTTTTG AAGGTAGTTT 180
15 TTCTGTGTGT ACTCTGTAAC ATGATTTTGC TTTCAAATCA TTGTGTGTGCC CCCATACAAA 240
ATGCCTTTTA TTTTGTAGGA TCGTGGACTT TTTAGTATGG CATGAGTGTG CTAAAAGCCA 300
GATATCTTTC CACATTCACT GGTGGCTTTG ACACCTAGTT TTTAATCTCC CATCCTTACT 360
20 TTAAACCCTG ACAGTGCAGT CCTCAGTCAG GGCCAGGACC GGGCTGAGGC CCTTTGTGGA 420
GATGCTGCAC CACCAGCAGA AGGCTGAGAC CTGGTTACCT GTACCTGTTT ACTTGTAAATA 480
AAAAGAATTA TCTAAAA 497
25

30

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAGGCAGA GGCAAGCTGC CTGCCAACCC CCTCCCTCAA GGAATGGCCT TGCCCAGGAA 60
40 TGCCCACCAC ACATACCCTC TTCTTTTTTT CTAGTCAAAC TCTTGTATTAT TCCTTGGCTT 120
GCCTCCCTCC TTTCCTCCCC TCTCAACCTT TTAATTCTGG TTTCTATTTC ATGGGATTTG 180
45 GGGTTGAAGT TAAACTTACA ACAGTGCCGC CAACACCAAG TCTTGCAGGA AAAAAATACA 240
AAGAAATTTA ACAAAAAAAA AAAAAAAA 269

50

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

	TTGATTGACT ATGGTCTCTC CGGCTACCAG GAAGAGTCTG CCGAAGTGAA GGCCATGGAC	60
5	TTCATCACCT CCACAGCCAT CCTGCCCCTG CTGTTGGGCT GCCTGGGCGT CTTGGGCCTC	120
	TTCCGGCTGC TGCAGTGGGT GCGCGGAAG GCCTACCTGC GGAATGCTGT GGTGGTGATC	180
	ACAGGCGCCA CCTCAGGGCT GGGCAAAGAA TGTGCAAAAG TCTTCTATGC TGCGGGTGCT	240
10	AAACTGGTGC TCTGTGGCCG GAATGGTGGG GCCCTAGAAG AGCTCATCAG AGAACTCACC	300
	GCTTCTCATG CCACCAAGGT GCAGACACAC AAGCCTTACT TGGTGACCTT CGACCTCACA	360
15	GACTCTGGGG CCATAGTTGC AGCAGCAGCT GAGATCCTGC AGTGCTTTGG CTATGTCGAC	420
	ATACTTGTCA ACAATGCTGG GATCAGCTAC CGTGGTACCA TCATGGACAC CACAGTGGAT	480
	GTGGACAAGA GGGTCATGGA GACAAACTAC TTTGGCCCAG TTGCTCTAAC GAAAGCACTC	540
20	CTGCCCTCCA TGATCAAGAG GAGGCAAGGC CACATTGTCG CCATCAGCAG CATCCAGGGC	600
	AAGATGAGCA TTCCTTTTCG ATCAGCATAT GCAGCCTCCA AGCAGCAAC CCAGGCTTTC	660
25	TTGACTGTC TGCGTGCCGA GATGGAACAG TATGAAATG AGGTGACCGT CATCAGCCCC	720
	GGCTACATCC ACACCAACCT CTCTGTAAAT GCCATCACCG CGGATGGATC TAGGTATGGA	780
	GTTATGGACA CCACCACAGC CCAGGGCCGA AGCCCTGTGG AGGTGGCCCA GGATGTTCTT	840
30	GCTGCTGTGG GGAAGAAGAA GAAAGATGTG ATCCTGGCTG ACTTACTGCC TTCCTTGGCT	900
	GTTTATCTTC GAACTCTGGC TCCTGGGCTC TTCTTCAGCC TCATGCCTCC AGGGCCAGAA	960
35	AAGAGCGGAA ATCCAAGAAC TCCTAGTACT CTGACCAGCC AGGGCCAGGG CAGAGAAGCA	1020
	GCACTCTTAG GCTTGCTTAC TCTACAAGGG ACAGTTGCAT TTGTTGAGAC TTTAATGGAG	1080
	ATTTGTCTCA CAAGTGGGAA AGACTGAAGA AACACATCTC GTGCAGATCT GCTGGCAGAG	1140
40	GACAATCAAA AACGACAACA AGCTTCTTCC CAGGGTGAGG GGAAACACTT AAGGAATAAA	1200
	TATGGAGCTG GGGTTTAACA CTAAAACTA GAAATAAACA TCTCAAACAG TAAAAAATAA	1260
45	AAAAAAAC	1269

50 (2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1944 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

60 AAAAGGCAAA CTATAGGATA ACACAGAGCC CTTTTTGAAA ATAAATTGGC ATTGGAGTGT 60

	TTTACCCTCT AGCTGTTTTA CTTAGAATGT AACATATGCT GCCTACCCAC CTCAAAATGT	120
	CTGTACTGCA AGAGGGCCCT GGGCCTCTGC TTTCCATATT CACGTTTGCC CAGAGTTGTA	180
- 5	GTCCCAAAGA AGAGCATGGG TGGCAGATGG TAGGGAATTG AACTGGCCTG TGCAATGGGC	240
	ATGGAGCACA AGGGGTCACA GCATGCCTCC TGCCTTACCG TGGCAGTACG GAGACAGTCC	300
10	AGAACATGGT CTTCTTGCCA CGGGTGTTG TTGTCTCTGG TGGTGCTGCA TGTCTGTGGC	360
	TCACCTTTAT TCTTGAAACT GAGGTTTACC TGGATCTGGC TACTGAGGCT AGAGCCCACA	420
	GCAGAATGGG GTTGGGCCTG TGGCCCCCAA ACTAGGGGGT GTGGGTCAT CACAGTGTG	480
15	CCTTTTGTCT CCTAAAGATA GGGATCTACT TTTGAAGGGA ATTGTTCTTC CCAAATAAAT	540
	TTGCTTTACC TTGGTCCTTT CTTTGTGCC AGTATTCAAG TGGTATAGCT CTGAGCAGGG	600
20	TCACATTTGG CCAAACCTGA CACTGTCTTG CTGCATTCTC CTTTGGCAAA CATCAGGGTC	660
	AGAATTCAGG ATAGCCCTTC CTAGGGCACT GGACTTTCTG GCATGGGGGC TGTGTTTGCA	720
	CAAGTTATTT TCATGTTACC TGGAGAGTGT CCAGAGGCTG CTCTGAGGCT GAGGTGTGTT	780
25	CCCCCTTGCC TGGTTCCAGC TGTCAGAGGG ATACCATCCT AGGGTCTGGG AATCCAAGGC	840
	CACGAGACTC CTTGGTTTGT GGTCCGAGAT CCTGTACTAA GGAGGGTCTG GCCAGAGGAA	900
30	CAGACCAGCT TTGACACAAT GAAGCGCAAG GGAACAAGTG GTTGCCTGG TGTCTTACCT	960
	GTCCTGAACC TGGTCTGTG GGCCATTGAA AAGTTAGATC TGTGATCTCT GGGGTTTGTG	1020
	TGGCTTTGTT CAATGCTTCC ACTCTAGGGC AGGCAGAGCA GTCTATACTC TCCCAAGCCT	1080
35	GCTTGACCTC CAAGTAGAGC TGATACAGAG ATCTGTGAAT ATTGTGATAG AAATTCTTTG	1140
	GTATTCATAC ATTTAGCTG CAAGTCAGCA ATTTCCAGG TACCATGTAA GCTATAAAAC	1200
40	AGTCATTCTT AAAGACAGAG GATAGCTGTG ACTCATGGGA TCATGAGGTC CATGGCTGGT	1260
	TGCAGGTTCC CTTTTTCTTT CCTCAGGTTT TGTCTCTTCC TGTGTTGTCC CCAGCAAGGG	1320
	AGAGACTGTG GGGTGGATTG GGAGAACAGA TTAGGAGTAT AGCAAATGAA CCCAGAATGG	1380
45	AACAGTGGGG AGCTAACTGT GAATGAGGAG AGTACCTGCT GCAGGACCTG GAGGTCAGGT	1440
	GTGAATGCTG TATTGGCACA GGAATAAAT ATCCTGGCGT CTGGAGCCTT CACCTCTCCG	1500
50	TCAAGTCTTT CCTGTGATAC TGCCATGGCA CAGGATCTGA GTTGCAGCTC TGCACCTTAA	1560
	ATCACACCTT GGGCATGTG TGGGCTGCAG GGCTGCCAGG TTCTGTACTT GTGTCCAGCT	1620
	GTGGCCCTGG ATGCTGGAGC TGGAGGGTTT TCTGTGCTCA GACTGTAGCC TGTAGCTCTT	1680
55	GGCCTGTGTA GAGCCCCCTC CTGTGCCCTC AGTGGCTGTC GTTGTGTTAA ATCATCAGGA	1740
	AGATGGGAAA GGTGAGGCAG AATTTTCTG CCCTACAAAG GGTGGAAGAG AAAGGACACA	1800
60	GTATTTTCAT GAATTTACCA TATATCTTTG TTTTCTTCA ACGAAAAAGT TAATTGAGGC	1860

AATGTCATCT GCTCAAAGTT GAGTGGTTTA TTCACAATAA ACTGTAAGTT TCTGATTATA 1920

AAAAAAAAAA AAAAAAAAAA AAAG 1944

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(2) INFORMATION FOR SEQ ID NO: 145:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1021 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

TCGACCCACG CGTCCGGGGT GCGCAACGGG GAGTTCGGC TGGAGACCCG TGCTCTGGGC 60
20 CGGCGCCTTC ACCATGGCCT CGGCAGAGCT GGACTACACC ATCGAGATCC CGGATCAGCC 120
CTGCTGGAGC CAGAAGAACA GCCCCAGCCC AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC 180
25 TGTGGTGATT CTYTTGGGCT GGGGTGGCTG CAAGGACAAG AACCTTGCCA AGTACAGTGC 240
CATCTACCAC AAAAGGGGCT GCATCGTAAT CCGATACACA GCCCCGTGGC ACATGGTCTT 300
CTTCTCCGAG TCACTGGGTA TCCCTTCACT TCGTGTTTTG GCCAGAAGC TGCTCGAGCT 360
30 GCTCTTTGAT TATGAGATTG AGAAGGAGCC CCTGCTCTTC CATGTCTTCA GCAACGGTGG 420
CGTCATGCTG TACCGCTACG TGCTGGAGCT CCTGCAGACC CGTCGCTTCT GCCGCCTGCG 480
TGTGGTGGGC ACCATCTTTG ACAGCGCTCC TGGTGACAGC AACCTGGTAG GGGCTCTGCG 540
35 GGCCCTGGCA GCCATCCTGG AGCGCCGGGC CGCCATGCTG CGCCTGTTC TGCTGGTGGC 600
CTTTGCCCTG GTGGTCGTCC TGTTCACGT CCTGCTTGCT CCCATCACAG CCNTCTTCCA 660
40 CACCCACTTC TATGACAGGC TACAGGACGC GGGCTCTCGC TGGCCCGAGC TCTACCTCTA 720
CTCGAGGGCT GACGAAGTAG TCCTGGCCAG AGACATAGAA CGCATGGTGG AGGCACGCCT 780
GGCACGCCGG GTCTGGCGC GTTCTGTGGA TTTCGTGTCA TCTGCACAG TCAGCCACCT 840
45 CCGTGACTAC CTTACTTACT ACACAAGCCT CTGTGTCGAC TTCATGCGCA ACTGCGTCCG 900
CTGCTGAGGC CATTGCTCCA TCTCACCTCT GCTCCAGAAA TAAATGCCTG ACACCTCCCC 960
50 ACAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGGCCCGTA CCAATTTCG CCTATAAAGG 1020
T 1021

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(2) INFORMATION FOR SEQ ID NO: 146:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

	GGCACGAGGA GGGCCACGGC AGCCATCGCG CTTTGCAGTT CGGTCTCCTG GTGTACGGCC	60
	AACGCCAAGT AGGGGATTGC GTTCCCTCCA GTCGCAGACC CTATCAGATT TGGATATGTC	120
10	CTTCATATTT GATTGGATTT ACAGTGGTTT CAGCAGTGTG CTACAGTTTT TAGGATTATA	180
	TAAGAAAAC TGGTAACTGG TATTTCTTGG ATTGGATAAT GCAGGAAAA CAACATTGCT	240
15	ACACATGCTA AAAGATGACA GACTTGGACA ACATGTCCCA ACATTACATC CCACTTCCGA	300
	AGAACTGACC ATTGCTGGCA TGACGTTTAC AACTTTTGAT CTGGGTGGAC ATGTTCAAGC	360
	TCGAAGAGTG TGGAAAAACT ACCTTCCTGC TATCAATGGC ATTGTATTTT TGGTGGATTG	420
20	TGCAGACCAC GAAAGGCTGT TAGAGTCAAA AGAAGAACTT GATTCATAA TGACAGATGA	480
	AACCATTGCT AATGTGCCTA TACTGATTCT TGGGAATAAG ATCGACAGAC CTGAAGCCAT	540
25	CAGTGAAGAG AGGTTGCGAG AGATGTTTGG TTTATATGGT CAGACAACAG GAAAGGGGAG	600
	TATATCTCTG AAAGAACTGA ATGCCCCGACC CTTAGAAGTT TTCATGTGTA GTGTGCTCAA	660
	AAGACAAGGT TACGGAGAAG GCTTCCGCTG GATGGCACAG TACATTGATT AACACAACT	720
30	CACATTGGTT CCAGGTCTCA ACGTTCAGGC TTACTCAGAG ATTTGATTGC TCAACATGCA	780
	TAACTTGAAT TCAATAGACT TTGCTGGTT ATAAACAGA TGTTTMTTAG ATTATTAATA	840
35	TTAAATCAAC TTAATTTGAA TGAGAATTGA AACTGATTC AAGTAAGTTT GAGTATCACA	900
	ATGTTAGCTT TCTAATCCA TAAAAGTACT TGGTTTTTAC AGTTTATAAT CTGACATCAC	960
	CCCAGCGCCA TTTGTAAAGA GCAACTTTCC AGCAGTACAT TTGAAGCACT TTTTAAACAAC	1020
40	ATGAAACTAT AAACCATATT TAAAAGCTCA TCATGTTAAA TTTTATATGT ACTTTTCTGG	1080
	AACTAGTTTT TAAATTTTAG ATTATATGTC CACCTATCKT AAGTGACAG TTAATAATTA	1140
45	GCTTATTCAA TGATTGCATG ATGCCTTACA GTTTTCAATA ACTTTTTTTC TTATGCAAAC	1200
	GTCATGCAAT AAAACAACT CTAATGTTTG GCAAAAAAAA AAAAAAAA NTCGAGGGGG	1260
50	GGCCCGTACC CAATTCGCCC TAAAG	1285

55 (2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

-5	GGCACGAGGT GCGCGAGGGG TCAGTGGTTC TCTCGGGTCT CGGGACAGGT GAGCACCTG	60
	ATGAAGGCCA CGGTCCTGAT GCGGCACCTG GCGGGGTGCA GGAGATCGTG GCGCCCTCC	120
	GCAAGGGCGS CGGAGACCGG TTACAGGTGA TTTCTGATTT TRACATGACC TTGAGCAGGT	180
10	TTGCATATAA TGGAAAGCGA TGCCCTTCTT CTTACAATAT TCTGGATAAT AGCAAGATCA	240
	TCAGTGAGGA GTGTGGGAAA GAGCTCACAG CGCTCCTTCA CCACTATTAC CCAATTGAGA	300
15	TCGACCCACA CCGGACCGTC AAGGAGAAGC TACCTCATAT GGTGGAATGG TGGACCAAAG	360
	CGCACAATCT CCTATGTCAG CAGAAGATTC AGAAGTTTCA GATAGCCCAG GTGGTTAGAG	420
	AGTCCAATGC AATGCTCAGG GAGGGATATA AGACCTTCTT CAACACACTC TACCATAACA	480
20	ACATTCCTCT TTTTCATCTT TCTGCGGGCA TTGGTGATAT CCTGGAAGAA ATTATCCGAC	540
	AGATGAAAGT GTTCCACCCC AACATCCACA TCGTGTCTAA CTACATGGAT TTTAATGAAG	600
25	ATGGTTTTCT CCAGGGATTT AAGGGCCAGC TGATACACAC ATACAACAAG AACAGCTCTG	660
	TGTGTGAGAA CTSTGGTTAC TTCCAGCAAC TTGAGGGCAA AACCAATGTC ATCCTGCTGG	720
	GAGACTCTAT CGGGGACCTC ACCATGGCCG ATGGGGTTCC TGGTGTGCAG AACATTCTCA	780
30	AAATTGGCTT CCTGAATGAC AAGGTGGAGG AGCGGCGGA NCGCTACATG GACTCCTATG	840
	ACATCGTGCT GGAGAAGGAC GAGACTCTGG ATGTGGTCAA CGGGCTACTG CAGCACATCC	900
35	TGTGCCAGGG GGTCCAGCTG GAGATGCAAG GCCCCGTAAG GCGCAGGCTN CCAGNCCGCC	960
	TGCAGGCCGT GGTGAGGAGG GCGCCTCCC CAGAGTCTGC TCCCCGTGA ACACAGAGCA	1020
	GANGCCAGGG TGGCCAGCAG TGGCTGGGTC CTTCCGCGCC CCTCCGTCCT CCTTTCCCTG	1080
40	AGCACCTTCA TCACCAGAGG CTTGAAGGAA CCCC GCCATG TGGCAGGGCA CAGGCACTGT	1140
	TCCTGGTGAA CCTTGGACCA CAGCATGTCA GTGCTCTAGG GATTGTCTAC TCCAGGGATT	1200
45	TTCTTCAAAA TTTTAAACA TGGGAAGTTC AAACAAATAT AATGTGTGAA ACAGATCAAA	1260
	ATTTTAAAAA TGAAAAAAA GCTGCTCTGA TTCAGGGGAT GTGGGTGGG GTAGAACCTG	1320
	GACCTCTTGG CCTGGGGGCA CATGGGATGC TTCTAGGAAC ACAGTTTGAG AACCACCAA	1380
50	AAAAAA	1386

55 (2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2098 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

5	AGCCCTTCTC CCCGCGCTTG GGA	CTCTGAC ATCTTAAGGC TGCACGGTCG	TGTCCTTGTC	60
	TGGGTGAGGC CATGTCTGTG ATCCAAGGTT	CCTGGA	ACTG ACACAGGAAG GGGCTGTGAA	120
10	CCCTAAGTGG GTGTMATCTC CTCCRACCGA	GGCTTCTMAC	CCTGGAGATG GCAGTTACTC	180
	CTGGCCATGG TTGCTGAGCA TGGGCAGACC	AGTGGAGGCC	ACCCTACTGT GTTATCTGCG	240
	CCTTCRATGA AGTGAGACCC TTGGGGAGAA	CGGGCTGTGG	ATGAAGGAGT GGACTGCAGC	300
15	CTTGGCCTAG CCACTGGGCT GGGATCTTCT	GGGTCATGTG	ACTGTGTATC CAGGAGCAGA	360
	AACTGTATT CTCAGGATTC AGGATCTACC	CAGCACCAA	GATGTATTTT CAGGAGAACA	420
	GACCTAGAAA TGGGCCTGTC TGGCATTTC	GAGTCAGGCA	AAGCAGGCAG GGCCAGGGAG	480
20	CTTCTGTGGG TCTACACAAG AAGGTTCCTG	TGAGGGCTAT	CAGTTGTGTC CTTCTAGCTT	540
	GCTGGTAACT TTGGCGCCTC CGCCAAGCCC	TGCCAGACTC	CCCTGGCTGT GATGGCATTC	600
25	TGTGCCATCC TGCCTTGTC CCAGCCTCTG	CAGGATGCCC	TCCCTACCCA MCTTYTCCTG	660
	GGCCTTCCCT GTCCACTGGG CTGGATTTCAT	GTTCAAACCA	CTGGACTGGC AGGGCAACGA	720
	CTTCTTCCCA CCTCAAGATG AGGTCCCTCGC	CCCCCTGTCT	TGGCATAAAA ACACCTTTAA	780
30	AGCATGAGCC ATGTGCTTCT TTGCCCTTCT	CTGTCTGTGT	CCAATCTTCT GCCTCCAGT	840
	CACCTCCCTGG GGA	CTATG TGGCCACAC CATGTGTCCT	900	
35	GTCAATCCAG AACTGCCTCT GAGCTCCAGG	CTGACCACAG	ATCAGCCACA GCCTGATGCC	960
	TGCAGCCCCA CTTTGCTCAC CCTTCCCCCTC	CCCTCCTCCT	TCCTTCCACA CAGCAAGCCT	1020
40	ACCTTTYTCC ATCCATGCTC ACCATAGCCC	CCTTCCTTGT	GACCTGGACC CTCCATGTGA	1080
	CCTGGCTGAG ACTGTCAGCC TCCTGGAGGA	GTGGGGTCCA	CCTTCTTCTT GCCCTATGCA	1140
	GTGCAAGCTT CACTTCTCAC CCAGCAAGGT	TGACTCATCT	GCCTCCATGT CTCTGGGGCT	1200
45	TTGCTGTTGC CCTGAAACCT AGCTGGGCTG	GTCTTGCTCC	CAGCTTGCTT CCCCCTCCTC	1260
	GGATGTCCCT TTGCAGGCC CTGTGCTTCC	TCCGGCACCA	GTGTCTTGG CTGCCATGGC	1320
	AAGCTCATCA GGGGCTTGTA CCTGGTCTAC	CAAGCATGGT	AGCAGCTGCC TGCATGTAT	1380
50	CTCCATCTGG TCACTGCAGG TGCCAACCT	TCATCCCCCA	TGTTTCTCTG GGCCATGGAG	1440
	GGCTGACCTC CGTTTCTGGG GAATGTGGCT	GAGCTGTGGT	AACCAGCTAC ACCCCAGGTG	1500
55	CTCTTTCCAT GGTGGTGCCT GCTCATCTTG	CTGATGCAAA	CTAGGAAGTT AGGCTGCATC	1560
	TGGAGTGGC TTTGCTGGA GAGGTGCTTT	GCTGTCTCTC	AGACTCAGTC ACTGTGTTCC	1620
60	CTCCCCGCCT CTCTTATCTC CATGGCTGTT	TGCAGCTCTC	CCAGGTACTT TGGGGTCTGA	1680

GCTGGAATTC CTTTGTGGTT TGCTCTTCTG CTTCTCACTC TTGTATTAAAG AAGGATTCCA 1740
 CAAAGGGAGA GTGGCATCCC TGCTGCTGCT GTGCCAGACC AGAGTTTCCT GAGGGGCCCT 1800
 5 GACCCTAACC CTCCAGCTCA GCCCTGTACA CCTGACCCTG TAAATGAGTG GGGTTTGCTG 1860
 ACTGTAATCC CTGACACCAG TAAAACCAA AGGACTCTTG GGGGCTCAGT GTGAGAGCCA 1920
 GGGTTACCTA CTCTGCCAAG TGAGGACAAA CTGCTAGGCT GTATCCATA ATTTTCAGGAT 1980
 10 GAGAAACATT AACAATAAAA ATTTGTAGTA AACATAACCT CATGANGACT AAAAAAAAAA 2040
 AAAAACYGG GGGGGGGCCC GTAACCCATT GGGCCCTTNG GGGGGGNGTT TTAAAATT 2098

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(2) INFORMATION FOR SEQ ID NO: 149:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCGACCCACG CGTCCGAAC T GAGGCGGCGG CGGGAGCCGG TTGGKGTCTG GTCTTCGCGT 60
 30 CGGCCCGCGG GACCAGACGC TGCCCCCGGC GCGGGGAGAA GATGGTGCK AGCGGCCTCG 120
 GGCCCGCCAC GCGCCGCCAC GAGTGAGCCC AGCGCGACCG CGGGCGTCCG CCGAGCAGCT 180
 GGCCCGGCTG GGCCCGGGG GCGCANTGCC CGCCGGGGCG GGGTGGAGCT GATCAGAATA 240
 35 ATGTTTCAGCA TCAACCCCTT GGAGAACCTG AAGGTGTACA TCAGCAGTCG GCCTCCCTG 300
 GTGGTCTTCA TGATCAGCGT AANGCCCATG GCCATAGCTT TCCTGACCCT GGGCTACTTC 360
 40 TTCAAAATCA AGGAGATTAA ATCCCCAGAA ATGGCAGAGG ATTGGAATAC TTTCTGCTA 420
 CGGTTCATG ATTTGGACTT GTGTGTATCA GAGAATGAAA CCCTCAAGCA TCTCACAAC 480
 GACACCACAA CTCCGGAAAG TACAATGACC AGCGGGCAGG CCCGAGCTTC CACCCAGTCC 540
 45 CCCCAGGCCC TGGAGGACTC GGGCCCGGTG AATATCTCAG TCTCAATCAC CCTAACCTG 600
 GACCCACTGA AACCTTCGG AGGTATTCC CGCAACGTCA CCCATCTGTA CTCAACCATC 660
 50 TTAGGGCATC AGATTGGACT TTCAGGCAGG GAAGCCACG AGGAGATAAA CATCACCTTC 720
 ACCCTGCCTA CAGCGTGGAG CTCAGATGAC TCGCCCTCC ACGGTCACTG TGAGCAGGTG 780
 GTATTACAG CCTGCATGAC CCTCACGGCC AGCCCTGGGG TGTTCCTCGT CACTGTACAG 840
 55 CCACCGCACT GTGTTCTGA CACGTACAGC AACGCCACGC TCTGGTACAA GATCTTCACA 900
 ACTGCCAGAG ATGCCAACAC AAAATACGCC CAAGATTACA ATCCTTTCTG GTGTTATAAG 960
 60 GGGGCCATTG GAAAAGTCTA TCATGCTTAA AATCCCAAGC TTACAGTGAT TGTTCAGAT 1020

5 GATGACCGTT CATTAATAAA TTTGCATCTC ATGCACACCA GTTACTTCCT CTTTGTGATG 1080
 GTGATAACAA TGTTTTGCTA TGCTGTTATC AAGGGCAGAC CTAGCAAATT GCGTCAGAGC 1140
 AATCCTGAAT TTTGTCCCGA GAAGGTGGCT TTGGCTGAAG CCTAATTCCA CAGCTCCTTG 1200
 TTTTTTGAGA GAGACTGAGA GAACCATAAT CCTTGCCTGC TGAACCCAGC CTGGGCCTGG 1260
 10 ATGCTCTGTG AATACATTAT CTTGCGATGT TGGGTTATTC CAGCCAAAGA CATTTCAAGT 1320
 GCCTGTAACCT GATTTGTACA TATTTATAAA AATCTATTCA GAAATTGGTC CAATAATGCA 1380
 CGTGCTTTGC CCTGGGTACA GCCAGAGCCC TTCAACCCCA CCTTGGACTT GAGGACCTAC 1440
 15 CTGATGGGAC GTTTCACGT GTCTCTAGAG AAGGATTCCT GGATCTAGCT GGTACGACG 1500
 ATGTTTTTAC CAAGGTCACA GGAGCATTGC GTCGCTGATG GGGTTGAAGT TTGGTTTGGT 1560
 20 TCTTGTTTCA GCCCAATATG TAGAGAACAT TTGAAACAGT CTGCACCTTT GATACGGTAT 1620
 TGCATTTCCA AAGCCACCAA TCCATTTTGT GGATTTTATG TGCTGTGGC TTAATAATCA 1680
 TAGTAACAAC AATAATACCT TTTTCTCCAT TTTGCTTGCA GGAAACATAC CTTAAGTTTT 1740
 25 TTTTGTTTTG TTTTGTTTT TTTGTTTTT GTTTTCCTTT ATGAAGAAAA AATAAAATAG 1800
 TCACATTTTA ATACTACCAA AAAATGGACA AAAAAAGTCG AGGGGGG 1847

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(2) INFORMATION FOR SEQ ID NO: 150:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

45

GACGCTGACG AGAGAAGGCC TCTTCCTTGA GGGTTGGTGC TGTGTTGCAG TGACCGTGCC 60
 GGATTACGCC AACTCGGATC CGGCGGTCGT GAGGTCTGGA CGAGTCAAGA AAGCCGTAGC 120
 CAACGCTGTT CAGCAGGAAG TAAAATCTCT TTGTGGCTTG GAAGCCTCTC AGGTTCTGTC 180
 AGAGGAAGCT CTTTCTGGGG CTGGTGAGCC CTGTGACATC ATCGACAGCA GTGATGAGAT 240
 50 GGATGCCCAG GAGGAAAGCA TCCATGAGAG AACTGTCTCC AGAAAAAGA AAAGCAAGAG 300
 ACACAAAGAA GAACTGGACG GGGCTGGAGG AGAAGAGTAT CCCATGGATA TTTGGCTATT 360
 GCTGGCCTCC TATATCCGTC CTGAGGACAT TGTGAATTTT TCCCTGATTT GTAAGAATGC 420
 CTGGA CTGTC ACTTGCACTG CTGCCTTTTG GACCAGGTTG TACCGAAGCA CTACACGCTG 480
 60 GATGCTTCCC TGCCTTTGCG TCTGCGACCA GAGTCAATGG AGAAGCTGCG CTGTCTCCGG 540

	GCTTGTGTGA TCCGATCTCT GTACCATATG TATGAGCCAT TTGCTGCTCG AATCTCCAAG	600
	AATCCAGCCA TTCCAGAAAG CACCCCCAGC ACATTAAAGA ATTCCAAATG CTTACTTTTC	660
5	TGGTGCAGAA AGATTGTTGG GAACAGACAG GAACCAATGT GGGAAITCAA CTTCAAGTTC	720
	AAAAAACAGT CCCCTAGGTT AAAGAGCAAG TGTACAGGAG GATTGCAGCC TCCCGTTCAG	780
10	TACGAAGATG TTCATACCAA TCCAGACCAG GACTGCTGCC TACTGCAGGT CACCACCCTC	840
	AATTCATCT TTATTCCGAT TGTCAATGGA ATGATATTTA CTCTGTTTAC TATCAATGTG	900
	AGCACGGACA TCGGGCATCA TCGAGTGAGA CTGGTGTTC AAGATTCCCC TGTCCATGGT	960
15	GGTCGGAAC TCGCAGTGA ACAGGGTGTG CAAGTCATCC TGGACCCAGT GCACAGCGTT	1020
	CGGCTCTTTG ACTGGTGGCA TCCTCAGTAC CCATTCTCCC TGAGAGCGTA GTTACTGCTT	1080
20	CCCATCCCTT GGGGGCAGCC TCGAGTGTAG TCCATTAGTA ATCAGATTCC AGTTTGGACA	1140
	GGGTGGCTGG ATTGTATATC TCGTTAGTAA TGTACATGCT CTTCAGGTTT TAGGGCTCCT	1200
	GTTAGGGGAG GGAGAAATGT TGAATCAAGA GGGAAAACAA CTAATATGAT TTATAAACAT	1260
25	ATTTTAATGT AAAAATTTGC ATTTAAAGG AGTGGCCCTG TTTTCTGTGT TAAAACCCCA	1320
	TTTGGTGCTA TTGAGTTTGT TCTTTATTCT TTTATCCCAG TGAAAATTGT TGATCTTGCT	1380
30	GTAGGAAAAA ATTAACTCT TTGAATCTCC AAACAAGGAA GTTTCAGCAT TCCCTTATGG	1440
	ATCAGAGGAA CCTTAGAGGC CTGAAATTGT TGCTTCCAGT TTAGCTGCCC CTCAAATTCA	1500
	AGTGAATATT TTCCCTTCTC CCTTTACCCT TCTCCAGAAA TAAAGCAGGT GACAGGGTTT	1560
35	CAGAATCTT	1569

40 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

50	CCCACGCGTC CGGAAGGATT GACCAGTTAA CCAACATCTT AGCCCCCATG GCTGTTGGCC	60
	AGATTATGAC ATTTGGCTCC CCAGTCATCG GCTGTGGCTT TATTTGGGGA TGGAAGTTGG	120
	TATCCATGTG CGTGGAGTAC GTCCTGCTCT GGAAGGTTTA CCAGAAAACC CCAGCTCTAG	180
55	CTGTGAAAGC TGGTCTTAAA GAAGAGGAAA CTGAATTGAA ACAGCTGAAT TTACACAAAG	240
	ATACTGAGCC AAAACCCCTG GAGGGAAGTC ATCTAATGGG TGTGAAAGAC TCTAACATCC	300
60	ATGAGCTTGA ACATGAGCAA GAGCCTACTT GTGCCTCCCA GATGGCTGAG CCCTTCCGTA	360

CCTTCCGAGA TGGATGGGTC TCCTACTACA ACCAGCCTGT GTTTCCTGGCT GGCATGGGTC 420
 TTGCTTTTCCT TTATATGA CTCTGGGCT TTGACTGCAT CACCACAGGG TACGCCTACA 480
 5 CTCAGGGACT GAGTGGGTTT CATCCTCAGT ATTTTGATGG GAGCATCAGC TATAACTGGA 540
 ATAATGGGAA CTGTAGCTTT TACTTGGCTA CGTCGAAAAT GTGGTTTGGT TCGGCAGGTC 600
 10 TGATCTCAGG ATTGGCACAG CTTTCCTGTT TGATCTGTG TGTGATCTCT GTATTCATGC 660
 CTGGAAGCCC CCTGGACTTG TCCGTTTCTC CTTTGAAGA TATCCGATCA AGGTTTCATT 720
 AAGGAGAGTC AATTACACCT ACCAAGATAC CTGAAATTAC AACTGAAATA TACATGTCTA 780
 15 ATGGGTCTAA TTCTGCTAAT ATTGTCCCGG AGACAAGTCC TGAATCTGTG CCCATAATCT 840
 CTGTCAGTCT GCTGTTTGCA GCGTCATTG CTGCTAGAAT CCGTCTTGG TCCTTTGATT 900
 20 TAACTGTGAC ACAGTTGCTG CAAGAAAATG TAATTGAATC TGAAAGAGGC ATTATAAATG 960
 GTGTACAGAA CTCCATGAAC TATCTTCTTG ATCTTCTGCA TTTTCATCATG GTCATCCTGG 1020
 CTCCAAATCC TGAAGCTTTT GGCTTGCTCG TATTGATTTC AGTCTCCTTT GTGGCAATGG 1080
 25 GCCACATTAT GTATTTCCGA TTTGCCCAA AACTCTGGG AAACAAGCTC TTTGCTTGGC 1140
 GTCCTGATGC AAAAGAAGTT AGGAAGGAAA ATCAAGCAA TACATCTGTT GTTTGAGACA 1200
 30 GTTTAACTGT TGCTATCTG TTACTAGATT ATATAGAGCA CATGTGCTTA TTTTGTACTG 1260
 CAGAATTCCA ATAAATGGCT GGGTGTTTTG CTCTGTTTTT ACCACAGCTG TGCCTTGAGA 1320
 ACTAAAAGCT GTTTAGGAAA CCTAAGTCAG CAGAAATTAA CTGGATTAAAT TTCCCTTATG 1380
 35 TTAGGGGCCA TGGRAAAAAA ATTGGGAAAA GGAAAACTC AGTTTTAAAT ACGGGAGACT 1440
 ATAATGGATA AACTGRATT CCCCTATTTT TCATGAGTAG ATACAATCTT ACGTAAAGA 1500
 40 GTGGTTAGTC ACGTGAATTC AGTTATCATT TGACAGATTC 1540

45 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

55 TACTTATGAG GTCAATTGGA AATAAGAACA CCATTTTACT GGGTCTAGGA TTTCAAATAT 60
 TACAGTTGGC ATGGTATGGC TTGGTTTCAG AACCTTGGAT GATGTGGGCT GCTGGGGCAG 120
 TAGCAGCCAT GTCTAGCATC ACCTTCTCTG CTGTCAGTGC ACTGTGTTCA CGAACTGCTG 180
 60

	ATGCTGATCA ACAGGGTGTC GTTCAAGGAA TGATAACAGG AATTCGAGGA TTATGCAATG	240
	GTCTGGGACC GGCCCTCTAT GGATTCAITTT TCTACATATT CCATGTGGAA CTTAAAGAAC	300
5	TGCCAATAAC AGGAACAGAC TTGGGAACAA ACACAAGCCC TCAGCACCAC TTTGAACAGA	360
	ATTCCATCAT CCCTGGCCCT CCCTTCCTAT TTGGAGCCTG TTCAGTACTG CTGGCTCTGC	420
10	TTGTTGCCTT GTTTATTCCG GAACATACCA ATTTAAGCTT AAGGTCCAGC AGTTGGAGAA	480
	AGCACTGTGG CAGTCACAGC CATCCTCATA ATACACAAGC GCCAGGAGAG GCCAAAGAAC	540
	CTTTACTCCA GGACACAAAT GTGTGACGAC TGAAATCAGG AAGATTTTTC TATCAGCACC	600
15	CAGGTCCTAG TTTTCACCTC TAGTTCTGGA TGTACATTCC ATTTCCATCC ACAGTGTACT	660
	TTAAGATTGT CTTAAGAAAT GTATCTGCAT GAACTCCGTG GGAATAAAG GAAGTGGGAA	720
20	CTTAGAACCA GACAGTTTTT CAAAGATGTT ACAATTTCTT TTGAAAAACC TTTTGTATTAT	780
	TAGCACCAAT TTCTYGCCAC TAAGCTATTT GTTTTATTAT ACATCCTTTA ATTAATAACT	840
	ATATATGTAA CTTCTTAGAT ATTAGCAAAT GTCTCTGCTA CCATTTCTTT AAGGTGTTGA	900
25	GCTTTAACTC TATGCTGACT CAGTGAGACA CAGTAGGTAG TATGGTTGTG GACCTATTIG	960
	TTTTAACATT GTAAAATTTT GAGTCAGATT TTAATATTGT AAAATCTTGG GTCAAATAAT	1020
30	TCAAAGCCTT AATGCAGATG CACTAAAACA AAGAAATGGT AAATGAATTG TTTGCATTTA	1080
	AAAAAAAAAA CTCCTAAGAA AACTGTACTA AATCTGAATC ATGTTTTGAG CTTGTTTGCA	1140
	GTACTTTTAA ACATTATTCA CTA CTGTTTTT TGAAGTGAGA AAGTATCAGC CATTTAGCAT	1200
35	TTAAGTTGGG GTATTTAGAG CCTGTAATCT AAATGCTGGC TCAAATTTAT TCCCCAGCTA	1260
	CTTCTTATAC CACTATTCTT TTAATGTTTG CATAATCATA AGCACCTCAA CACTTGAATA	1320
40	CATAATCTAA AAATTATATA GTAAAGCTGG TAGCCTTGAA AATGTCAGTG TGATATCTAT	1380
	TATGTAGATA AATATATATA GTGGCCTTTC AGGACTGTCA CAGTAACACT TTATTTACAG	1440
	AGCTAATGTT TGTCCTAAAT TTTCAGGACC CTAGAGGAGA GCTTTATACA ATTACCGATG	1500
45	TGAATTTCTC TAAAGTGTAT ATTTTGTGT CCAGTTATAT TATTTAAAAA AGTGTTACTT	1560
	TGTAAAAATT GTATATAAAG AACTGTATAG TTTACACTGT TTTCATCTTG TGTGTGGTTA	1620
50	TTGCTTAATG CTTTTTAAAC TTGGAACACT CACTATGGTT AAATAAGGTC TTAAAAGAAA	1680
	TGTAAATATT YGTTAATAA AGTTAAATAT TTTAATGAT	1719

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(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 863 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

5
GGCACGAGGG AAGCCGGGAC GATGTCCGCA TGACAACCGA CGTTGGAGTT TGGAGGTGCT 60
TGCCTTAGAG CAAGGGAAAC AGCTCTCATT CAAAGGAACT AGAAGCCTCT CCCTCAGTGG 120
10 TAGGGAGACA GCCAGGAGCG GTTTCTGGG AACTGTGGGA TGTGCCCTTG GGGGCCGAG 180
AAACAGAAG GAAGATGCTC CAGACCAGTA ACTACAGCCT GGTGCTCTCT CTGCAGTTCC 240
15 TGCTGCTGTC CTATGACCTC TTTGTCAATT CCTTCTCAGA ACTGCTCAA AAGACTCCTG 300
TCATCCAGCT TGTGCTCTTC ATCATCCAGG ATATTGCAGT CCTCTTCAAC ATCATCATCA 360
TTTTCTCAT GTTCTTCAAC ACCTTCGTCT TCCAGGCTGG CCTGGTCAAC CTCCTATTCC 420
20 ATAAGTTCAA AGGGACCATC ATCCTGACAG CTGTGTACTT TGCCCTCAGC ATCTCCCTTC 480
ATGTCIGGGT CATGAACPTA CGCTGGAAAA ACTCCAACAG CTTCATATGG ACAGATGGAC 540
25 TTCAAATGCT GTTTGTATT CAGAGACTAG CAGCAGTGTT GTACTGCTAC TTCTATAAAC 600
GGACAGCCGT AAGACTAGGC GATCCTCACT TCTACCAGGA CTCTTTGTGG CTGCGCAAGG 660
AGTTCATGCA AGTTCGAAGG TGACCTCTTG TCACACTGAT GGATACTTTT CCTTCCTGGA 720
30 TAGRAGCCA CATTTGCTGC TTTGCAGGGG AGAGTTGGGC CCTATGCATG GGGCAAAACA 780
GGTGGGATTT TCCAAGGGAA GGGTTCAGAA TTAGGCTGTG TGTTCAGCC ATTTCCAAGG 840
AAGGGGAAGG GTTTCCTTNC CCT 863
35

(2) INFORMATION FOR SEQ ID NO: 154:

40
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

50 AACAGCAAAA AAGAATGATT TCTTCTGAAA TTGTGGAACA TGAGGATTCA AGTTTTTATT 60
TGTTACTAG GTGCTGGAGG AACATCCAG TTCACAAAGC CCCATCTCT TCCTCTGGAG 120
CCAGAGCCTG CGGTGGAATC AAGTCCAAC TAAACATCAG AACAAATAAG AGAGAAATAA 180
55 GAATAGAATG AATGACCCCA AAATARGGTT TTCTTGGGCG AGGATGTGCT GGATTAGGAA 240
AGGTGACATG ACACAGGCAG AGCAGAGTGG CAGCCACCAC AGAATACAGT GTGTGTTATT 300
ACGAGGAGCC AGCAGTTGAG CCTAAGGTCC TTCTACCTAC CTGGTATTGG CATTTGAGGT 360
60

	CGGAAACCCCT CTAAGTCCCC ATAAGCCAGG AAAAGTGAAA AGAGAACACA GTTCCTTTAA	420
	GAAGTGGCAG CAAGGCTTGA GGCCTTATGT ATGTAGCTGA GTCAGCAAGG TACATGATGC	480
5	TGCTCTGCTTT CAAAAGGACT TTTCTCTCCT AGCTGACTGA CTCCTTCCTT AGTTCAAGGA	540
	ACAGCTGAGA CAGACCTCTG CTGAGTAGCT CTGTGATGAC AAAGCCTTGG TTAACTGAG	600
10	GTGATCCTCA GGTGTGAGG TTTATTAGTC CCCAAGGCAA ACACAAATAT TAGATTAATA	660
	ATCCAACCTT AATAGTATAC ATTAAAAGA AAAAAACAA AAGCCCTGGA AGNITGAGGC	720
	CAAGCCTGCT GAGTATTGCA GCTGCATTTG CCCAAAGGGA ATCCAGAACA AGTCCCTCCC	780
15	TGTATTTTGT TCTTGAGAGG GGTCACTCTA GAAGCTAGAT CCTATCAGGA TGAGGAGCAG	840
	CAGCCCAGGG CTTGTCTGGA TCAGCACCAA CGATTTTAAA GAAAAAGGA AGAGTTTCTT	900
20	AGATGAGTAA TTGTTATTGA AGATAGTCAG TGATAACCAC TGACCAGATG CTATCAATAC	960
	ACTATGTGTC CTTTTTAGAA TAAAGATTAC ATATCATCAT TCCTTTGGGG AAAATTGTTA	1020
	TTCAGGTATA AAAACAAGAG ATTATAATAA AAAANTAAA GAACCCTAAA AAAAAAAAC	1080
25	CTCGTGCCGA ATCCCTGCA G	1101

30 (2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2031 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

40	CAATTAACCC GTTTGAGGCC TAGGTTGTTT GGCAAGCCCC NGGCCTAAAG TTTTAATTCG	60
	GCAGAGCCAA GGGCTGAAA GGAAGGGAAA GGGGAGGTA GCGGGAGGGT AGCAGGTGAG	120
45	TTCCTAGGGC TGGAAGGTTT AGCAGCAGCC TGGTGCAGTG CCCTGTCATC AAGACAAACC	180
	CACGGTCCTC CTGGGTGCCT ACCAAGCTTG GTTTGTACAA AAGCAAGGTG GGAGTCTATT	240
	TTTGTACATG AGATACATCA CACTTACCTG TGGGCCAGTA TTGTGAAGTG AGTCTGAGTT	300
50	GTTTACTACTG ATGCCTTCCC TGCCCACCAC AAATTGTGTA CATAGTCTTC AGAATGATAC	360
	CACCCCTTTC CCCAGCTCCC AACCAAGAGC TGGTTCTAGG CCTGTGTTAT ATGTCATATT	420
55	TAGCGTTTTT ATATATGACC TTTGATTTCT GTTGTGTTGTA TTTTAGCACA GTGTATGCAC	480
	CTTCATTTAA ATACATCTGT GTGCATACAG ATACGCATAT ATGTGTGTGC GTATGCATAT	540
	ATCTCTCATC TGTAGTTTCC AAGAGTTCAG CTGAAGCAGA TGGAGTCCTG CAGCCCAGGA	600
60	GACACCTGTC ATCCCTGCTA ATAGTGTGTTG CCACAAGTAT TAGTGAGTCT TCCTTATTAA	660

TATTTTCATT TCAGAAGACT GAAGCAAAGC TGATAGTGTT TGCTGTTTCT TTGGCAGCTA 720
 AGTGAGGGTC TTGGGATGAC TTGCTGTGTT CCTCAAGCTG CACTTTGGGG CCATCTCTGC 780
 -5 AGTATTAAGC CCCCTTTTGT CTGGTGGTA CTCTGTCTGT GCCTGTGTGT GTGTGTGATA 840
 GTCACCTCTG CATGGCTTCC ATGTCTGGTT TGTGGCATT TGGGATAAGT GCTGAACCAG 900
 10 AGCATTTCGA GTTTGTTTGA GGCTCGTTG CCAATGATAG ATCACTCCTG TTGACCTGGT 960
 ATGTCTGCTT GCTTGCTGCT TTTCTTGCT TTCTCTTGA AGAGGAAAGG ACTCTGGTCA 1020
 GGCCAGGCT GAGTGAGATG AGCTGCAGCT GGCTCATGGC CTTCTTAGAG CAGAGAGAGG 1080
 15 AGTATGTCAT TTTACTAAGT TCCTAAACAA ACATTTATGC AGGCAACACT CCTTCAGAT 1140
 CCAGAACTG AGGCACAATA GGGTTATGAC TTGCTCAAGA ATATGTAGCT GCTAGGGGGT 1200
 20 AAATCAAGGC ATCACAATTT CTGTCAGCG GGCAGGAATA GGCTGTGAAT TGCTAGCACT 1260
 TTTTTTTTAA GCAATTACTT TTTGACTTGT TCCTCTGAAA GTGCAAGAGG CGTACACCTT 1320
 TCCCAAATGT AGACTAGAAT CTGCAGGATG CCACCCACTG TATAGTTCTG CTTTCCAGA 1380
 25 GAGGAAGAAC TTTTAGAAAC CAAATGATCT TAATTGTTAT TGCCACCCC TGGCTTTTCC 1440
 GGGTAGAAAA TTCACAGTAG GAATGATTGT TAAGAGAGAG TGCTTGAAC CATGGGTAA 1500
 30 CAGGAAAGGC TACCTAACTT CACATATCTG CAACCAGAGC AGCCACCAAG CATTACTTAG 1560
 CAGCAGGAAA ATGATTGTAT TTGAGTTCCT GTGTGTCCAA AACTGAGGCA CCATGTTCTT 1620
 TGAAAACATG CCACCTCAAG GCTGGGCGCG GTGGCTCACA CCTGTTAATC CCAGCACTTT 1680
 35 GGGAGGCCGA GCGGGGCGGA TCACCGGAGT CGGGGAGTTT GAGACCAGCC TGGACCAACA 1740
 TGGGAGAAAC CCCATCTCTA CCTAAAAATA CAAAATTAGC CGGGCGTGGT GGCAATGCGCC 1800
 40 TATAATCTCA GCTACTTGGG AGGGYTGAGG CAGGRGAATT GCTTGAACCC RGGANGGCGG 1860
 AGGTTTGC GG TTGAGTTGAG GATCGTGCCA TTGCACTTCC GGGCCTTGGG GCAACAACAG 1920
 CAAAAAYTCC GTCTTCAAMW MRTGCCGAAT TCGATATCAA GCTTATCGAT ACCGTCGACC 1980
 45 TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGNGATC GTATTACAAT C 2031

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(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

	CCTGCACCCCT GAGCCCTTCA CCCCTCCGAG TTCCCCCAG GTTGGCTTCC TTCGATTCCCT	60
	TTTCTTGGTA TCAACGTTTG ATTGGAAGAA CAACCCCTC TTTGTCAACC TCAATAATGA	120
-5	GCTCACTGTG GAGGAGCAGC TCGGGCACAG CTCMCCGTYA TGGTCATTGT TACCCCCCAA	180
	GACCGCAAAA ACTCTGTGTG GACACAGGAT GGACCCTCAG CCCAGATCCT GCAGCAGCTT	240
10	GTGGTCTCTGG CAGCTGAAGC CCTGCCCATG TTAGAGAAGC AGCTCATGGA TCCCCGGGA	300
	CCTGGGGACA TCAGGACAGT GTTCCGGCCG CCCTTGGACA TTTACGACGT GCTGATTCCG	360
	CTGTYTCCTC GCCATATCCC GCGGCACCGC AGGCTTGTGG ACTCGCCAGY TGCTCTCCTC	420
15	TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC TCATCCCTGA TGCCCGTGCT GGGTNATGAT	480
	CCTNCTCAGC TCTATCTGAC GCAGCTCAGG GAGGCCTTTG GGGATCTGGC CCTTTTCTTC	540
20	TATGACCAGC ATGGTGGAGA GGTGATTGGT GTCTCTGGA AGCCACCAG CTTCAGCCG	600
	CAGCCCTTCA AGGCCTCCAG CACAAAGGGG CGCATGGTGA TGTCTCGAGG TGGGGAGCTA	660
	GTAATGGTGC CCAATGTTGA AGCAATCCTG GAGGACTTTG CTGTGCTGGG TGAAGGCCTG	720
25	GTGCAGACTG TGGAGGCCCG AAGTGAGAGG TGGACTGTGT GATCCCAGCT CTGGAGCAAG	780
	CTGTAGACGG ACAGCAGGAC ATTGGACCTC TAGAGCAAGA TGTCAGTAGG ATGACCTCCA	840
30	CCCTCCTTGG ACATGAATCC TCCATGGAGG GCCTGCTGGC TGAACATGCT GAATCATCTC	900
	CAACAAAACC CAGCCCCAAC TTTCTCTCTG ATGCTCCAGC ATTGGGGCAG GGGCATGGTG	960
	GCCCATGTAG TCTCCTGGGC CTCACCATCC CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA	1020
35	GGAAGTGAAC CCAGGAGATC CATCCACCTA TTAGCCCTGG GCCTGGACCT CCCTGCGATT	1080
	TCCCACTCCT TTCTTAGTCT TCTTCCAGAA ACAGAGAAGG GGATGTGTGC CTGGGAGAGG	1140
40	CTCTGTCTCC TTCTGTCTGC CAGGACCTGT GCCTAGACTT AGCATGCCCT TCACTGCAGT	1200
	GTCAGGCCTT TAGATGGGAC CCAGCGAAAA TGTGGCCCTT CTGAGTCACA TCACCGACAC	1260
	TGAGCAGTGG AAAGGGGCTA TATGTGTATG AATAGACCAC ATTGAAGGAG CACAATGCCC	1320
45	TCCTGTGTTG ATGCCACTTC CCAGGGTGGA GACAGTGGA AAGAACCGAG GACAGGAAAG	1380
	GATTGGGTAG GTGAAGGGGT CAGGGGACTG GTAGTCACCC AATCTTGGAG AGGTGCAAAA	1440
50	AGCACTGGGG GCTACCCGTT AGCTGCATCT GCCCTGGCTG TTTGCCCGTT CATGTCACAA	1500
	ACTGCCACTA CTATGTACCT GCAGTGGGGT TGCAGAGATG GGGGAGACTC AAGTCTTACT	1560
	CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG AATGCTGCCT CCTTTCAGTC TGGTCTACAC	1620
55	CCACTTTCTG GTAGCCTCTC TGCTTCTGTG AATTCTGGCT GTTTTTCAG ACTCAGCTCA	1680
	AATAGTGCCC CTCCTTAAGC CCATCCCTCG CCCCCAGCCT GAGGTGATCT TTCCCTCCTC	1740
60	TGAAGTATTA GAGCAGTTAC TGTCTGTTCA GTTCGTTTGG CAGGCACACA CAGTGGCATA	1800

AATTCTATTG TTTTGAAGTC TGATTTAAAA TTAAATTGCA GCTGGGCGTG GTGGCTCATG 1860
 CTTGTAATCC CAACACTTAG GGAGTMAGGR GAATCACTTG ASCYCAGGAG TYCTAGACCA 1920
 -5 ATCTGGGCAA MAGAGAGACC CCATCTCTTT TAAATAAAAA GTTAAATTGC TTAAAAA 1980
 A 1981

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(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 915 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTCGG TGCTGCGTGT ACTGCTGGGC 60
 GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120
 25 GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180
 TACCAGCCAG ATCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAAC TCTGGCTGGG 240
 30 TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAAC TTGTT CTTGATTCTG 300
 CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360
 CCAGCCATG TCTGCCTGGG GTTCCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG 420
 35 ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480
 AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540
 40 ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600
 ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660
 ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720
 45 TTAAATCAA CCAAAATTCT GATGCCCAA ATAACCACIT TTAATGCCTT GGTGTAAGTA 780
 TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840
 50 AACCATATAT CCTATTTTAT TTCTCCTTT TAAACCTTA TAACTATAA MAAAAA 900
 AAAAAA CCGA 915

55

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 2117 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

	AGAGCGAAGC GAGGGTGGCG CGGGTCCGGG CATGAAGCTG GGCCGGGCCG TGCTGGGCCT	60
	GCTGCTGCTG GCGCCGTCCG TGGTGCAGGC GGTGGAGCCC ATCAGCCTGG GACTGGCCCT	120
10	GGCCGGCGTC CTCACCGGCT ACATCTACCC GCGTCTCTAC TGCTCTTCG CCGAGTGCTG	180
	CGGGCAGAAG CGGAGCCTTA GCCGGGAGGC ACTGCAGAAG GATCTGGACG ACAACCTCTT	240
15	TGGACAGCAT CTTGCAAAGA AAATCATCTT AAATGCCGTG TTTGGTTTCA TAAACAACCC	300
	AAAGCCCAAG AAACCTCTCA CGCTCTCCCT GCACGGGTGG ACAGGCACCG GCAAAAATTT	360
	CGTCAGCAAG ATCATCGCAG AGAATATTTA CGAGGGTGGT CTGAACAGTG ACTATGTCCA	420
20	CCTGTTTGTG GCCACATTGC ACTTTCCACA TGCTTCAAAC ATCACCTTGT ACAAGGATCA	480
	GTTACAGTTG TGGATTGAG GCAACGTGAG TGCCTGTGCG AGGTCCATCT TCATATTTGA	540
25	TGAAATGGAT AAGATGCATG CAGGCCTCAT AGATGCCATC AAGCCTTTCC TCGACTATTA	600
	TGACCTGGTG GATGGGGTCT CCTACCAGAA AGCCATGTTT ATATTTCTCA GCAATGCTGG	660
	AGCAGAAAGG ATCACAGATG TGGCTTTGGA TTTCTGGAGG AGTGGAAAGC AGAGGGAAGA	720
30	CATCAAGCTC AAAGACATTG AACACGCGTT GTCTGTGTCG GTTTTCAATA ACAAGAACAG	780
	TGGCTTCTGG CACAGCAGCT TAATTGACCG GAACCTCATT GATTATTTTG TTCCCTTCCT	840
35	CCCCCTGGAA TACAAACACC TAAAAATGTG TATCCGAGTG GAAATGCAGT CCCGAGGCTA	900
	TGAAATTGAT GAAGACATTG TAAGCAGAGT GGCTGAGGAG ATGACATTTT TCCCCAAGA	960
	GGAGAGAGTT TTCTCAGATA AAGGCTGCAA AACGGTGTTC ACCAAGTTAG ATTATTACTA	1020
40	CGATGATTGA CAGTCATGAT TGGCAGCCGG AGTCACTGCC TGGAGTTGGA AAAGAAACAA	1080
	CACTCAGTCC TTCCACACTT CCACCCCCAG CTCCTTTCCC TGAAGAGGA ATCCAGTGAA	1140
45	TGTTCTGTGTT TGATGTGACA GGAATTCTCC CTGGCATTGT TTCCACCCCC TGGTGCCTGC	1200
	AGGCCACCCA GGGACCACGG GCGAGGACGT GAAGCCTCCC GAACACGCAC AGAAGGAAGG	1260
	AGCCAGCTCC CAGCCCACTC ATCGCAGGGC TCATGATTTT TTACAAATTA TGTTTTAATT	1320
50	CCAAGTGTTT CTGTTTCAAG GAAGGATGAA TAAGTTTAT TGAAAATGTG GTAACTTTAT	1380
	TTAAAATGAT TTTTAACATT ATGAGAGACT GCTCAGATTC TAAGTTGTTG GCCTTGTGTG	1440
55	TGTGTTTTTT TTTAAGTTCT CATCATTATT ACATAGACTG TGATGTATCT TTAAGTGAAA	1500
	TGAGCCCAAG CACACATGCA TGGCATTGTG TCCACAGGAG GGCATCCCTG GGGATGTGGC	1560
60	TGGAGCATGA GCCAGCTCTG TCCCAGGATG GTCCCAGCGG ATGCTGCCAG GGGCAKTGAA	1620

GTGTTTAGGT GAAGGACAAG TAGGTAAGAG GACGCCCTTCA GGCACCACAG ATAAGCCTGA 1680
 AACAGCCTCT CCAAGGGTTT TCACCTTAGC AACAAATGGGA GCTGTGGGAG TGATTTTGGC 1740
 -5 CACACTGTCA ACATTTGTGA GAACCAGTCT TTTGAAAGAA AAGTATTTCC AACTTGTCAC 1800
 TTGCCAGTCA CTCGGTTTTG CAAAAGGTGG CCCTTCACTG TCCATTCCAA ATAGCCCACA 1860
 10 CGTGCTCTCT GCTGGATTCT AAATTATGTG AATTTTGCCA TATTAAATCT TCCTCATTTA 1920
 TACTATTATT TGTACGTTT AATCAGAATC CCCGAAACCT CCTATAAAGC TTAGCTGCCC 1980
 CTTCTGAGGA TGCTGAGAAC GGTGTCTTTC TTTATAAATG CAAATGGCTA CCGTTTTTACA 2040
 15 ATAAAATTTT GCATGTGCAA AAAAAAAAAA ANAAAAAAAA AAAATCCCGG GGGGGGGCCG 2100
 GTAACCAATT TGNCCCC 2117

20

(2) INFORMATION FOR SEQ ID NO: 159:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TGTTCCTTAA TCCCTTTTCT AAAAAGGGGG GAAAATCCGG ATGGATTTTA GGGATTGGTC 60
 TGGTGTGAGC TGTGTTTAT TGACACCTA AATCCTGATT ATAGGCTTTT CATTTCTCCG 120
 35 CAAAGCCTTT ATTTTGGCAG TTAAGCCAAA TGTGTTTTC AGAAAGTTAG TTATTTTCTC 180
 CTCTTTCTTT CCTTCTTTC CTCCTTTTT CCCGTCTGAC CCCAAACGTT ATTGTCCAAA 240
 40 CATGACTGGA CAGCAGCTTT TGTTCCTTGA CCCTGTAATA TGACAGTCTG CTAATATTGA 300
 CAGAAGGTGC AGTTTTTGGG TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA 360
 45 AAAAAAAGKA CTTGTTTCTG TTGFACTTGA GTCCTAAGAA AAAGTGGCCC ATAGTTTAGT 420
 GGACAATTTT CAAAGGCTTT AGTACCACCT GTATTTCAAA ATGGGGGACC CAAACTCCCG 480
 GAAGAAACAA GCTCTGAACA GACTACGTGC TCAGCTTAGA AAGAAAAAG AATCTCTAGC 540
 50 TGACCAGTTT GACTTCAAGA TGTATATTGC CTTGTATTTC AAGGAGAAGA AGAAAAAGTC 600
 AGCACTTTTT GAAGTGTCTG AGGTTATACC AGTCATGACA AATAATTATG AAGAAAATAT 660
 CCTGAAAGGT GTGCGAGATT CCAGCTATTC CTTGGAAAGT TCCCTAGAGC TTTTACAGAA 720
 55 GGATGTGGTA CAGCTCCATG CTCCTCGATA TCAGTCTATG AGAAGGGATG TAATTGGCTG 780
 TACTCAGGAG ATGGATTTC TTTTGGCC TCGGAATGAT ATTGAAAAA TCGTCTGTCT 840
 60 CCTGTTTCT AGGTGGAAG AATCTGATGA GCCTTTTAGG CCTGTTTTCAGG CAAATTGAG 900

	TTTCATCATG GTGACTATGA AAAACAGTTT CTGCATGTAC TGAGCCGCAA GGACAAGACT	960
5	GGAATCGTTG TCAACAATCC TAACCACTCA GTGTTTCTCT TCATTGACAG ACAGCACTTG	1020
	CAGACTCCAA AAAACAAAGC TACAATCTTC AAGTTATGCA GCATCTGCCT CTACCTGCCA	1080
	CAGGAACAGC TCACCCACTG GGGCAGTTGG CACCATAGAG GRTCACCTCC GTCCTTATAT	1140
10	GCCAGAGTAG AGTACTGACC AGCAAAATGG AGAAGATCAG AGAATGCAGC AGCAGTTTTT	1200
	TTTCTTGTTT TCTTACCACT TTATTCTTTC AGAGTTTAAA GAAAATGGAC TCATGCACAG	1260
15	AACACTATGC ATTTTGAAAC TTGTTTCATCC TGGATTTTTT TAAATCATTT TTATCTCAGA	1320
	ACTTAAACAA AAATTAGATG TCGTGCACGG ACTGTGTGAA AGAAGATGCT TTGCATATTT	1380
	GCTGCACTGC ATCAGTATCT TACTAAAAAT GTGAAATGAA AGGACTATTG TACACTGAAA	1440
20	TGCTTAAATG TATCTGAAAG CACAAGGTGA TACTCATTTT TATGGTCTTC CCATTTGTGC	1500
	TGGTTTTTGC CTCTTTGACA TCTGTCATCA GTATTTAGAG GGTGAGAAGT GAATGTAACA	1560
25	GGTATAAATA ACATTTTTAA AAACAATAAC TTTGCTATAA TCACAGTTGT TCCAGAGCAC	1620
	TGTCAGATAC ATTCTAATGA CCAGAACTGG TTTAAAAAAA GAAAATACAA CCATGGGAAA	1680
	GAAATCTTAA ATGAAAAACG CATCTCATTG TAGGCATTTT TGCCTCATAT TTTACTGGGC	1740
30	CATGTTTGTT TCCTGGTACT CATGTATTTT TTTTTCAG ATCTCTTTCC CCAAGTTGCT	1800
	ATTGTAAGAG TATCTGCTG CGTGTGGATG CAGTTATACA CATTAAAGCA GATCTGGAGT	1860
35	CTGAAGTAGC TATAAAGCAG CTATAAAACA GAAATACATG CATAGCTGCA GAAACCATGA	1920
	TAGGTAGAGG ACTTTTCTTT TGGTTTTGTT TTGTTTTGTT TTGTTTTGTT TTTGGTTTTA	1980
	CAGAGAAGAG ATTTTATTA CAAAGAAAAA AATTCCAGTG AATGTGCAG AAATGCTGGT	2040
40	TTTACACCA TCCTAAAGAA AACTTTTACA AGGGTGTTT GGAGTAGAAA AAAGTTATA	2100
	AAGTTGGAAT CTTAAATTGT AAAATTAACC ATTGAGTGT AAAGTTCTAA AAGCAGAACT	2160
45	CATTTTGTGC AATGAACATA AGGAAAGACT ACTGTATAGG TTTTMTTTT TTCTCCTTTT	2220
	AAATGAAGAA AAGCTTTGCT TAAGGGTTGC ATACTTTTAT TGGAGTAAAT CTGAATGATC	2280
	CTACTCCTTT GGAGTAAAC TAGTGCTTAC CAGTTTCCAA TTGTATTTAG CTTCTGGTTG	2340
50	GAATTTGAAA AAAAAAGAAA AAAAGAAAAA GAAACCTAA ATAAATAGG TGAAA	2395

55 (2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

5	CCCCGGATAC CGCCTGACGT AGTGCCAATC ACACCTCTCG CGTCTCGGCG CCTCGGAGGC	60
	TAATGAGGAC GCCTGGCGAA ACGCAGTAAC GGATTTCGG GTGGACCTTC GCTTTACGGC	120
10	TCGTGAGTTC TTCCGCCCAA CCCAGAGGAA GCGGGAGAGC AGTTTACGAC AGCGCCGGTC	180
	GTGTTTACGG CGGCGCCCGC TCGCGCGCA TGTTCCTCT TTTCTGGTT TCTCAAGAGT	240
	GCTGCTGCTA ACGCGGTCCC CGGCACGCAC CATCTGTTGC CATCCCGGCC GGCCGAGGCA	300
15	TTGCAGATTT TGAAGATGG CAAAGTTCAT GACACCCGTG ATCCAGGACA ACCCCTCAGG	360
	CTGGGGTCCC TGTGCGGTC CCGAGCAGTT TCGGGATATG CCCTACCAGC CGTTCAGCAA	420
20	AGGAGATCGG CTAGGAAAGG TTGCAGACTG GACAGGAGCC ACATACCAAG ATAAGAGGTA	480
	CACAAATAAG TACTCCTCTC AGTTTGGTGG TGAAGTCAA TATGCTTATT TCCATGAGGA	540
	GGATGAAAGT AGCTTCCAGC TGGTGGATAC AGCGCGCACA CAGAAGACGG CCTACCAGCG	600
25	GAATCGAATG AGATTTGCCC AGAGGAACCT CCGCAGAGAC AAAGATCGTC GGAACATGTT	660
	GCAGTTCAAC CTGCAGATCC TGCCTAAGAG TGCCAAACAG AAAGAGAGAG AACGCATTCTG	720
30	ACTGCAGAAA AAGTTCAGA AACAATTGG GGTAGGCAG AAATGGGATC AGAAATCACA	780
	GAAACCCCGA GACTCTTCAG TTGAAGTTCG TAGTGATTGG GAAGTGAAAG AGGAAATGGA	840
	TTTTCTCAG TTGATGAAGA TCGCTACTT GGAAGTATCA GAGCCACAGG ACATTGAGTG	900
35	TTGTGGGGCC CTAGAATACT ACGACAAAGC CTTTGACCGC ATCACCACGA GGAGTGAGAA	960
	GCCACTGCGG ASATNCAAGC GCATCTTCCA CACTGTCAAC ACCACAGACG ACCCTGTCAT	1020
40	CCGCAAGCTG GCAAAACTC AGGGGAATGT GTTTGCCACT GATGCCATCC TGGCCACGCT	1080
	GATGAGCTGT ACCCGCTCAG TGTATTCTTG GGATATTGTC GTCCAGAGAG TTGGGTCCAA	1140
	ACTCTTCTTT GACAAGAGAG ACAACTCTGA CTTTGACCTC CTGACAGTGA GTGAGACTGC	1200
45	CAATGAGCCC CCTCAAGATG AAGGTAATTC CTTCAATTCA CCCCACAACC TGGCCATGGA	1260
	GGCAACCTAC ATCAACCACA ATTTCTCCCA GCAGTGCTTG AGAATGGGGA AGGAAAGATA	1320
50	CAACTTCCCC AACCCAAACC CGTTGTGGA GGACGACATG GATAAGAATG AAATCGCCTC	1380
	TGTTGCGTAC CGTTACCGCA GTGGNAAGCT TGGAGATGAT ATTGACCTTA TTGTCCGTTG	1440
	TGAGCACGAT GGCCTCATGA CTGGAGCCAA CGGGGAAGTG TCTTCATCA ACATCAAGAC	1500
55	ACTCAATGAG TGGGATTCCA GGCCTGTAA TGGCGTTGAC TGGCGTCAGA AGCTGGACTC	1560
	TCAGCGAGGG GCTGTCAATTG CCACGAGCT GAAGAACAAC AGCTACAAGT TGGCCCGGTG	1620
60	GACCTGCTGT GCTTGCTGG CTGGATCTGA GTACCTCAAG CTTGGTTATG TGTCTCGGTA	1680

CCACGTGAAA GACTCCTCAC GCCACGTCAT CCTAGGCACC CAGCAGTTCA AGCCTAATGA 1740
 GTTTGCCAGC CAGATCAACC TGAGCGTGGA GAATGCCTGG GGCATTTTAC GCTGCGTCAT 1800
 5 TGACATCTGC ATGAAGCTGG AGGAGGGCAA ATACCTCATC CTCAAGGACC CCAACAAGCA 1860
 GGTATCCGT GTCTACAGCC TCCCTGATGG CACCTTCAGC TCTGATGAAG ATGAGGAGGA 1920
 AGAGGAGGAG GAAGAAGAGG AAGAAGAAGA GGAAGAACT TAAACCAAGT ATGTGGAGCT 1980
 10 GGAGTTGTG CTTCACCGA GACTACGAGG GCCTTTGATG CTTAGTGGAA TGTGTGTCTA 2040
 ACTTGCTCTC TGACATTTAG CAGATGAAAT AAAATATATA TCTGTTTAGT CTTAAAAAAA 2100
 15 AAAAAAAAAA AAAAAAAAAA 2120

20 (2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

30 GGAAGCTGAA GTCCTTCCAG ACCAGGGACA ACCAGGGCAT TCTCTATGAA GCTGCACCCA 60
 CCTCCACCCT CACCTGTRAC TCAGGACCAC AGAAGCAAAA GTTCTCACTC AAAGTGGATG 120
 CCAAGGATGG GCGCTTGTTC AATGAGCAGA ACTTCTTCCA GCGGGCCGCC AAGCCTCTGC 180
 35 AAGTCAACAA GTGGAAGAAG CTGTACTCGA CCCCCTGCT GGCCATCCCT ACCTGCATGG 240
 GTTTCGGTGT TCACCAGGAC AAATACAGGT TCTTGGTGT ACCCAGCCTG GGGAGGAGCC 300
 40 TTCAGTCGGC CTGGGATGTC AGCCCAAAGC ATGTGCTGTG CAGAGAGGTC TGTGCTGCAG 360
 GTGGCCTGCC GGCTGCTGGA TGCCCTGGAG TTCCTCCATG AGAATGAGTA TGTTCATGGA 420
 AATGTGACAG CTGAAAATAT CTTTGTGGAT CCAGAGGACC AGAGTCAGGT GACTTTGGCA 480
 45 GGCTATGGCT TCGCINTCCG CTATTGCCCA AGTGGCAAAC ACGTGGCCTA CGTGAAGGC 540
 AGCAGGAGCC CTCACGAGGG GGACCTTGAG TTCATTAGCA TGGACCTGCA CAAGGGATGC 600
 50 GGGCCCTCCC GCCGCRGCGA CCTCCAGAGC CTGGGCTACT GCATGCTGAA GTGGCTCTAC 660
 GGGTTTCTGC CATGGACAAA TTGCCTTCCC AAMAMTGAGG ACATCATGAA GCAAAAACAG 720
 AAGTTTGTG ATAAGCCGGG GCCCTTCGTG GGACCCTGCG GTCACCTGGAT CAGGCCCTCA 780
 55 GAGACCCTGC AGAAGTACCT GAAGGTGGTG ATGGCCCTCA CGTATGAGGA GAAGCCGCCC 840
 TACGCCATGC TGAGGAACAA CCTAGAAGCT TTGCTGCAGG ATCTGCGTGT GTCTCCATAT 900

60

(2) INFORMATION FOR SEQ ID NO: 162:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GGCACGAGAT GAGGGGCACC CAGTGCTTCT AGGGCAGGCT GGGTGGTGGT CCCCTAGGTA 60
15 TCAGCCTCTC TTA CTGTACT CTCCGGGAAT GTTAACCTTT CTATTTTCAG CCTGTGCCAC 120
CTGTCTAGGC AAGCTGGCTT CCCATTGGC CCCTGTGGGT CCACAGCAGC GTGGCTGCCC 180
20 CCCAGGGCCA CCGCTTCTTT CTGATCCTC TTTCCTTAAC AGTGACTTGG GCTTGAGTCT 240
GGCAAGGAAC CTTGCTTTTA GCTTCACCAC CAAGGAGAGA GGTGACATG ACCTCCCCGC 300
CCCCTACCA AGGCTGGGAA CAGAGGGGAT GTGGTGAGAG CCAGGTTCTT CTGGCCCTCT 360
25 CCAGGGTGTT TTCCACTAGT CACTACTGTC TTCTCCTTGT AGCTAATCAA TCAATATTCT 420
TCCCTTGCTT GTGGGCAGTG GAGAGGCTGC TGGGTGTACG CTGCACCTGC CCACTGAGTT 480
GGGGAAGAG GATAATCAGT GAGCACTGTT CTGCTCAGAG CTCCTGATCT ACCCCACCCC 540
30 CTAGGATCCA GGA CTGGGTC AAAGCTGCAT GAAACCAGGC CCTGGCAGCA AACCTGGGAA 600
TGGCTGGAGG TGGGAGAGAA CCTGAACTTC TCTTTCCCTC TCCCTCCTCC AACATTACTG 660
35 GAACTCTATC CTGTTAGGAT CTTCTGAGCT TGT TTCCCTG CTGGGTGGGA CAGAGGACAA 720
AGGAGAAGGG AGGGTCTAGA AGAGGCAGCC CTTCTTTGTC CTC TGGGGTA AATGAGCTTG 780
ACCTAGAGTA AATGGAGAGA CAAAAGCCT CTGATTTTAA ATTTCCATAA AATGTTAGAA 840
40 GTATATATAT ACATATATAT ATTTCTTTAA ATTTTGTAGT CTTTGATATG TCTAAAAATC 900
CATTCCTCTT GCCCTGAAGC CTGAGTGAGA CACATGAAGA AAAGTGTT TCATTTAAAG 960
45 ATGTTAATTA AATGATTGAA ACTTGAAAAA AAAAAAAAAA AAA 1003

50 (2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2196 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

60 AAGAAGCGGC ACACGGATGT GCAGTTCTAC ACAGAAGTGG GAGAGATAAC CACGGACTTG 60

	GGGAAACATC AGCATATGCA TGACCGAGAT GACCTCTATG CTGAGCAGAT GGAACGAGAA	120
5	ATGAGGCACA AACTGAAAAC AGCCTTTAAA AATTTTCATTG AGAAAGTAGA GGCTCTAACT	180
	AAGGAGGAAC TGGAATTTGA AGTGCCCTTTT AGGGACTTGG GATTTAACGG AGCTCCCTAT	240
	AGGAGTACCT GCCTCCTTCA GCCCACTAGT AGTGCGCTGG TAAATGCTAC GGAATGGCCA	300
10	CCTTTTGTGG TGACATTGGA TGAGGTAGAG CTGATCCACT TTRAGCGGGT CCAGTTTCAC	360
	CTGAAGAACT TTGATATGGT AATCGTCTAC AAGGACTACA GCAAGAAAGT GACCATGATC	420
15	AACGCCATTG CTGTAGCCTC TCTTGACCCC ATCAAGGAAT GGTGAATTG CTGCGACCTG	480
	AAATACACAG AAGGAGTACA GTCCCTCAAC TGGACTAAAA TCATGAAGAC CATTGTGTGAT	540
	GACCCTGAGG GCTTCTTCGA ACAAGGTGGC TGGTCTTTCC TGGAGCCTGA GGGTGAGGGG	600
20	AGTGATGCTG AAGAAGGGGA TTCAGAGTCT GAAATGAAG ATGAGACTTT TAATCCTTCA	660
	GAAGATGACT ATGAAGAGGA AGAGGAGGAC AGTGATGAAG ATTATTCATC AGAAGCAGAA	720
25	GAGTCAGACT ATTCTAAGGA GTCATTGGGT AGTGAAGAAG AGAGTGGAAG GGATTGGGAT	780
	GAACTGGAGG AAGAAGCCCG AAAAGCGGAC CGAGAAAGTC GTTACGAGGA AGAAGAAGAA	840
	CAAAGTCGAA GTATGAGCCG GAAGAGGAAG GCATCTGTGC ACAGTTCGGG CCGTGGCTCT	900
30	AACCGTGGTT CCAGACACAG CTCTGCACCC CCAAGAAAA AGAGGAAGTA ACTTCTGAAC	960
	TTTGGCCCTG AGCTCCATTG TTCCTCCAGC CAACCCCTGA AAATTTTACA TGACATAGAA	1020
35	ACTGTATTTT TCCTTTCGTT TTCATTTGAA GTTTTGCCAT TTGTGTTTAT GGGTTTAGGG	1080
	GGCCATTTGT GTGGACCAAT CTA CTCTCGGGG AATTCAGGC CCACCAGGAC ACGTGCCAAT	1140
	GGCCCCATTC AGATGGCAAG GGAGGAGGTG TTCTTGAAGA CAGGAGGAGG CTCCCGCTGT	1200
40	TAATAAATAT TGTTTCATTG TTCTCTCTTC CTGTACCTT CTGCCAAGAC ATTGATGGCT	1260
	TCTGACATCT TATTTGGTGT CTCAAAGCTG TATTTCGAAG ACAGTGGTAC AAGGTGACCC	1320
45	TTAATTACCC GTATCATGGT TCTTGACCAG CACATTCAAT CCTCCAACCT ACCCTACTGC	1380
	CATGACCTTC CGCACATCTC TAAGTTTTAT CTTTGCAATA CTCAAGGTTG TCGGAAATTT	1440
	GCTAATGGTT GTGATAAACC ATACAGCTTG AGCCAGTGAG GCAGATTGGG CTGGTGCTTT	1500
50	CGTCTGAGTT TTCCTGCTTT CCTGCCTCGT GCAGATTCTG AGGTATATCT GCTGCCTTGG	1560
	AAGACATAAG AAGCAGTGAT ACTCCCTGGC TCGGTTATTT TCTCCATACA ATGCACACAT	1620
55	GGTACAATGA TAGAAGGCAA AATTGCCACT GTCTTCTTTT TTTTCTCATA TATCTAAGGA	1680
	AGATATATCA GGTGTGTCCT CATGTACCGC TTCTAGTGAA ATGTAGAGGA AGGCTCAAAG	1740
	GAGTCAACAT TTAGATCTGG AAGGGACAAG TCATGCCTTG GGCCTAGAAT ACCCTGATGA	1800
60	GAAAAGAGAA GAGGAAGGGA GGCCATATCT ACAACANCAN CCTCTCGGCA CTGCTGCTCC	1860

TTATTTTAAC TTTGTCCTGC ATGTCTCTGT ATTTATCACA GTTCTCTGTG AACAGCTTTT 1920
 CAAGTATTTG GGGAGTTTAT CTGCCATCC TCCCCTCTG GTTCTCTGCA CCCACCTGTC 1980
 -5 CCACTGCAGT TCCTTCCGTG CTCTGTGACT TTAAGAGAAG AAGGGGGGAG GGGTCCCGGA 2040
 TTTTATGTTT GTTTGTTTTT TCTCCTTAGC AGTAGGACTT GATATTTTCA ATTTTGGAAG 2100
 10 AACTAAAAGA TGAATAAACT GGGTTTTTTT TGTGTGTTGT TTTGTAAAA AAAAAAAAAA 2160
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2196

15

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1945 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCACAGAGTC GGGCGGACGG ACAGGGAGAG GAGGAGAGGG GGTCTGCGCG CGGCCGCTAC 60
 CCAGAAGCCA GCGGACGGCA GCACGGAGTG GGCTGTCCCC GAGCCCAGCC CCGAGCGAGC 120
 30 CCCCCCCCCG CCCCCGMAGG ACGCGCCTYC CAGCCAGCCC GACTYCTAGG AGGAGGGGAG 180
 GCGGGAAAGC AGCTCAAGCC TCACCCACCG CCCTGCCCCC AGCCCCGCCA CTCCCAGGCT 240
 35 CCTCGGGACT CGGCGGGTCC TCCTGGGAGT CTCGGAGGGG ACCGGCTGTG CAGACGCCAT 300
 GGAGTTGGTG CTGGTCTTCC TCTGCAGCCT GCTGGCCCCC ATGGTCCTGG CCAGTGCAGC 360
 TGAAAAGGAG AAGGAAATGG ACCCTTTTCA TTATGATTAC CAGACCCTGA GGATTGGGGG 420
 40 ACTGGTGTTC GCTGTGTGCC TCTTCTCGGT TGGGATCCTC CTTATCCTAA GTCGCAGGTG 480
 CAAGTGCAGT TTCAATCAGA AGCCCCGGGC CCCAGGAGAT GAGGAAGCCC AGGTGGAGAA 540
 45 CCTCATCACC GCCAATGCAA CAGAGCCCCA GAAAGCAGAG AACTGAAGTG CAGCCATCAG 600
 GTGGAAGCCT CTGGAACCTG AGGCGGCTGC TTGAACCTTT GGATGCAAAT GTCGATGCTT 660
 AAGAAAACCG GCCACTTCAG CAACAGCCCT TTCCCCAGGA GAAGCCAAGA ACTTGTGTGT 720
 50 CCCCCACCCT ATCCCCTCTA ACACCATTC CACCTGAT GATGCAACTA ACACCTGCCT 780
 CCCCCTGCA GCCTGCGGTC CTGCCACCT CCCGTGATGT GTGTGTGTGT GTGTGTGTGT 840
 55 GTGACTGTGT GTGTTTGCTA ACTGTGGTCT TTGTGGCTAC TTGTTTGTGG ATGGTATTGT 900
 GTTTGTAGT GAACTGTGGA CTCGCTTTC CAGGCAGGGG CTGAGCCACA TGGCCATCTG 960
 60 CTCTCCCTG CCCCCGTGGC CCTCCATCAC CTTCTGCTCC TAGGAGGCTG CTTGTGCCCC 1020

	GAGACCAGCC CCCTCCCCTG ATTTAGGGAT GCGTAGGGTA AGAGCACGGG CAGTGGTCTT	1080
	CAGTCGTCTT GGGACCTGGG AAGGTTTGCA GCACTTTGTC ATCATTCTTC ATGGACTCCT	1140
-5	TTCACTCCTT TAACAAAAAC CTTGCTTCCT TATCCACCT GATCCCAGTC TGAAGGTCTC	1200
	TTAGCAACTG GAGATACAAA GCAAGGAGCT GGTGAGCCCA GCGTTGACGT CAGGCAGGCT	1260
10	ATGCCCTTCC GTGGTTAATT TCTTCCCAGG GGCTTCCAG AGGAGTCCCC ATCTGCCCCG	1320
	CCCCCTCACA GAGCGCCCGG GGATTCCAGG CCCAGGGCTT CTA CTCTGCCC CCTGGGGAAT	1380
	GTGTCCCCTG CATATCTTCT CAGCAATAAC TCCATGGGCT CTGGGACCTT ACCCCTTCCA	1440
15	ACCTTCCCTG CTTCTGAGAC TTCAATCTAC AGCCCAGCTC ATCCAGATGC AGACTACAGT	1500
	CCCTGCAATT GGTCTCTGG CAGGCAATAG TTGAAGGACT CCTGTTCCTT TGGGGCCAGC	1560
20	ACACCGGGAT GGATGGAGGG AGAGCAGAGG CCTTTGCTTC TCTGCCTACG TCCCCTTAGA	1620
	TGGGCAGCAG AGGCAACTCC CGCATCCTTT GCTCTGCCTG TCRGTGGTCA GAGCGGTGAG	1680
	CGAGGTGGGT TGGAGACTCA GCAGGCTCCG TGCAGCCCTT GGGAACAGTG AGAGGTTGAA	1740
25	GGTCATAACG AGAGTGGGAA CTCAACCCAG ATCCCGCCCC TCCTGTCTCTC TGTGTTCCCG	1800
	CGGAAACCAA CCAAACCGTG CGCTGTGACC CATTGCTGTT CTCTGTATCG TGATCTATCC	1860
30	TCAACAACAA CAGAAAAAAG GAATAAAATA TCCTTTGTTT CCTAGTGAAA AAAAAAAAAA	1920
	AAAAAAAAA AAAAAAAAAA CTCGA	1945

35

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

45

	GGGTCGACCC ACGCGTCCGG CAGCCGTCTG TTGAGTCGTT GCTGCCGCTG CCCCCTCCCG	60
	GATCAGGAGC CAGTGTATAC CGCCCGCCA CCGCCTTGGT GCCGCTAGAG GAAACGAGAA	120
50	GGAGGCCGCC TGCGGTTTGT CGCCGCAGCT CGCCCMYGY CYGGRAGAGC CGAGCCCCGG	180
	CCCAGTCGGT CGCTTGCCAC CSCTCGTAGC CGTTACCCGC GGGCCGCCAC AGCCCGCCGC	240
55	CGGGAGAGGC GCGCGCCATG GCTTCTGGAG CCGATTCAAA AGGTGATGAC CTATCAACAG	300
	CCATTCTCAA ACAGAAGAAC CGTCCCAATC GGTTAATTGT TGATGAAGCC ATCAATGAGG	360
	ACAACAGTGT GGTGTCCTTG TCCAGCCCA AGATGGATGA ATTGCAGTTG TTCCGAGGTG	420
60	ACACAGTGT GCTGAAAGGA AAGAAGAGAC GAGAAGCTGT TTGCATCGTC CTTTCTGATG	480

	ATACTTGTTC TGATGAGAAG ATTCCGATGA ATAGAGTTGT TCGGAATAAC CTTCGTGTAC	540
5	GCCTAGGGGA TGTCA TCAGC ATCCAGCCAT GCCCTGATGT GAAGTACGGC AAACGTATCC	600
	ATGTGCTGCC CATTGATGAC ACAGTGGAA G CATTACTGG TAATCTCTTC GAGGTATACC	660
	TTAAGCCGTA CTTCCTGGAA GCGTATCGAC CCATCCGGAA AGGAGACATT TTTCTTGTC	720
10	GTGGTGGGAT GCGTGCTGTG GAGTTCAAAG TGGTGGAAAC AGATCCTAGC CCTTATTGCA	780
	TTGTTGCTCC AGACACAGTG ATCCACTGCG AAGGGGAGCC TATCAAACGA GAGGATGAGG	840
15	AAGAGTCCTT GAATGAAGTA GGGTATGATG ACATTGGTGG CTGCAGGAAG CAGCTAGCTC	900
	AGATAAAGGA GATGGTGGAA CTGCCCCCTGA GACATCCTGC CCTCTTTAAG GCAATTGGTG	960
	TGAAGCCTCC TAGAGGAATC CTGCTTTACG GACCTCCTGG AACAGGAAAG ACCCTGATTG	1020
20	CTCGAGCTGT AGCAAATGAG ACTGGAGCCT TCTTCTTCTT GATCAATGGT CCTGAGATCA	1080
	TGAGCAAATT GGCTGGTGAG TCTGAGAGCA ACCTTCGTAA AGCCTTTGAG GAGGCTGAGA	1140
25	AGAATGCTCC TGCCATCATC TTCATTGATG AGCTAGATGC CATCGCTCCC AAAAGAGAGA	1200
	AAATCATGG CGAGGTGGAG CGGCGCATTG TATCACAGTT GTTGACCCTC ATGGATGGCC	1260
	TAAAGCAGAG GGCACATGTG ATTGTTATGG CAGCAACCAA CAGACCCAAC AGCATTGACC	1320
30	CAGCTCTACG GCGATTGGT CGCTTTGACA GGGAGGTAGA TATTGGAATT CCTGATGCTA	1380
	CAGGACGCTT AGAGATTCTT CAGATCCATA CCAAGACAT GAAGCTGGCA GATGATGTGG	1440
35	ACCTGGAACA GTAGCCAATG AGACTCACGG GCATGTGGGT GCTGACTTAG CAGCCCTGTG	1500
	CTCAGAGGCT GCTCTGCAAG CCATCCGCAA GAAGATGGAT CTCATTGACC TAGAGGATGA	1560
	GACCATTGAT GCCGAGGTCA TGAAGTCTCT AGCAGTTACT ATGGATGACT TCCGGTGGGC	1620
40	CTTGAGCCAG AGTAACCCAT CAGCACTGCG GGAAACCGTG GTAGAGGTGC CACAGGTAAC	1680
	CTGGGAAGAC ATCGGGGGCC TAGAGGATGT CAAACGTGAG CTACAGGAGC TGGTCCAGTA	1740
45	TCCTGTGGAG CACCCAGACA AATTCTGAA GTTTGGCATG ACACCTTCCA AGGGAGTTCT	1800
	GTTCATGGA CCTCCTGGCT GTGGGAAAAC TTTGTTGGCC AAAGCCATTG CTAATGAATG	1860
	CCAGGCCAAC TTCATCTCCA TCAAGGTCC TGAGCTGCTC ACCATGTGGT TTGGGGAGTC	1920
50	TGAGGCCAAT GTCAGAGAAA TCTTTGACAA GGCCCGCCAA GCTGCCCCCT GTGTGCTATT	1980
	CTTTGATGAG CTGGATTGCA TTGCCAAGGC TCGTGGAGGT AACATTGGAG ATGGTGGTGG	2040
55	GGCTGCTGAC CGAGTCATCA ACCAGATCCT GACAGAAATG GATGGCATGT CCACAAAAA	2100
	AAATGTGTTT ATCATTGGCG CTACCAACCG GCCTGACATC ATGATCCTG CCATCCTCAG	2160
	ACCTGGCCGT CTTGATCAGC TCATCTACAT CCCACTTCCT GATGAGAAGT CCCGTGTGTC	2220
60	CATCCTCAAG GCTAACCTGC GCAAGTCCCC AGTTGCCAAG GATGTGGACT TGGAGTTCTT	2280

5 GGCTAAAATG ACTAATGGCT TCTCTGGAGC TGACCTGACA GAGATTTGCC AGCGTGCTTG 2340
 CAAGCTGGCC ATCCGTGAAT CCATCGAGAG TGAGATTAGG CGAGAACGAG AGAGGCAGAC 2400
 AAACCCATCA GCCATGGAGG TAGAAGAGGA TGATCCAGTG CCTGAGATCC GTCGAGATCA 2460
 CTTTGAAGAA GCCATGCGCT TTGCGCGCCG TTCTGTCACT GACAATGACA TTCGGAAGTA 2520
 10 TGAGATGTTT GCCCAGACCC TTCAGCAGAG TCGGGGCTTT GGCAGCTTCA GATTCCCTTC 2580
 AGGGAACCAG GGTGGAGCTG GCCCCAGTCA GGGCAGTGA GCGGCACAG GTGGCAGTGT 2640
 ATACACAGAA GACAATGATG ATGACCTGTA TGGCTAAGTG GTGGTGGCCA GCGTGCAGTG 2700
 15 AGCTGGCCTG CCTGGACCTT GTTCCCTGGG GGTGGGGGCG CTGCCCCAGG AGAGGGACCA 2760
 GGGGTGCGCC CACAGCCTGC TCCATTCTCC AGTCTGAACA GTTCAGCTAC AGTCTGACTC 2820
 20 TGGACAGGGG GTTCTGTGTG CAAAAATACA AAACAAAAGC GATAAAATAA AAGCGATTTT 2880
 CATTGTGTAA AAAAAAAAAA AAAAAAAAAAT CCGGGGGGGG GCCCGAACCA TTT 2933

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(2) INFORMATION FOR SEQ ID NO: 166:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TCGGAGAGCC GCGGGGCGNG CGCCTCTCGG CCAGGAAGCG CCTCTTGGAC GCGTGTNACC 60
 40 GATGCCCAGA AGTGGCCTTG GGCTGGGGAT CACCATAGCT TTTCTAGCTA CGCTGATCAC 120
 GCAGTTTCTC GTGTATAATG GTGTCTATCA GTATACATCC CCAGATTTCC TCTATATTCG 180
 TTCTTGGCTC CCTTGTATAT TTTTCTCAGG AGGCGTCACG GTGGGGAACA TAGGACGACA 240
 45 GTTAGCTATG GGTGTCCTG AAAAGCCCCA TAGTGATTGA GTCTTCAAAA CCACCGATTC 300
 TGAGAGCAAG GAAGATTTTG GAAGAAAATC TGA CTGTGGA TTATGACAAA GATTATCTTT 360
 TTTCTTAAGT AATCTATTTA GATCGGGCTG ACTGTACAAA TGA CTCTCTGG AAAAAACTCT 420
 50 TCACCTAGTC TAGAATAGGG AGGTGGAGAA TGATGACTTA CCCTGAAGTC TTCCCTTGAC 480
 TGCCCGCACT GCGCCTGTC TGTGCCCTGG AGCATTCCTG CCAGGCTACG TGGGTTTCAGG 540
 55 CAGGTGGCAG CTTCCCAAGT ATTGATTTTC ATTCATGTGA TTAACAACAG TTGCCATATT 600
 TCAAAGCCTT GAACTAAGAC TCAATTACCA ACCCGCAGTT TTGTGTCAGT GCCCAAAGGA 660
 60 GGTAGGTTGA TGGTGCTTAA CAAACATGAA GTATGGTGTA ATAGGAATAA TATTTATCCA 720

	AAAGATTTTT AAAAATAGGG CTGTGTTTAA AAAAAAAAC AAAACARGAA AAGCAGCAGT	780
	GATTATAGAG AGGTCACACT CTAAGTGGGG TCGCGGCGTG GCCACGCTTC ACGGTCACGC	840
-5	TCGTCCGTCC TGCAGTGGCG TGTTTACATG GTCACACGTG TGTGTATCAC CAGTGGGTCA	900
	ACTGCTGTG ATTCTCCCG TGGCAGTTTG TGTAACAAT CTTACTGAGC AAAAGGCAAT	960
10	GAAAAGTCTT GGTTCACACA CTGCGATATA TTGGAATTTT CACCTCAGTT TATGAAGTTT	1020
	ATTTGAAAT CCATAGTCAT CTAAGAATGA ATACCTGTCT GCCATGTATT TCAATCTTAG	1080
	TGAGCCAAAA TTGTTTGTTC GTTACTACAG AATAGAGATG ACTGTTTTTT GCCACAGCCC	1140
15	TATGGRATTT GCAATCTGTG ATTGCCTTGT AAAAAGGAGA GTGCATATGG CACTGCATTA	1200
	AACGTGTGGT GTTCTAGTC AATGATATTG GTGAGCACA TGTATTCATT TAATGGCATA	1260
20	GACCATACCA GACCTAATTT GCAAGTATTG GGTCTTAAAC TTCAAGTGCA ATGTATATGA	1320
	AAACCAATCT GAGCCTTGTA TCTCTTAAAT ATTTATTTTT TTTAACGTGT GAGATGTTG	1380
	AGAGAAGGTT CTCCATTCAT TTCAGTGCTG CCTGGAGGAA ACTCGGCAAT GATTTCTTTC	1440
25	AGTTGTGAAG TTCCTTTCGT GTTACACCCT CCACTGAACC CTCAACCTTC GAAATACTCC	1500
	AGTTTTGTGG GTTGGTCAT TTTTACTTAT AAATTTACCT TTTGTATTT TGCAATTTAC	1560
30	ATGTGTTGG TTTGTTTTAA ATTCTGTGAA AGTGGCTGA TTAAGAACT CCTTTTAAAT	1620
	GGAAGCCACC AGTCAGCAGA ATGGAAGCTT AGAGGAAGCT GCCTGTGAGC GCTGGTCTTT	1680
	GTGTTTGGTT TTGTGATGTA ACGATCTTTG CTGGGGTTTT TTGCTTTGTT TTGAGGGAAA	1740
35	TGTCTTGAG TAAATTTTAA GTTCTGGAG TTAATTTGTT TTACAGGAAT TTTGTTTTTT	1800
	AAAAAATAG GATCATCTG AACTTTGGAA TGACCCCTT ATATATTTTC TGAAAAATGAA	1860
40	AACAGTTACA TGAAAAAAT TTCCAATGAA GATGTCAGCA TTTTATGAAA AACCAGAAGT	1920
	TATTAGATGA AAGCAGCGAG TGAATCTTTA AACAGACTT GATCAGCAC ACACAATAAG	1980
	TCTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG AAATAATGTA GCCAAAAGAA	2040
45	TGTAAATTTG AGGATTTTTT TGCCAATAGT TTATAGAAAA TATATGAACC AAAGTGATTT	2100
	GAGTTTGTA AAATGTAAAA TAGTATGAAC AAAATTTGCA CTCTACCAGA TTTGAACATC	2160
50	TAGTGAGGTT CACATTCATA CTAAGTTTTT AACATTGTGT TCTTTTGTGA TTCATTTTTT	2220
	ACTTTTATTA AAGGTTCAAA ACC	2243

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

5	GGTGGGNAGC TTTNAAATTTC CCCTTACWGG GGCCTNTAA GGGGAAACCT TCCCGGAATT	60
	TTCCGGGTCGA CCCACGCGTC CGGCCAGCCT AGGAGAAGAA GTTCGTAGTC CCAGAGGTGA	120
10	GGCAGGAGGC GGCAGTTTCT GCGGGGTGAG GCGGAGCTG AAGTGACAGC GGAGGCGGAA	180
	GCAACGGTCG GTGGGGCGGA GAAGGGGGCT GGCCCCAGGA GGAGGAGGAA ACCCTTCCGA	240
15	GAAAACAGCA ACAAGCTGAG CTGCTGTGAC AGAGGGGAAC AAGATGGCGG CGCCGAAGGG	300
	GAGCCTCTGG GTGAGGACCC AACTGGGGCT CCCGCCGCTG CTGCTGCTGA CCATGGCCTT	360
	GGCCGGAGGT TCGGGGACCG CTTCGGCTGA AGCATTTGAC TCGGTCTTGG GTGATACGGC	420
20	GTCTTGCCAC CGGGCCTGTC AGTTGACCTA CCCCTTGAC ACCTACCCTA AGGAAGAAGA	480
	GTTGTACGCA TGTACAGAGG GTTGCAGGCT GTTTTCAATT TGTCAAGTTG TGGATGATGG	540
	AATTGACTTA AATCGAACTA AATTGGAATG TGAATCTGCA TGTACAGAAG CATATTCCCA	600
25	ATCTGATGAG CAATATGCTT GCCATCTTGG KTGCCAGAAT CAGCTGCCAT TCGCTGAACT	660
	GAGACAAGAA CAACTTATGT CCTGATGCC AAAAATGCAC CTAATCTTTC CTCTAACTCT	720
30	GGTGAGGTCA TTCTGGAGTG ACATGATGGA CTCCGCACAG AGCTTCATAA CCTCTTCATG	780
	GACTTTTTTAT CTTCAAGCCG ATGACGGAAA AATAGTTATA TTCCRGTTCTA AGCCCAGRAA	840
	TCCCAGGTAC GCACCACATT TGGAGCCAGG AGCCCTACCA AATTGGRGRG RAWCMCTCT	900
35	AAGCAAAATG TCCNTCAKMT CGSMAATGAG AAATTCACAA GCGCACAGGA ATTTTCTTTGA	960
	AGATGGAGAA AGTGATGGCT TTTTAAGATG CCTCTCTCTT AACTCTGGGT GGATTTTAAC	1020
40	TACAACTCTT GTCCTCTCGG TGATGGTATT GCTTTGGATT TGTGTGCAA CTGTGTGCTA	1080
	CACGCTGTTG GACGCAGTAT AGTTCCCTC TGAGAAGCTG AGTATCTATG GTGACTTGGA	1140
	GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTGTGG TTGTTAGATC	1200
45	TAAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC TTGCTCATTC	1260
	TGAAATTTAA GCATTTTTCT TTTAAAAGAC AAGTGAATA GACATCTAAA ATTCCACTCC	1320
50	TCATAGAGCT TTTAAATGG TTTCATTGGA TATAGGCCTT AAGAAATCAC TATAAAATGC	1380
	AAATAAGTT ACTCAAATCT GTGAAAAAAA AAAAAAAAAA AAAAAAAC TCGAGGGGGG	1440
	GCCCGTTACC AAKTCGCCCT ATWGTGADTB GTATTMITAT TTTACTAATA TCTGTAGCTA	1500
55	TTTTGTTTTT KGCTTKGGTT ATKGTMTTYY TCCCTTYTCT WAGCTATFRAG CTGATCATKG	1560
	CYSCTTCTCA CCTCTGCCA TGATACTGTC AGTTACCTTA GTTAACAAGC TGAATATTTA	1620
60	GTAGAAATGA TGCTTCTGCT CAGGAATGGC CCACAAATCT GTAATTTGAA ATTTAGCAGG	1680

AAATGACCTT TAATGACACT ACATTTTCAG GAACTGAAAT CATTAAAATT TTATTTGAAT 1740
AATTATGTGC TGAAAAAAAA AAAAAAAAAA AMWMRARASK RRWWACTCGA GGGGGGGCCC 1800
-5 GGTACCCNAT TCGCCG 1816

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(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

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AGAAACCGTT GATGGGACTG AGAAACCAGA GTTAAACCT CTTTGAGCT TCTGAGGACT 60
CAGCTGGAAC CAACGGGCAC AGTTGGCAAC ACCATCAACT TCTCCAAGC AGAGAAACCC 120
25 GAACCCACCA ACCAGGGGCA GGATAGCCTG AAGAAACATC TACACGCAGA AATCAAAGTT 180
ATTGGGACTA TCCAGATCTT GTGTGGCATG ATGGTATTGA GCTTGGGGAT CATTTTGGCA 240
TCTGCTTCCT TCTCTCCAAA TTTTACCCAA GTGACTTCTA CACTGTTGAA CTCTGCTTAC 300
30 CCATTCATAG GACCCTTTTT TTTTATCATC TCTGGCTCTC TATCAATCGC CACAGAGAAA 360
AGGTTRACCA AGCTTTTGGT GCATAGCAGC CTGGTTGGAA GCATTCTGAG TGCTCTGTCT 420
35 GCCCTGGTGG GTTTCATTAT CCTGTCTGTC AAACAGGCCA CCTTAAATCC TGCCTCACTG 480
CAGTGTGAGT TGGACAAAAA TAATATACCA ACAAGAAGTT ATGTTTCTTA CTTTATCAT 540
GATTCACTTT ATACCACGGA CTGCTATACA GCCAAAGCCA GTCTGGCTGG AWCTCTCTCT 600
40 CTGATGCTGA TTGCACTCT GCTGGAATTC TGCTAGCTG TGCTCACTGC TGTGCTGCGG 660
TGAAACAGG CTTACTCTGA CTTCCCTGGG AGTGTACTTT TCCTGCCTCA CAGTTACATT 720
45 GGTAATTCTG GCATGTCCTC AAAAATGACT CATGACTGTG GATATGAAGA ACTATTGACT 780
TCTTAAGAAA AAAGGGAGAA ATATTAATCA GAAAGTTGAT TCTTATGATA ATATGGAAAA 840
GTTAACCATT ATAGAAAAGC AAAGCTGAG TTTCTTAAAT GTAAGCTTTT AAAGTAATGA 900
50 ACATTAAAAA AAACCATTAT TTCCTGTCA TTAAAGATA ATGTG 945

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(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 902 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

-5
GGCAGAGCCA CAGGAAGGAT GAGGAAGACC AGGCTCTGGG GGCTGCTGTG GATGCTCTTT 60
GTCTCAGAAC TCCGAGCTGC AACTAAATTA ACTGAGGAAA AGTATGAACT GAAAGAGGGG 120
10 CAGACCCTGG ATGTGAAATG TGA CTACACG CTAGAGAAGT TTGCCAGCAG CCAGAAAGCT 180
TGGCAGATAA TAAGGGACGG AGAGATGCCC AAGACCCTGG CATGCACAGA GAGGCCTTCA 240
AAGAATTCCC ATCCAGTCCA AGTGGGGAGG ATCATACTAG AAGACTACCA TGATCATGGT 300
15 TTA CTGCGCG TCCGAATGGT CAACCTTCAA GTGGAAGATT CTGGACTGTA TCAGTGTGTG 360
ATCTACCAGC CTCCCAAGGA GCCTCACATG CTGTTGCATC GCATCCGCTT GGTGGTGACC 420
20 AAGGGTTTTT CAGGGACCCC TGGCTCCAAT GAGAATTCTA CCCAGAATGT GTATAAGATT 480
CCTCCTACCA CCACTAAGGC CTGTGCCCCA CTCTATACCA GCCCCAGAAC TGTGACCCAA 540
GCTCCACCCA AGTCAACTGC CGATGTCTCC ACTCCTGACT CTGAAATCAA CCTTACAAAT 600
25 GTGACAGATA TCATCAGGGT TCCGGTGTTC AACATTGTCA TTCTCCTGGC TGGTGGATTG 660
CTGAGTAAGA GCCTGGTCTT CTCTGTCTCG TTGCTGTCA CGCTGAGGTC ATTGTACCC 720
30 TAGGCCCACG AACCCACGAG AATGTCCTCT GACTTCCAGC CACATCCATC TGGCAGTTGT 780
GCCAAGGGAG GAGGGAGGAG GTAAAAGGCA GGGAGTTAAT AACATGAATT AAATCTGTAA 840
TCACCRGCTA AAAAAAAAAA AAAAAAACN CGANCCTNGG TTTTCAGCTC CATCAGCTCC 900
35 TT 902

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(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 1883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

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AGAAAACAAC TGAAAACCA CATTTTTCTA CATA CAGCTG GGGAGGTAGC TGAGAACTTG 60

GCACTGCGCA CACATACTAG GTTGAAAGAG AGTTGAGGAA ACCAGAAGGC CAAGTGGATC 120

TGCTGGCAAA CCCTGAACCT GTCTCCTGCG CTGCTCTAC AGTCTGAAG TTGAAAATCC 180

TTTTCATGCC TAGCATCTGC TTGAGTTATA AACCCCAAGG CAGCCATGTC ATAGACTAGT 240

60

GTTTACTCTT GTTTTGA CTT TTTTAATG CTTCTAAGA CCCAAGTGCC TCCTGCTGTT 300

	TCCTCCTTTG TGGTAGCCTC TGGCCATCTG GGACCTCAAT CCCAGCTTT CCCACTTTCA	360
	GCAGTCCTTT GCTCTCTTTG CTTCTACCTC AAATAGCCCC AGGAGTGGGC TTTAGTCTCC	420
-5	AATATGGAGC ATYTCAAGCT TCTCCTGGGG GATGGGGATT GGGATGGGCA GAATCTGTTT	480
	TGGWCTCCG GGTATTTTCC AGTGGGTGTA AAAGCAGAGC TGGGCCTTTC CCTCTCTTAT	540
10	CCCTGAGGGT GGGTAAGAAG GACTGTATCT ACACCTGTTC TTCCCTACCT TCTCTTTTGT	600
	TAGGGAGGCC TCATTCTAAG TTCCTCAAGA GAGTCCTTGG CTAAAGCTG TAGCAAGGGT	660
	GTGCTAGGTG GGGGATTTGG AGCAAAACCG TCGAGTAGGC ATGATACTGG TATGGAGTGG	720
15	GCCTGCAAAA TCAGACAGAA ATGGCTTGAG AAGCCGAGG GGAGCATGCC TGTCTCTCAG	780
	TGATAGAGTA TGGGAGGGAC CTCCTAGCT TGGAAAATGA GAATTGAAGG GGTATGAAC	840
20	AAATAGGATG CCTAGTTGAG GATGTTCCCA AAGTTTGTG CAATCTTATC ATTAGTAGAT	900
	TTTATAAGCC ACAGAGACAA ACCAGAAACG GAATAATGTT ACTTTGGATG CTTTATTTT	960
	TTGTTCTAGG TGTGGCTTTG TACATGCAGA AGAATGCTAT ATGCTGCACA TTTTGCCTTT	1020
25	AAAGTCTTAC GACTTTCCCC ATTTTAGTCT AATGGGAAGA TACAGATGTG CAAGTCTGCT	1080
	TTTTTGTTTT TTGTTATTAT TTTTTTTTTT TTGCTCTGTG TTATGGACAT TTTCAGACAT	1140
30	GCACAGAAGT GGAGAGGATG GTCCTTGGAC CCCATGTGTC CATCACCTAG CTGCATCACT	1200
	TATCAGCTAT GGTCAACCTG GTTTCATCTG TATCTCTCTC TTTTCACCTG TATTGTTTAT	1260
	TGAAAATCCA AGACACTATG CCAATGCAAC CGTGACTION TTGGGAGATT GGTAGTCTCT	1320
35	TTTGATGGTG ATAGTGATGG GGTGCACTAT CATAATCACA TCAGGTCTGC TTTTGTCTTT	1380
	TAATGTTAAC TAATGAAGTT CCAGAGATGG GCCTTAGAAA TGTGTTTTAA GAATTAACAA	1440
40	GGAGTCTCAA AAAGAAATGA GAGGGATGCT TCCTTTCCCC TTGCATCTAC AAAACAAGAG	1500
	AGAGACTGTT CTGTTGTAAA ACTCTTTCOA AAATTCTGAT ATGGTAAGGT ACTTGAGACC	1560
	CTTCACCAGA ATGTCAATCT TTTTTTCTGT GTAACATGGA AACTTGTTGT ACCATTAGCA	1620
45	TTGTTATCAG CTTGTACTGG TCTCATAACT CTGGTTTTGG AAGAATAATT TGGAAATTGT	1680
	TGCTGTGTTT TGTGAAAATA ACCTCCCCAA AATAATTAGT AACTGGTTGT TCTACTTGGT	1740
50	AATTTGACAC CCTGTTAATA ACGCAATTAT TTCTGTGTTT TTAAACAGTA TAAATAGTTG	1800
	TAAGTTTGCA TGCATGATGG AAAAATAAAA ACCTGTATCT CTGTTAAAAA AAAAAAAAAA	1860
	AAAAAAAAA AAAAAAAAAA AAA	1883

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(2) INFORMATION FOR SEQ ID NO: 171:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

	TACTTTTAGA TTTACTGCCT TCAAAAAGTG CCTATTCTGA GCAACATAAA CGTTATTCCT	60
10	TACATATGTA TGTACACACG GTACCCAGAG TCGTACTGTG GCAGCCTTCA AAAACATACC	120
	ATCAGAAAGA GTAGGTGCTG AGATAAGGNA ACTTTGCCAA ATGNAAGAAA GTCACTCACT	180
15	TCCAATATCC CCTCTTCAAG CGGCTACCGT GRAASGGGCT GCAAACACAT TCCCTGAGCA	240
	TCCCTTGCTG ATACAGCTTC TTTATATTTA TATCCTACTG GATGGTAGCA TATTGCTAAG	300
	GTTTCTGTGA CTCTGCTTCA AGGGAATGTA AGYTTTATGG CATTGAAACA TTTAGGAAAA	360
20	AAAAAGATGT TTAAGAGAAT TAATAGAGCC GTAGTCTGTA TTAGGATGTG TGTCATATGT	420
	GTGTCTTATA AACTAAGCAT CGGTGGGTTT AGAGTGTTAA AGTGTGAGCA CATTCCTTCT	480
25	CCTTTTGTCT CTCAGGCTAA CATGAGAGAA AATAGAAAAG TCTTGGCTGT GGGGATTGGA	540
	AGCTCAGGGG GCCAAATGTC CTTGCCAGAT CCTTAGAGCA TTTACTTTGAC TCCTAAAAAT	600
	AGTAGTGTAT GTTATTTGAT GGCTTTTGTT TCCATAGTTC CATCACTGAC AAAACTGTCA	660
30	ATACTGTTGA TGGAGCAGCA GCATAGCCTA GAGTGATGCA TTCTTACCCA GAGGTGGCAA	720
	TAGGAGAGGG TCCATGTAAA TAGGACGAGG TAGACAGTGC ATGATTGTAG GAGAAGGGTT	780
35	GAAGGGAGGA CATGATTCCA AAAAAGATCG TTCTCAATGT GTCGTCTGAC TCAACCAGCT	840
	GGCAGATTAC ACTTGCCAAG TCGTTCCCTT TCCTTCTAAG TCAGTTGGCT CCATATTCAC	900
	TTGAATATGC CTCTGTTTGG GCAAAGCAAG ATACCTCCAC TTAACCTTTA TCCAAGGAAG	960
40	CTCTTGGTGT CCTCTTGGTC ATAAAGTTGT CTCCTACCTA ACCCAGTTTT ACCAAATGGA	1020
	AGTAAAAGGG GACAAACTAT GGAAGATGGA CTCCATGCCA TTGCAGTCAG CCACCATTCT	1080
45	CTTTTCCATA TAAGGAGCCC CATTACATAA GCTACGGGTG AGGTGGAAC AGCTATGTTT	1140
	CATAATTICA AGAGTGTGAC CACCCTGCTC TAGTCATCAT CATTGGATGA ATCCAGTTGA	1200
	CTCTTTGGCA AAAGGGTGAT ACTTTTCACT AAAAATGCCT ACTCTTCCTG TTGATGTTCC	1260
50	TTTTCTGTTT TTACCTTGTC CAATTTCCAC ACTAGTCATT TTTTTATTT TTTAGAGGAT	1320
	CAGATTTTAG CGCTGGAAAA TGAGTTCAAA AATTTCACTG TAATGTCATA AGGATGTTGG	1380
55	GATACAGAGA TTTTTTTTTT CCTTGGAAAC AAATGGACTG GGAAGAAACA CAGCATGGCT	1440
	TGCTCTGAG TTTCAATCTG ATGATTATGA CCATGGAAGA TAGTCTTATG TAAAGGTTAA	1500
	ATGGTGTTTA CAAGTGATA GATAAGGCGG AGATGGTGAG AAGCCGGGTT TTCTCTATGC	1560
60	TAAATGTGTC TACTAAGAGC AGCACTTCCT ACTAGCTAAG CACAATCATA GCCCCACCGT	1620

-5 GATGAGCTGC TAGTCTGAAT AACATTCCCT GACTTAGGGA AAGGCACACA AAAACATATA 1680
AAGAATATGT CTATTTTCAT ATGTGTGATA CTGACAGAGC CATGGTATTC CTAAAATATA 1740
GGTTTCTCTT TTTTCTTGTA TTCTTAGCAA ATTGCATTTA TTCACTACAT TACAAACCAT 1800
CACTGATGTA TCCAAAATAG CACACATAGT TCAGTATGAA AATAAGAGAA TAAAATCTGT 1860
10 TATAAGCAAG TGATTTAGGT ATTTTCTTTT GTGTTTATGC ATTATCTGAC TATATTAAAA 1920
CCTGTTTTTC TATTACCTT CTATCAGTTT TCTCTACCAA TTATGTTTTT TCAATGCTCT 1980
ATAAGAATGA ATATGGAAAT TATATTTCTT TTTTCTGTAA AAGAGTTGCA ACTACTTTAT 2040
15 TATATTTAGA AATCCAATAA ACTTCTTATT ACATTTAAAA AAAAAAAAAA AAAACTCGAA 2100

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(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

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CCTTTGANTG TGGTCCCGGG TGCNGATTGG CAGCGCCTCC GCCGCGGCTC GTGGTTGTCC 60
CGCCATGGCA CTGTCGCGGG GGCTGCCCGG GGAGCTGGCT GAGGCGGTGG CCGGGGGCCG 120
GGTGCTGGTG GTGGGGGCGG GCGGCATCGG CTGCGAGCTC CTCAAGAATC TCGTGCTCAC 180
CGGTTTCTCC CACATCGACC TGATTGATCT GGATACTATT GATGTAAGCA ACCTCAACAG 240
ACAGTTTTTG TTTCAAAAGA AACATGTTGG AAGATCAAAG GCACAGGTTG CCAAGGAAAG 300
TGTAAGTCAG TTTTACCCGA AAGCTAATAT CGTTGCCTAC CATGACAGCA TCATGAACCC 360
TGACTATAAT GTGGAATTTT TCCGACAGTT TATACTGGTT ATGAATGCTT TAGATAACAG 420
AGCTGCCCCG AACCATGTTA ATAGAATGTG CCTGGCAGCT GATGTTCCCTC TTATTGAAAG 480
TGGAACAGCT GGGTATCTTG GACAAGTAAC TACTATCAA AAGGGTGTGA CCGAGTGTTA 540
TGAGTGTCAT CCTAAGCCGA CCCAGAGAAC CTTTCCTGGC TGTACAATTC GTAACACACC 600
TTCAGAACCT ATACATTGCA TCGTTTGGGC AAAGTACTTG TTCAACCACT TGTTTGGGGA 660
AGAAGATGCT GATCAAGAAG TATCTCCTGA CAGAGCTGAC CCTGAAGCTG CCTGGGAACC 720
AACGGAAGCC GAAGCCAGAG CTAGAGCATC TAATGAAGAT GGTGACATTA AACGTATTTT 780
TACTAAGGAA TGGGCTAAAT CAACTGGATA TGATCCAGTT AAACTTTPTA CCAAGCTTTT 840
TAAAGATGAC ATCAGGTATC TGTGACAAT GGACAACTA TGGCGGAAAA GGAAACCTCC 900

AGTTCCGTTG GACTGGGCTG AAGTACAAAG TCAAGGAGAA GAAACGAATG CATCAGATCA 960
 ACAGAATGAA CCCAGTTAG GCCTGAAAGA CCAGCAGGTT CTAGATGTAA AGAGCTATGC 1020
 -5 ACGTCTTTTT TCAAAGAGCA TCGAGACTTT GAGAGTTCAT TTAGCAGAAA AGGGGGATGG 1080
 AGCTGAGCTC ATATGGGATA AGGATGACCC ATCTGCAATG GATTTTGTCA CCTCTGCTGC 1140
 10 AAACCTCAGG ATGCATATTT TCAGTATGAA TATGAAGAGT AGATTGATA TCAAATCAAT 1200
 GGCAGGGAAC ATTATTCTTG CTATTGCTAC TACTAATGCA GTAATTGCTG GGTGATAGT 1260
 ATTGGAAGGA TTGAAGATTT TATCAGGAAA AATAGACCAG TGCAGAACAA TTTTMTTGAA 1320
 15 TAAACAACCA AACCCAAGAA AGAAGCTTCT TGTGCCTTGT GCACTGGATC CTCCCAACCC 1380
 CAATGTTTAT GTATGTGCCA GCAAGCCAGA GGTGACTGTG CGGCTGAATG TCCATAAAGT 1440
 GACTGTTCTC ACCTTACAAG ACAAGATAGT GAAAGAAAAA TTTGCTATGG TAGCACCAGA 1500
 20 TGTCCAAATT GAAGATGGGA AAGGAACAAT CCTAATATCT TCCGAAGAGG GAGAGACGGA 1560
 AGCTAATAAT CACAAGAAGT TGTCAGAATT TGGAATTAGA AATGGCAGCC GGCTTCAAGC 1620
 25 AGATGACTTC CTCCAGGACT ATACTTTATT GATCAACATC CTTCATAGTG AAGACCTAGG 1680
 AAAGGACGTT GAATTTGAAG TTGTTGGTGA TGCCCCGGA AAAGTGGGS CCAAACAAGC 1740
 TGAAGATGCT GCCAAAAGCA TAACCAATGG GCAGTGATGA TGGGAGCTTC AGCCCTCCAC 1800
 30 CTYCACAGCT TCAAGGAGGC AAGATGGACG TYTCYCATAG TTGATYCGGR TGAAGAAGRT 1860
 TCTCCAATAA TGCCCCGACG TTCATTGAAG GAAGGAGGAG GAGGCCCGCC AAGAGGGGAA 1920
 35 TTTAGGNTTG 1930

40 (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

50 GGGCCTGGCC TCTGGGCTGA GGCTTGCTAG GGA CTGGGG TGGCTCTAAG GGGCAGGGAT 60
 AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG ACCAGCCCCT TCTCGTGCRG GTTCCACCCC 120
 GATGCAGGTG GTCACGTGCT TGACGCGGGA CAGTACCTG ACGCACTGCT TCCTCCAGCA 180
 55 CCTCATGGTC GTGCTGTCCT CTCTGGAACG CACGCCCTCG CCGGAGCCTG TTGACAAGGA 240
 CTTCTACTCC GAGTTTGGGA ACAAGACCAC AGGGAAGATG GAGAACTACG AGCTGATCCA 300
 60 CTCTAGTCGC GTCAAGTTTA CCTACCCAG TGAGGAGGAG ATTGGGGACC TGACGTTTAC 360

TGTGGCCCAA AAGATGGCTG AGCCAGAGAA GGCCCCAGCC CTCAGCATCC TGCTGTACGT 420
 GCAGGCCTTC CAGGTGGGCA TGCCACCCCC TGGGTGCTGC AGGGGCCCCC TGCGCCCCAA 480
 - 5 GACACTCCTG CTCACCAGCT CCGAGATCTT CCTCCTGGAT GAGGACTGTG TCCACTACCC 540
 ACTGCCCGAG TTTGCCAAAG AGCCGCCGCA GAGAGACAGG TACCGGCTGG ACGATGGCCG 600
 10 CCGCGTCCGG GACCTGGACC GAGTGCTCAT GGGCTACCAG ACCTACCCGC AGCCCTCACC 660
 CTCGTCTTCG ATGACGTGCA AGGTCATGAC CTCATGGGCA GTGTCACCC T GGACCACTTT 720
 GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG 780
 15 TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG CTCATCTCGC TGTGGGCTCG CCAGTGGGAG 840
 GCCCTGTGTG GCCGTGAGCT GCCTGTCGAG CTCACCGGCT AGCCAGGCC ACAGCCAGCC 900
 20 TGTGCTGTCC AGCCTGACGC CTA CTG GGGC AGGGCAGCAG GCTTTTGTGT TCTCTAAAAA 960
 TGTMTTATCC TCCCTTTGGT ACCTTAATTT GACTGTCTC GCAGAGAATG TGAACATGTG 1020
 TGTGTGTTGT GTTAATCTT TCTCATGTTG GGAGTGAGAA TGCCGGGCCC CTCAGGGCTG 1080
 25 TCGGTGTGCT GTCAGCCTCC CACAGGTGGT ACAGCCGTGC ACACCAGTGT CGTGTCTGCT 1140
 GTTGTGGGAC CGTTGTAAAC ACGTGACACT GTGGGTCTGA CTTTCTCTTC TACACGTCTT 1200
 30 TTCCTGAAGT GTCGAGTCCA GTCTTTTGTT GCTGTTGCTG TTGCTGTGTC TGTGCTGTT 1260
 GGCATCTTGC TGCTAATCCT GAGGCTGGTA GCAGAATGCA CATTGGAAGC TCCCACCCCA 1320
 TATTGTTCTT CAAAGTGGAG GTCTCCCTG ATCCAGACAA GTGGGAGAGC CCGTGGGGGC 1380
 35 AGGGGACCTG GAGCTGCCAG CACCAAGCGT GATTCTGCT GCCTGTATTC TCTATTCCAA 1440
 TAAAGCAGAG TTTGACACCG TCAAAAAAAAA AAAAAAAAAA AAAAAAAAAA ATTNCTGCGG 1500
 40 CCTCAAGGG 1509

45 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3173 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

55 TCGACCCAS GCGTCCGTGC TTTTCCACAG AAGGTTAGAC CCTGAAAGAG ATGGCTCAGC 60
 ACCACCTATG GATCTTGCTC CTTTGCTGCA AAACCTGGCC GGAAGCAGCT GGAAAAGACT 120
 60 CAGAAATCTT CACAGTGAAT GGGATTCTGG GAGAGTCAGT CACTTTCCCT GTAAATATCC 180

	AAGAACCACG	GCAAGTTAAA	ATCATTGCTT	GGACTTCTAA	AACATCTGTT	GCTTATGTAA	240
	CACCAGGAGA	CTCAGAAACA	GCACCCGTAG	TTACTGTGAC	CCACAGAAAT	TATTATGAAC	300
-5	GGATACATGC	CTTAGGTCCG	AAC TACAATC	TGGTCATTAG	CGATCTGAGG	ATGGAAGACG	360
	CAGGAGACTA	CAAAGCAGAC	ATAAATACAC	AGGCTGATCC	CTACACCACC	ACCAAGCGCT	420
10	ACAACCTGCA	AATCTATCGT	CGGCTTGGA	AACCAAAAAT	TACACAGAGT	TTAATGGCAT	480
	CTGTGAACAG	CACCTGTAAT	GTCACACTGA	CATGCTCTGT	AGAGAAAGAA	GAAAAGAATG	540
	TGACATACAA	TTGGAGTCCC	CTGGGAGAAG	AGGGTAATGT	CCTTCAAATC	TTCCAGACTC	600
15	CTGAGGACCA	AGAGCTGACT	TACACGTGTA	CAGCCCAGAA	CCCTGTCAGC	AACAATTCTG	660
	ACTCCATCTC	TGCCCCGGCAG	CTCTGTGCAG	ACATCGCAAT	GGGCTTCCGT	ACTCACCACA	720
20	CCGGGTGCT	GAGCGTGCTG	GCTATGTTCT	TTCTGCTTGT	TCTCATTTCTG	TCTTCAGTGT	780
	TTTGTGCCG	TTGTTCAAG	AGAAGACAAG	ATGCTGCCTC	AAAGAAAACC	ATATACACAT	840
	ATATCATGGC	TTCAAGGAAC	ACCCAGCCAG	CAGAGTCCAG	AATCTATGAT	GAAATCCTGC	900
25	AGTCCAAGGT	GCTTCCCTCC	AAGGAAGAGC	CAGTGAACAC	AGTTTATTCC	GAAGTGCAGT	960
	TTGCTGATAA	GATGGGGAAA	GCCAGCACAC	AGGACAGTAA	ACCTCCTGGG	ACTTCAAGCT	1020
30	ATGAAATTGT	GATCTAGGCT	GCTGGGCTGA	ATTCTCCCTC	TGGAACTGA	GTTACAACCA	1080
	CCAATACTGG	CAGGTTCCCT	GGATCCAGAT	CTTCTCTGCC	CAACTCTTAC	TGGGAGATTG	1140
	CAAACTGCCA	CATCTCAGCC	TGTAAGCAA	GCAGGAAACC	TTCTGCTGGG	CATAGCTTGT	1200
35	GCCTAAATGG	ACAAATGGAT	GCATACCCTT	CCTGAAATGA	CTCCCTTCTG	AATGAATGAC	1260
	AAAGCAGGTT	ACCTAGTATA	GTTTTCCCAA	ACTTCTTCCC	ATCATAGCAC	ATGTAGAAAA	1320
40	TAATATTTTT	ATGGCACACT	GGGATAAACA	AGCAAGATTG	CTCACTTCTG	GAAGCTGCAT	1380
	ATGACTAGAG	GCCTCTTG TG	ACTGGAGGTA	ACAACCCTGC	CCAGTAACTG	TGGGAGAAGG	1440
	GGATCAATAT	TTTGACACCC	TGTAATAGGC	CATGGCACAC	CAGCCAAGAT	GCTCTGCTCA	1500
45	CAGTCAGTAT	GTGTGAAGAT	CCCTGGTGCG	TGGCCTTCAC	CACGCATCTT	GAGCAAATTA	1560
	GGAAAATGTA	CCCTTCGCTT	GAGGCAGATG	CAGCCCTTCC	CCCGAGTGCA	TGGCTTGGAG	1620
50	AGCAGAATGT	GGGCTGCATA	TAAGCACACT	CATCCCTTTG	TCTGGGAATC	TTTGTGCAGG	1680
	GCATAACAGG	CTTAGTAAGT	CCAAACACAG	ATGACAGTGC	TGTGTGGGTC	TCTGTCAGAG	1740
	TTGTGGCTCT	CAGCCATGTA	GACACACTCT	CCAAATGGAG	TGTTGGAAAA	TGTTCTTTCT	1800
55	GCAGGGTCTA	GAGACTGCTG	GGACACTTTT	CTTGGAGTGC	TACTTCAGAA	GCCTTATAGG	1860
	ATTTTCTTTC	TGGCCAAGAT	TTCTTCTGT	ATCACTCCAA	GCAGCCTCAG	CAGAAGAAGC	1920
60	AGCCATGCCC	AGTATTCCCA	CTCTCCAAAA	GGAAGTGACC	AGCTTATATT	TCTCACACTT	1980

	CTGGGGA	ACT	GGGTATAATC	CAACCATCAA	AATAGAAGAC	CTTGCAAGAA	GCAGAGTCAT	2040
	TCTCCAGAAG	GA	ACTTGGGA	GATGATGGTG	CAGATGATGA	AACTGGGTTC	ATCCCAGTTC	2100
-5	CAAAGACTCA	GAGA	ACTAGA	GTTTAAGCTG	AGGCAGAGTG	CGCCACCCCT	GGCATGCCCC	2160
	ACAAACAGAT	CACCAGCCAG	CTTACACAGG	CATTA	ACTCT	CCTCAATGAG	GAAGAATCAT	2220
10	TCACAACTGA	GCAAGACATT	CATATGATCA	TTTAAGGAAG	TGTTTCCCTT	ATGTGTTAGC		2280
	AAGTATAATC	GGCTAACTCC	TAAATCCCAA	TGAATAGTCC	TAGGCTGGAC	AGCAATGGGC		2340
	TGCAATTAGG	CAGATAAAGA	CATCAGTCCC	AGTAAATGAA	TCCATAGACT	CATCTAGCAC		2400
15	CAACTACCAT	TAGCACTATG	TTAGGAGCTG	CAAGGCCCCA	AAGTAGAAGA	TGTGCATAAT		2460
	GTCTGCTCTT	GTGTAGCTCA	GGAGACAATT	CCAGCACAGA	CACTACAGTT	AACGCTGAAC		2520
20	TGCAGCTGCA	AGTAATAGCA	TGAACAGTCA	GAAAAATACC	TTATGAGGGG	GCAGGGCTGA		2580
	AGCTGGGCCT	TGAAGGATGG	ATGAAATTTG	GATAGAGAAT	GAGGAAGACA	GAGGGCCTCC		2640
	AAGTGAGAGA	AGCATGAAAA	ATGAGCAGGG	GCCTGGATCA	GTGGGGTGTA	TTCAGAGCAC		2700
25	CTCTCCAGAT	GCACCATGCA	TGCTCACAGT	CCCTTGCCCTA	TGTGTGGCAG	AGTGTCCCAG		2760
	CCAGATGTGT	GGCCCCACCC	CATGTCCATT	TACATGTCCT	TCAATGCCCC	CCTCAAAAGG		2820
30	TACCTCTTCT	GTAAAGCTTT	CCCTGGTATC	AGGAATCAAA	ATTAATCAGG	GATCTTTTCA		2880
	CACTGCTGTT	TTTTCTCTT	TGGTCCTTCT	ATCACTAAAA	CTCATCTCAT	TCAGCCTTAC		2940
	AGCATAACTA	ATTATTGT	TTCTCACTA	CATTGTACAT	GTGGGAATTA	CAGATAAACG		3000
35	GAAGCCKGCT	GGGGTGGTGG	CTCAGCCTG	TAATCCCAAC	ACTTTGGGAG	GCCAAGGCAG		3060
	GCGGATCACC	TGAGGTCAGG	ARTTCGAGAT	TARTCTGGCC	AACATGGTGA	AACCCCATNT		3120
40	NTACTAAAAA	TACGAAATTA	GCCAGGTGTG	GTGGCACACA	TCTGTAGTCC	CAG		3173

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

55	AAATTCGGCA	CAGCTGAGAG	GAGACACAAG	GAGCAGCCCG	CAAGCACCAA	GTGAGAGGCA	60
	TGAAGTTACA	GTGTGTTTCC	CTTTGGCTCC	TGGGTACAAT	ACTGATATTG	TGCTCAGTAG	120
	ACAACCACGG	TCTCAGGAGA	TGTCTGATTT	CCACAGACAT	GCACCATATA	GAAGAGAGTT	180
60	TCCAAGAAAT	CAAAAGAGCC	ATCCAAGCTA	AGGACACCTT	CCCAAATGTC	ACTATCCTGT	240

CCACATTGGA GACTCTGCAG ATCATTAAAGC CCTTAGATGT GTGCTGCGTG ACCAAGAACC 300
 TCCTGGCGTT CTACGTGGAC AGGGTGTTC AAGATCATCA GGAGCCAAAC CCCAAAATCT 360
 TGAGAAAAAT CAGCAGCATT GCCAACTCTT TCCTCTACAT GCAGAAAACT CTGCGGCAAT 420
 GTCAGGAACA GAGGCAGTGT CACTGCAGGC AGGAAGCCAC CAATGCCACC AGAGTCATCC 480
 ATGACAACTA TGATCAGCTG GAGGTCCACG CTGCTGCCAT TAAATCCCTG GGAGAGCTCG 540
 ACGTCTTTCT AGCCTGGATT AATAAGAATC ATGAAGTAAT GTCCTCAGCT TGATGACAAG 600
 GAACCTGTAT AGTGATCCAG GGATGAACAC CCCCTGTGCG GTTTACTGTG GGAGACAGCC 660
 CACCTTGAAG GGAAGGAGA TGGGAAGGC CCCTTGACG TGAAAGTCCC ACTGGCTGGC 720
 CTCAGGCTGT CTTATTCCGC TTGAAAATAG CCAAAAAGTC TACTGTGGTA TTTGTAATAA 780
 ACTCTATCTG CTGAAAGGCG CTGCAGGCCA TCCTGGGAGT AAAGGGCTGC CTTCCCATCT 840
 AATTATTGT GAAGTCATAT AGTCCATGTC TGTGATGTGA GCCAAGTGAT ATCCTGTAGT 900
 ACACATTGTA CTGAGTGGTT TTTCTGAATA AATTCCATAT TTTACCTAAA AAAAAAAAAA 960
 AAAAAGCTGA GGGGGGGCCC GTACCCAATT T 991

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(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

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ACAGCCCTCT TCGGAGCCTG AGCCCGGCTC TCCTCACTCA CCTCAACCCC CAGGCGGCCC 60
 CTCCACAGGG CCCCTCTCCT GCCTGGACGG CTCTGCTGGT CTCCCCGTCC CCTGGAGAAG 120
 AACAAGGCCA TGGGTGCGCC CCTGCTGCTG CCCCTRCTGC YCCTGCTGCW GCCGCCAGCA 180
 TTTCTGCAGC CTRGTGGCTC CACAGGATCT GGTCCAAGCT ACCTTTATGG GGTCACTCAA 240
 CCAAAACACC TCTCAGCCTC CATGGGTGGC TCTGTGGAAA TCCCCTTCTC CTTCTATTAC 300
 CCCTGGGAGT TAGCCAYAGY TCCCRACGTG AGAATATCCT GGAGACGGGG CCACTTCCAC 360
 GGGCAGTCCT TCTACAGCAC AAGGCCGCCT TCATTTCACA AGGATTATGT GAACCGGCTC 420
 TTTCTGAACT GGACAGAGGG TCAGGAGAGC GGCTTCCTCA GGATCTCAA CCTGCGGAAG 480
 GAGGACCAGT CTGTGTATTT CTGCCGAGTC GAGCTGGACA CCCGGAGATC AGGGAGGCAG 540
 CAGTTGCAGT CCATCAAGGG GACCAAACTC ACCATCACCC AGGCTGTCAC AACCACCACC 600

ACCTGGAGGC CCAGCAGCAC AACCACCATA GCCGGCCTCA GGGTCACAGA AAGCAAAGGG 660
 CACTCAGAAT CATGGCACCT AAGTCTGGAC ACTGCCATCA GGGTTGCATT GGCTGTGCGCT 720
 5 GTGCTCAAAA CTGTCAATTT GGGACTGCTG TGCCTCCTCC TCTGTGGTGG AGGAGAAGGA 780
 AAGGTAGCAG GGCGCCAAGC AGTGACTTCT GACCAACAGA GTGTGGGGAG AAGGGATGTG 840
 10 TATTAGCCCC GGAGGACGTG ATGTGAGACC CGCTTGTGAG TCCTCCACAC TCGTTCCCCA 900
 TTGGCAAGAT ACATGGAGAG CACCCTGAGG ACCTTTAAAA GGCAAAGCCG CAAGGCAGAA 960
 GGAGGCTGGG TCCCTGAATC ACCGACTGGA GGAGAGTTAC CTACAAGAGC CTTTCATCCAG 1020
 15 GAGCATCCAC ACTGCAATGA TATAGGAATG AGGTCTGAAC TCCACTGAAT TAAACCACTG 1080
 GCATTTGGGG GCTGTTYATT ATAGCAGTGC AAAGAGTTCC TTTATCCTCC CCAAGGATGG 1140
 20 AAAATACAAT TTATTTTGCT TACCATACAC CCCTTTCTC CTCGTCCACA TTTTCCAATC 1200
 TGTATGGTGG CTGTCTTCTA TGGCAGAAGG TTTTGGGGAA TAAATAGCGT GANATGNTNC 1260
 TGACTNAAAA AAAAAAAAAA AAAAATCGA 1290

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(2) INFORMATION FOR SEQ ID NO: 177:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TGGGGCCCCCT TTTGGATGCT CTGGGTGTTT TTGCCAAGAG TTACAGGATG TCAAGTGTGG 60
 40 GGAGCTCAGC ACCCTTGCTG TGGACCAAGT AAGGCTGTTC CAGACCAGGT GCTTCCAGAC 120
 ATTTCCAGGC TCCAGGAGAG AGGCTGGGAG CCCCCACAGA AAGCACAGGA AAATGCAAAA 180
 45 AAAAAACAGT CTTTTTTTTT TTTTGCTTT TTATTATGAA AACAAAACAA ATGCCCCAGG 240
 AGAAGGTCC ATGATTACCA GAAACATCAA AGAGTACTTT CTACCATTTT TATTCTGTTG 300
 TGTTGAGGCC AGCATTGCAA TAAACAAGCT AACTACTTA CATGGACTC ATTTTCAGTA 360
 50 ACTGACATTT ACAGGAATAT ACTAGAAACG GCACTAAAAA GTTTAAGAAA AGTTACGGTA 420
 AACTTGCATG CACATCATAC AGAAAAGTAA CATTTTAAAT ATAAAAAGA AAAACTTCCT 480
 55 GGAAGCATTA TGCCAGTATT AAGGAACAGT GCTACTCTGG ATGTGACAAA TTCTGTATGT 540
 GGGTGTACT CTTTCCCAA AGACTGTCAG AGGCGTGAGT GCTGCAAAAG AACAACAACA 600
 AAAACAAACA CACAAAAAAA TGTGTCTTAC AGTTTGTAAAG CAAGATGACA CTGCCCAACA 660
 60 CAAAGAGGGG TCTGGAGTTC AGTTCACGCC CGAAGCCTGC CCCCTCGGCC TCCAGGGGTC 720

	ATTTCAGAGTG TTCTCAAATC CAATTCCGAC ACACGACTTG TCACTACTCC TCTCCCCTTG	780
- 5	AAAAAAGCAT GTTAGAAGCT GCCCTACAGG TCTCAGCAGT GGGACAATCT AATTGAATCA	840
	CCGCAGCCTT CTAATACAGA AGAAACGGAC GTGACTGTCA CCCTCAGCCC GCCAGCAAGG	900
	GCGCTGAGGA AGTCATTAAT CCTTCGAAAC TCTGAAAAGA AACCAGTGTT GAAGTCTGGA	960
10	CAGAAAGCCT TAAAAAAGTG ACAGCACCAA TGCAGCTGCT CAGTGTACCC NCCGTGGGCT	1020
	GTCAGGGTCA GTGGCTTCTT TCTAGATGAA AGGAGCAGAG GCGAGCCGAC GCCACCGTCA	1080
15	CAGAGAACCA GCCGAGAAGG AAAGGCCCCA CGATGCTCCC TGTGCGCTGC CCCCACAGCC	1140
	GGCCGCTCCC CCGACGGCTC ACACAGGCAG CACCTCACTG CCCTGTGGCT GGAGGGGCAT	1200
	TGCAAGGAGC GCCCCCAGC CCCAGGCACC CCCGGCTTAG GGTGTACGTA TCACCCAGCC	1260
20	CTGTGCTGGC AGCACGTTAC CAACCAGCCT GCGTGAAGAC CTGTCAACTG TCGTGTGTGA	1320
	ATTCTTAA TCGGTTTAA ATAGTCCATT AAAGATCTGT TTAGAAAATA CCTTTGAAAA	1380
25	CGAGGGTAAC TTTAAAAAAT GGAACTTTT AAATCCATTT ATATTTTAT TATAAACAA	1440
	ACTTAATTAA AAGTTTAA AACTGGCTGA AAATCACCA AGTGTACAGC TCACCAGCAA	1500
	TTTAAAAAAT GATAATTTAC CAGCATCTCC TCATCAGAGT TCCCTCTCCA GTAAGGGTAT	1560
30	ACCTACATCT GTAAGGGTCA GTGGACTCTG AATCAATTTT ATGGTTGTTT TAAAATCACC	1620
	GTGTATTAGG ATACTAATGA TAGTCCCTAT ATCCATCCAG AAATGCTGGC AGAAAGCACT	1680
35	GGCCACCATA CAGGACAGAC CACACCACAG CTCCATACCC AGCGTCTGCC TGGAGGCTCC	1740
	CCCACGCTGA GGTCCGGGAG AATGCCTGGT TTCAGTCATT TCCGGACTAA CTGTGACAAC	1800
	GCGTGAGCAG GGAGCACCGT GCGAGTCTCC GGGAGGGAAT CCTCCTGGGG CCCAGAGACT	1860
40	CCTCCACCCC TGGGGAGGGC AGACAGGCTC GGGARGGCCT GGCCAGGCCA CTGGAGGCTG	1920
	GCAGGGAGCA GGCATGTCCA CCCGCAAGCC TGGGAGGCTA ACTCTGGCAT TCCTGGCCGG	1980
45	AGCCGCCATG CTCATTGGTG GGCCAGTTTG GGACATCCCC GTA CTCAAAG ACCATATGGC	2040
	AGCCTCTGGG AAAACAAAAC CAAAACATCA CCTTCTATTA AACTCTGTAT ATTATTATTT	2100
	TTTACAATAG AAAGTTAAAA ATCAAGACTT AGATTACTA TACATTTTTT CTCTCAGATT	2160
50	ACAAAGTTTA TATTATATAA CTGGGGTTCC CTAAATTGAT TTCTTTTAAA ACAGTCTTAA	2220
	AGAGACCAGA AGTGAATACA AAAGAACTAA ACAAATAAAA AAATTAGAAT GTGCTGTAGC	2280
55	TGAAAGCTGT	2290

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(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GGCACGAGCC ATGCCTGGCC TCTCCTTGAT TCTTACAGTC ACTTTGTTGG CTGTTTCTGA 60
 CTCAGCAGCT ACCTGCATTG TGGCCAAAGG ATGACCTATT CCTTCTCAGG AGGGCAAAAA 120
 TGTGGAATAG TGTCTGTCCA TGCCTCTCCT CATGGGCTAC CACCTCTGCC ACCGTGGTTA 180
 ATCAGTAACA ACCAGGAGAG AAGCTGCTGG AACTGACCTC TGGGAACTCC CTGGGATGGT 240
 TTGGTGCAGG AATGTAGTAG GCATACACGT GGTGCGTGG ATCTGGGCCC TCCTGATGTG 300
 AGTAGAGAGG TAAAGGCCA CCATCTCCTT GACCTCTGGG GAACTCATCC ACAAAGAAGA 360
 TGTTCCTCAAG ATGCTTCTGA AGATTGCCTA AAAATAGCCG GTTTCACCCC CCGTGAATGC 420
 ATCCATTCTA GAATGCTCCT TCACCAGGAC CAGAGAACTG ATTTACAGAA GTGACATGAA 480
 AACATTCCAT CCCAGAATTT GCAGTAGCTC AAATTAAGTT TCTAGCTATT AAAAAGAAAA 540
 AAAAAAAAAA 549

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GGCACGAGGG CTCATTTCATT CCGCGCCGGG CCGCCAGAC ACCTGCGCCC TTCTGCAGCC 60
 GCCCGCCGCA TCCGCCGCGG CAGCCCCCAG CATGTCGGGC CCAGACGTCG AGACGCCGTC 120
 CGCCATCCAG ATCTGCCGGA TCATGCGGCC AGATGATGCC AACGTGGCCG GCAATGTCCA 180
 CGGGGGGACC ATCCTGAAGA TGATCGAGGA GGCAGGCGCC ATCATCAGCA CCCGGCATTG 240
 CAACAGCCAG AACGGGGAGC GCTGTGTGGC CGCCCTGGCT CGTGTGAGC GCACCGACTT 300
 CCTGTCTCCC ATGTGCATCG GTGAGGTGGC GCATGTCAGC GCGGAGATCA CCTACACCTC 360
 CAAGCACTCT GTGGAGGTGC AGGTCAACGT GATGTCCGAA AACATCCTCA CAGGTGCCAA 420
 AAAGCTGACC AATAAGGCCA CCCTGTGGTA TGTGCCCTG TCGCTGAAGA ATGTGGACAA 480
 GGTCTCTGAG GTGCCTCCTG TTGTGTATTG CCGGCANGAG CAGGAGGAGG AGGGCCGGAA 540
 GCGGTATGAA GCCCAGAAGC TGGAGCGCAT GGAGACCAAG TGGAGGAACG GGGACATCGT 600

CCAGCCAGTC CTCAACCCAG AGCCGAACAC TGTCAGCTAC AGCCAGTCCA GCTTGATCCA 660
 CCTGGTGGGG CCTTCAGACT GCACCCCTGCA CGGCTTTGTG CACGGAGGTG TGACCATGAA 720
 -5 GCTCATGGAT GAGGTCGCCG GGATCGTGGC TGCACGCCAC TGCAAGACCA ACATCGTCAC 780
 AGCTTCCGTG GACGCCATTA ATTTTCATGA CAAGATCAGA AAAGGCTGCG TCATCACCAT 840
 10 CTCGGGACGC ATGACCTTCA CGAGCAATAA GTCCATGGAG ATCGAGGTGT TGGTGGACGC 900
 CGACCCCTGTT GTGGACAGCT CTCAGAAGCG CTACCGGGCC GCCAGTGCCT TCTTCACCTA 960
 CGTGTGCTG AGCCAGGAAG GCAGGTCGCT GCCTGTGCCC CAGCTGGTGC CCGAGACCGA 1020
 15 GGACGAGAAG AAGCGCTTTG AGGAAGGCAA AGGGCGGTAC CTGCAGATGA AGGCGAAGCR 1080
 ACAGGGCCAC GCGGASCYTC AGCCCTAGAC TCCCTCCTCC TGCCACTGGT GCCTCGAGTA 1140
 20 GCCATGGCAA CGGGCCCACT GTCCAGTCAC TTAGAAGTTC CCCCCTTGGC CAAAAACCA 1200
 ATTCACATG AGAGCTGGTG TTGTCTGAAG TTTTCGTATC ACAGTGTAA CCTGTACTCT 1260
 CTCCTGCAA CCTACACACC AAAGCTTTAT TTATATCATT CCAGTATCAA TGCTACACAG 1320
 25 TGTGTCCCG AGCGCCGGA GCGTTGGGC AGAAACCTC GGAATGCTT CCGAGCACGC 1380
 TGTAGGTAT GGAAGAACC CAGCACCCT AATAAGCTG CTGCTGGCT GGAAAAAAA 1440
 30 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AGAAAAAAN 1509

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(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 1316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

AGCTGTATCA TAGGAAAGAT GGCCACACCG GCGGTACCAG TAAGTGCTCC TCCGGCCACG 60
 CCAACCCAG TCCGGCGGC GGCCCAAGCC TCAGTTCAG CGCCAACGCC AGCACCGGCT 120
 50 GCGGCTCCGG TTCCCGCTGC GGCTCCAGCC TGCATCCTCA GACCCTGCGG CAGCAGGGC 180
 TGCAACTGCG GCTCTGGCC AGACCCGGC CTCAGCGCAA NTCCAGCGCA GACCCAGCG 240
 55 CCCGCTCTGC CTGGTCTGC TCTTCAGGG CCCTTCCCCG GCGGCCCGT GGTGAGGCTG 300
 CACCCAGTCA TTTTGGCCTC CATTGTGGAC AGCTACGAGA GACGCAACGA GGGTGTGCTC 360
 CGAGTTATCG GGACCCTGTT GGAAGTGTG GACAAACACT CAGTGGAGGT CACCAATTGC 420
 60

	TTTTCAGTGC CGCACAAATGA GTCAGAAGAT GAAGTGGCTG TTGACATGGA ATTTGCTAAG	480
	AATATGTATG AACTGCATAA AAAAGTTTCT CCAAATGAGC TCATCCTGGG CTGGTACGCT	540
5	ACGGGCCATG ACATCACAGA GCACTCTGTG CTGNATCCAT GAGTACTACA GCCGAGAGGC	600
	CCCCAACCCC ATCCACCTCA CTGTGGACAC AAGTCTCCAG AACGGCCGCA TGAGCATCAA	660
10	AGCCTACGTC AGCACTTTAA TGGGAGTCCC TGGGAGGACC ATGGGAGTGA TGTTCACGCC	720
	TCTGACAGTG AAATACGCGT ACTACGACAC TGAACGCATC GGAGTTGACC TGATCATGAA	780
	GACCTGCTTT AGCCCCAACA GAGTGATTGG ACTCTCAAGT GACTTGCAGC AAGTAGGAGG	840
15	GGCATCAGCT CGCATCCAGG ATGCCCTGAG TACAGTGTG CAATATGCAG AGGATGTACT	900
	GTCGGAAG GTGTCAGCTG ACAATACTGT GGGCCGCTC CTGATGAGCC TGGTTAACCA	960
20	AGTACCGAAA ATAGTTCCCG ATGACTTTGA GACCATGCTC AACAGCAACA TCAATGACCT	1020
	TTTGATGGTG ACCTACCTGG CCAACCTCAC ACAGTCACAG ATTGCACTCA ATGAAAACT	1080
	TGTAAACCTG TGAATGGACC CCAAGCAGTA CACTTGCTGG TCTAGGTATT AACCCAGGA	1140
25	CTCAGAAGTG AAGGAGAAAT GGGTTMTTG TGGTCTTGAG TCACACTGAG ATAGTCAGTT	1200
	GTGTGTGACT CTAATAAACG GAGCCTACCT TTTGTAAATT AAAAAAAAAA AAAAAACCN	1260
30	SGRGGGGGG CCCGGTCCA TTSSCCCTT NGTAATTCGT NTTACAATCC CCNGGC	1316

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

45	GGCATGWKCA GACATGACTT CTATTGCCAG GCTGGTCAAG TGGCAGGGTC ATGAGGGAGA	60
	CATCGATAAG GGTGCTCCTT ATGCTCCCTG CTCTGGAATC CACCAGCGGG CTATCTGCGT	120
	TTATGGGGCT GGGGACTAGA ATTGGATGCT TCAAAACCAT CACCTGTTGG CCAACAAGTT	180
50	TGACCCAAAG GTAGATGATA ATGCTCTTCA GTGCTTAGAA GAATACCTAC GTTATAAGGG	240
	CCATTCTATT GGGACCTGAA CTTTGAAGAC CACAMTATTG AAGAGGCGTT GCTTACCYGT	300
55	TGGGGGCCAA GAGGCATGTT ACCAAACATG GYYCARGAAM YTTGGYKGGG AMCARKKKKG	360
	GKKGGGARRM CMRGGGYTTG SCAAWTTCCK KGGCMWCCYT TTAGGGTAAR RRGGGCKGTW	420
	ATTAGATGT GGGTAAAGTA GGATCTTTTG CCCTTGCAAA TTTGCTGCCT GGGTGAATGY	480
60	TGCTTGTTCC TTCTCMACCC CTAACCCTAG TAGTTCTCTC ACTAACTTTC TCACTAAGTG	540

5 AGAATGAGAA CTGCTGTGAT AGGGAGAGTG AAGGAGGGAT ATGTGGTAGA GCACTTGATT 600
 TCAGTTGAAT GCCTGCTGGT AGCTTTTCCA TTCTGTGGAG CTGCCGTTCC TAATAATTCC 660
 AGGTTTGGTA GCGTGGAGGA GAACTTTGAT GGAAAGAGAA CCTTCCCTTC TGTACTGTTA 720
 ACTTAAAAAT AAATAGCTCC TGATTCAAAG TAAAAA AAAA AAAAAA 777
 10

(2) INFORMATION FOR SEQ ID NO: 182:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GGCACAGATA ACTATGTACA TGTATTCCTT AAATGTTTTT TTAAGTTTTA TATTCCTGGC 60
 25 ACTGGTCTTC AAATGTGTAC ATGTGTGCCA GGGAGCAAAT GCCTTCTTGT TTCTGAAATT 120
 GGTCTTTTAG ACTGTTCTTT TTTCCCATCT TCTCACCTCC TGCCCTCCTC TCAGGGTACT 180
 TCCGTGGCCA GAACCCCTCC AGGTCAGAGG CAGAAGAGAA GCCTCATGGG TCACAGCAGC 240
 30 AGATGTGGGC TGGAGATCTA TTCATTGGT TTTGGCTTGA ATTTTCTGRA TGGTTTACTT 300
 GATCYTGGGA AAGANATATC TTGCCAGGAA AAATGATAGN CCTTGACAAT GTTGAATGAT 360
 35 CCTGCACCAC CTTGAAAGAC ATTTCTAATA TGGTTTGTCA GGCAAAGTGG TTAGTAGTCA 420
 TTTGTGGCCT GAGGTAGAAG TCCTCAGAAA TCAGCAGACT TCACTGATAA AATGCTGACT 480
 TGCCCTGGA CTGGGCTCTG TGAGAGTGGC CTCTGCACT GTGCACAGTA GGTGTGAACA 540
 40 CACCACACCT ACAGGGACCA CGTGGTGGGC TGTGGACTAG CGGCCAAGCT CCCTGCAGGC 600
 CCACTAATAG AATTCAGCTT TTAGCATGGG CTGTTTCATA CTGTTCTGAT GAAACTGATT 660
 45 TGGTTTCTTT CCTCCATACC CCTTCTGCAT TTCAGTGTTC TTGTTTAGTT TTCCTGGTTT 720
 TTAATTATAA CTACAAAATA AAATCTTTAG GCTATTCACC TTAGCTTAGT AAAAAAAAAA 780
 AAAAAAACT C 791
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55 (2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

5	GTCATGCAGT GCGCCGGAGA ACTGTGCTCT TTGAGGCCGA CGCTAGGGGC CCGGAAGGGA	60
	AACTGCGAGG CGAAGGTGAC CGGGGACCGA GCATTTTCAGA TCTGCTCGGT AGACCTGGTG	120
	CACCACCACC ATGTTGGCTG CAAGGCTGGT GTGTCTCCGG ACACTACCTT CTAGGGTTTT	180
10	CCACCCAGCT TTCACCAAGG CCTCCCCTGT TGTGAAGAAT TCCATCACGA AGAATCAATG	240
	GCTGTTAACA CCTAGCAGGG AATATGCCAC CAAAACAAGA ATTGGGATCC GCGTGGGAG	300
15	AACTGGCCAA GAACTCAAAG AGGCAGCATT GGAACCATCG ATGGAAAAA TATTTAAAAT	360
	TGATCAGATG GGAAGATGGT TTGTTGCTGG AGGGGCTGCT GTTGGTCTTG GAGCATGTG	420
	CTACTATGGC TTGGGACTGT CTAATGAGAT TGGAGCTATT GAAAAGGCTG TAATTGGCC	480
20	TCAGTATGTC AAGGATAGAA TTCATTCCAC CTATATGTAC TTAGCAGGGA GTATTGGTTT	540
	AACAGCTTTG TCTGCCATAG CAATCAGCAG AACGCCTGTT CTCATGAACT TCATGATGAG	600
25	AGGCTCTTGG GTGACAATTG GTGTGACCTT TGCAGCCATG GTTGGAGCTG GAATGCTGGT	660
	ACGATCAATA CCATATGACC AGAGCCCAGG CCCAAAGCAT CTTGCTTGGT TGCTACATTC	720
	TGGTGTGATG GGTGCAGTGG TGGCTCCTCT GACAATATTA GGGGGTCTC TTCTCATCAG	780
30	AGCTGCATGG TACACAGCTG GCATTGTGGG AGGCCTCTCC ACTGTGGCCA TGTGTGCGCC	840
	CAGTGAAG TTTCTGAACA TGGGTGCACC CCTGGGAGTG GGCCTGGGTC TCGTCTTGT	900
35	GTCTCATG GGATCTATGT TTCTTCCACC TACCACCGTG GCTGGTGCCA CTCTTTACTC	960
	AGTGGCAATG TACGGTGGAT TAGTTCTTTT CAGCATGTTT CTCTGTATG ATACCCAGAA	1020
40	AGTAATCAAG CGTGCAGAAG TATCACCAAT GTATGGAGTT CAAAAATATG ATCCCATTA	1080
	CTCGATGCTG AGTATCTACA TGGATACATT AAATATATTT ATGCGAGTTG CAACTATGCT	1140
	GGCAACTGGA GGCAACAGAA AGAAATGAAG TGAATCAGCT TCTGGCTTCT CTGCTACATC	1200
45	AAATATCTTG TTTAATGGGG CAGATATGCA TTAAATAGTT TGTACAAGCA GCTTTCGTTG	1260
	AAGTTTAGAA GATAAGAAAC ATGTCATCAT ATTTAAATGT TCCGGTAATG TGATGCCTCA	1320
	GGTCTGCCTT TTTTCTGGA GAATAAATGC AGTAATCCTC TCCCAAATAA GCACACACAT	1380
50	TTTCAATTCT CATGTTTGTG TGATTTTAAA ATGTTTGGT GAATGTGAAA ACTAAAGTTT	1440
	GTGTCATGAG AATGTAAGTC TTTTCTTCTAC TTAAATTTT AGTAGGTTCA CTGAGTAACT	1500
55	AAAATTTAGC AAACCTGTGT TTGCATATTT TTTKGGAGTG CAGMMTAWTG TAATTARAGC	1560
	ATTCCAGTAA NAGTGTNTTT AAAGTTGNTC TATATN	1596

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

	GCGCAGAGCC CGYACGAGCA GGACGACGAC GACAAGGGCG ACTCCAAGGA AACGCGGCTG	60
	ACCTTGATGG AGGAAGTGCT CCTGCTGGGC CTCAAGGACC GCGARGGTTA CACATCATT	120
5	TGGAATGACT GTATATCATC TGGATTACGT GGCTGTATGT TAATTGAATT AGCATTGAGA	180
	GGAAGGTTAC AACTAGAGGC TTGTGGAATG AGACGTAAAA GTCTATTAAAC AAGAAAGGTA	240
10	ATCTGTAAGT CAGATGCTCC AACAGGGGAT GTTCTTCTTG ATGAAGCTCT GAAGCATGTT	300
	AAGGAACTC AGCCTCCAGA AACGGTCCAG AACTGGATTG AATTACTTAG TGGTGAGACA	360
15	TGGAATCCAT TAAAATTGCA TTATCAGTTA AGAAATGTAC GGAACGATT AGCTAAAAAC	420
	CTGGTGGAAG AGGGTGTATT GACAACAGAG AAACAGAACT TCCTACTTTT TGACATGACA	480
20	ACACATCCCC TCACCAATAA CAACATTAAG CAGCGCCTCA TCAAGAAAGT ACAGGAAGCC	540
	GTTCCTGACA AATGGGTGAA TGACCCTCAC CGCATGGACA GCGCCTGCT GGCCTCATT	600
25	TACCTGGCTC ATGCCTCGGA CGTCCTGGAG AATGCTTTTG CTCCTCTTCT GGACGAGCAG	660
	TATGATTTGG CTACCAAGAG AGTGCGGCAG CTTCTCGACT TAGACCCTGA AGTGAATGT	720
30	CTGAAGGCCA ACACCAATGA GGTTCCTGTGG GCGGTGGTGG CGGCGTTCAC CAAGTAACTC	780
	TGCTCGGGGT GAACCATCTCT CTTTCTCTC AAGTAAACCA GTAGTTTTTC TTCTGTGAC	840
35	TTCTGGTTTT CTGTAATTTG TACTTTCCCA CACTATAATT GGCTTCTGTT TTACAAAATG	900
	GTGGGTGGCT TTTCTTTTT TGTACGTGTA CAGGATTCTG CTGGTACGAG AGGCCTTCCT	960
40	CTTCTGTTT TAAAAAAG TTTTACTGCC ATATTGGCAT TCCATTCCCT GTTGCCATCC	1020
	TCACGTGTTAC CTGTTTGGG TTTCTGGTCT ACTTTGACTT TCAAAGTACC TCCAGCCTCC	1080
45	TCATACGCAC AGCTTTTGA TGACCTCAGC TTGAGTTTCT CCATATGTGC ATGTACATCT	1140
	AGCATCTGTC CTACAGTTCA GACAGAAGTC AAAAAAGGC CTTCAACTCA CCAAAGGTAA	1200
50	ATATCTGTAT CTATTAGGAC ATTTTTTACA TAGACTTCAG TTGAGATGTA TACTTAGCAA	1260
	AATTATTTTT AAATGAAAC AGCACAGTAA ATACTTAATA TAAATGTCC CTTGGATTTT	1320
55	GCTTCCCATG TAAATCTATT GTATTATTAC ACTTGTATA ATTTTAACTA TAAAGGTCCA	1380
	ATTGTTTCAC AGAGCCAGTT TGGGATGGGC TGCAATCCAT TTATGCTGTA TATAGTTTGA	1440
60	ATTATATATA AATTACCCCT TCTTCTGGCC ACCCCTGCTC CCATCTTAGT ATTTTGCAAG	1500

5 ATCTAATCAG TTGTACACCT GGTGCCCCCTC GCTTGCTTCA ATCATGGTTA TTTGATGGCA 1560
 AAATCGACCT CTTGTGCGCTG AAGGAGAGAG AAAAGATGTG TGTCTGATTG GTCCTGGGAT 1620
 TTTTGTAGCT GTGCCATTTA TGGTACTCTT TGCCTATGCA TCCCCTTTTT AGATTTTTTTT 1680
 TAAATTTTAT CTTACTGTTT TTATAATTTT TATTGGGAAG AGGCTGTGA CCAGTACCAA 1740
 10 TCTTGAGTTT CTTTTCTGT CCACAAGTAA ATTAATATCT GCTCTGAAAT GTCATTTATC 1800
 TACTCACACA TTCTTGGGA AAAAATCAA ATGTCAGTCC TAGCAGATGT TGCATGTAAA 1860
 TTGGTAGCAA GTAATGATTA CAACCCAGAG GATTAAGAAT TTTGTAACAG AAAGCTCTAT 1920
 15 GTTTTAATTT TTTATATACA ATTAGGATAA TTAGCATGT CAGACTATAA ACCTTTGCTT 1980
 TTAAAGTTT ATTTTACTA TTTCTTATC ACTTTATGT ATCATCACCA TTGGTTTCAT 2040
 20 AATGTAAATA CTATATGTTG AACAAATTAA ATGTCAAAT TTTTATTAC CATAGTCCAT 2100
 GTTAATAGTG GGGCTTCAG GTGTTAGAG ATTTTTTTTG TTGTTGTTAA CATTGATGC 2160
 AAAAGTACTA GATGGTGTAT AACTCTAGAG TTGAATTTTA AGGGATTCCC TAATATGTAT 2220
 25 ACTATCTTTT TATCTGAAGT AATAAATAA CAATGATCTT GAAAGTGCCY RAAAMAAAAA 2280
 AAAAAAAAAA AAA 2293

30

(2) INFORMATION FOR SEQ ID NO: 186:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

45

GGCACGAGGC GAGCCGGCGC ACCGTACGCT GGGACGTGTG GTTTCAGCTC GTGCGCCTCC 60
 CCGTGGGTTT GCGACGTTTA GCGACTATTG CGCCTGCGCC ACGCCGGCTG CGAGACTGGG 120
 GCCGTGGCTG CTGGTCCCGG GTGATGCTAG GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG 180
 GTGTAGGTGG GAGTCACGGA CGGTTCTGGG CCCGAGGTGT CCGCGAAGGT GGCGCACATG 240
 50 GGCGGCAGGG GAGAGCATGG CTCAGCGGAT GTTCTGGGTG GACCTGGAGA TGACAGGATT 300
 GGACATTGAG AAGGACCAGA TTATTGAGAT GGCCTGTCTG ATAAGTACT CTGATCTCAA 360
 55 CATTTTGGCT GAAGGTCCTA ACCTGATTAT AAAACAACCA GATGAGTTGC TGGACAGCAT 420
 GTCAGATTGG TGTAAGGAGC ATCACGGGAA GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG 480
 60 TACAATTACA TTGCAGCAGG CAGAGTATGA ATTCTGTCC TTTGTACGAC AGCAGACTCC 540

	TCCAGGGCTC TGTCCACTTG CAGGAAATTC AGTTCATGAA GATAAGAAGT TTCTTGACAA	600
	ATACATGCCC CAGTTCATGA AACATCTTCA TTATAGAATA ATTGATGTGA GCACTGTTAA	660
5	AGAACTGTGC AGACGCTGGT ATCCAGAAGA ATATGAATTT GCACCAAAGA AGGCTGCTTC	720
	TCATAGGGCA CTTGATGACA TTAGTGAAAG CATCAAAGAG CTTCAGTTTT ACCGAAATAA	780
10	CATCTTCAAG AAAAAAATAG ATGAAAAGAA GAGGAAAATT ATAGAAAATG GGGAAAATGA	840
	GAAGACCGTG AGTTGATGCC AGTTATCATG CTGCCACTAC ATCGTTATCT GGAGGCAACT	900
	TCTGGTGGTT TTTTTTCTC ACGCTGATGG CTTGGCAGAG CACCTTCGGT TAACTTGCAT	960
15	CTCCAGATTG ATTACTCAAG CAGACAGCAC ACGAAATACT ATTTTCTCTC TAATATGCTG	1020
	TTTCCATTAT GACACAGCAG CTCCTTTGTA AGTACCAGGT CATGTCCATC CCTTGGTACA	1080
20	TATATGCATT TGCTTTTAAA CCATTCTCTT TGTTTAAATA AATAAATAAG TAAATAAAGC	1140
	TAGTTCTATT GAAATGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1200
	AAAAAAAAAA AN	1212

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(2) INFORMATION FOR SEQ ID NO: 187:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

	GCTTCCGGAA GTTGCTTTTG TCCAAACATC CGGGCTTCTC CTTTTTGTT TCCGGCCGAT	60
40	CCCACCTCTC CTCGACCTTG GACGCTACC TTCCGGAGGC CCACATCTTG CCCACTCCGC	120
	GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA GGGACATGGC AACTACAGCG	180
45	GCGCCGGCGG GCGGCGCCCG AAATGGAGCT GGCCCGGAAT GGGGAGGGTT CGAAGAAAAC	240
	ATCCAGGGCG GAGGCTCAGC TGTGATGAC ATGGAGAACA TGGATGATAC CTCAGGCTCT	300
	AGCTTCGAGG ATATGGGTGA GCTGCATCAG CGCCTGCGCG AGGAAGAAGT AGACGCTGAT	360
50	GCAGCTGATG CAGCTGCTGC TGAAGAGGAG GATGGAGAGT TCCTGGGCAT GAAGGGCTTT	420
	AAGGGACAGC TGAGCCGGCA GGTGGCAGAT CAGATGTGGC AGGCTGGGAA AAGACAAGCC	480
55	TCCAGGGCCT TCAGCTTGTA CGCCAACATC GACATCCTCA GACCCTACTT TGATGTGGAG	540
	CCTGCTCAGG TGCGAACAGG GCTCCTGGAG TCCATGATCC CTATCAAGAT GGTCAACTTC	600
	CCCCAGAAAA TTGCAGGTGA ACTCTATGGA CCTCTCATGC TGGTCTTCAC TCTGGTTGCT	660
60	ATCCTACTCC ATGGGATGAA GACGTCTGAC ACTATTATCC GGGAGGGCAC CCTGATGGGC	720

	ACAGCCATTG GCACCTGCTT CGGCTACTGG CTGGGAGTCT CATCCTTCAT TTACTTCCTT	780
5	GCCTACCTGT GCAACGCCCA GATCACCATG CTGCAGATGT TGGCACTGCT GGGCTATGGC	840
	CTCTTTGGGC ATTGCATTGT CTTGTTTCATC ACCTATAATA TCCACCTCCA CGCCCTCTTC	900
	TACCTCTTCT GGCTGTTGGT GGGTGGACTG TCCACACTGC GCATGGTAGC AGTGTGGTG	960
10	TCTCGGACCG TGGGCCCCAC ACAGCGGCTG CTCCTCTGTG GCACCCTGGC TGCCCTACAC	1020
	ATGCTCTTCC TGCTCTATCT GCATTTTGCC TACCACAAAG TGGTAGAGGG GATCCTGGAC	1080
15	AACTGGAGG GCCCAACAT CCCGCCCATC CAGAGGGTCC CCAGAGACAT CCCTGCCATG	1140
	CTCCCTGCTG CTCGGCTTCC CACCACCGTC CTCAACGCCA CAGCCAAAGC TGTGCGGTG	1200
	ACCCTGCACT CACACTGACC CCACCTGAAA TTCTTGCCA GTCTCTTTC CCGCAGCTGC	1260
20	AGAGAGGAGG AAGACTATTA AAGGACAGTC CTGATGACAT GTTTCGTAGA TGGGGTTTGC	1320
	AGCTGCCACT GAGCTGTAGC TGCCTAAGTA CCTCCTTGAT GCNTGTGGC ACTTCTGAAA	1380
25	GGCACAAGGC CAAGAACTCC TGGCCAGGAC TGCAAGGCTC TGCAGCCAAT GCAGAAAATG	1440
	GGTCAGCTCC TTGAGAACC CCTCCCCACC TACCCCTTCC TTCTCTTTA TCTCTCCAC	1500
	ATTGTCTTGC TAAATATAGA CTTGGTAATT AAAATGTTGA TTGAAGTCTG GAAAAAATA	1560
30	AAAAAATAA AAAAAATAA AAAAAATAA AAAAAATAA TCGAG	1605

35 (2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

45	ATTGCGCATG AGGGGGTCAC GTGGTGGCTG GGCCGGGGAA ATGGCGGCTT CAGGAGAGAG	60
	CGGGACTTCA GCGGGCGGAG GCAGACCGA GGAAGCATTT ATGACCTTCT ACAGTGAGGT	120
50	GAAACAAATA GAGAAGAGAG ACTCGGTTCT AACTTCGAAA AATCAGATTG AAAGACTGAC	180
	CCGTCTGGT TCCTCTTACT TCAATTTGAA CCCATTTGAG GTTCTTCAGA TAGATCCTGA	240
	AGTTACAGAT GAAGAAATAA AAAAGAGGTT TCGGCAGTTA TCCATCTTGG TGCATCCTGA	300
55	CAAAAATCAA GATGATGCTG ACAGAGCACA AAAGGCTTTT GAAGCTGTGG ACAAAGCTTA	360
	CAAGTTGCTA CTGGATCAGG AGCAAAAGAA GAGGGCCCTG GATGTAATTC AGGCAGGAAA	420
60	AGAATACGTG GAACACACTG TGAAAGAGCG AAAAAACAA TTAAAGAAGG AAGGAAAACC	480

	TACAATTGTA GAGGAGGATG ATCCTGAGCT GTTCAAACAA GCTGTATATA AACAGACAAT	540
	GAAACTCTTT GCAGAGCTGG AAATTAAAAG GAAAGAGAGA GAAGCCAAAG AGATGCATGA	600
- 5	AAGGAAACGA CAAAGGGAAG AAGAGATTGA AGCTCAAGAA AAAGCCAAAC GGGAAAGAGA	660
	GTGGCAGAAA AACTTTGAGG AAAGTCGAGA TGGTCGTGTG GACAGCTGGC GAAACTTCCA	720
10	AGCCAATACG AAGGGGAAGA AAGAGAAGAA AAATCGGACC TTCCTGAGAC CACCGAAAGT	780
	AAAAATGGAG CAACGTGAGT GACCGCCCAA GGTACAGGC ACAGAACCTT TCCCTGCTA	840
	TCTCCCTTCC TGCTTCGAAG GACTCATTCT TTCCTCCAC TTCCACCCCA ACATAGAGTA	900
15	GTATTGCTT TTAGTCCAT TTTGTTTCA ATACGATTTA ATATCGATCA GAGTAATTCT	960
	TTTGACATT GAAATGAGGG GCTTGGTTTA AAAAAAGACC TTTCCCTCTC CCTGCCCTTA	1020
20	GAACAACCAG TATTAGAAGG TGCCACCATT GGTGCTGCCT TCTCTCCCA CAGCCTGTAA	1080
	CTCAGTGTTC TGTACTTCAC TGAATTGTGA TGGTTAGAAA CTTCTGGAT AGTTTGTGGA	1140
	AATCATCCAA TTAAACATAC TGCTTAAAC AGTGTGCTG TGAATCAGA GACAAGCCTG	1200
25	GAAGGGGCAC CTTAGGAAGC CCCTTCGCTT CAGTTGCTCG CTTCTGGGTG TGCTCCCTTC	1260
	GAAGGCCAG ATAAGACAGG GAACACTTGT GAGCACACAG AGCAGCATCT GATGCCCTGT	1320
30	GGTGTGTCG ATGTGCCCC TGTCTACTGA CCAATCAGTG TGGCATGAGG CCCACGCCAC	1380
	CCAAACCTTT CACTTTCCAA AGAGCTAGCC GTCCTCCACC CAGTACCATG TCCTAGCCTG	1440
	TCTGCATTTG TTAGTGGTAA TATCTTTAT GTATAATAAA TTTTATACC CAAAAAAAAA	1500
35	AAAAAAAAA ACTCGA	1516

40 (2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50	GCTCCCATGT TGCTGGCTGT CCGTACATCA CCCTGTCCCC TGCAGGAGGG GGCTACAGGC	60
	CATCTCCCTC CTGTAGGCCT CTGACTCCCC TCCACTTTTG GGCCCTCAGC TTATCTGGG	120
55	CAGGGGACCA TTGCAGCATC CTCCCCTCCT CNGGACTCAA GGTGCTGAGG TATAAGCCCT	180
	GGGCCCCAGA TCCCTGRTKA CACCTTCCTG GAGAAGACTC TCAAAAGTGA CTGTATATTT	240
	GAGTTACCA GCAATAACTC CCCACACTCG AAGCAGGTCC AAACCCMAGG ATCCCAGGGT	300
60	CCTTGGGCTC TGTGGCACTG TCTTCCCAAG ATCCTTCCTG TTGCACAATG GGAAACCTAA	360

5 GAGGAAAAAG ACAGGGGCCCT GCTTGCCCAG CCATGCGAGG GATTCCATGC CCACCTGCCC 420
 TCTGYCTGCC TCGCTGGAAT GTGGGCCCCCT GCTCCCCGTC AGGTTGTGCT GTCTCTGACC 480
 TATGTTTACA TCCCCGAGGG GTTCTGTCCT CCTCCCCACC CAGGTCAGGG TGTGGTCCAG 540
 CAGCTTGCTG TGGGGTGCTG ACATGTGTCA CCACTGCCCC CCTTGCCCCC GGGGGGTCA 600
 10 TGGTCTCCTC CTGGATGCTG CTCCTTGAAT YTTTTTYYTT GAWAAACCYT TTAMAATTAA 660
 AAAAAAAAAA AAAAAACTCG A 681

15

(2) INFORMATION FOR SEQ ID NO: 190:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

GCCTCAAGCC ACGCATATGA TAATTTTCTG GAACATTCAA ATTCAGTGTT TCTACAGCCA 60
 GTTAGTCTAC AAACCATGTC AGCAGCACCA TCAAACCAGA GTCTGCCACT TTTTGTATC 120
 30 GCTGGATGAT TGCTGGGCAA AGGTGGCCTT TTAGAGCTCT TAAAAGCCCA CAAAAGGCT 180
 ATTCGTAGAG CCACAGTCAA CACATTTGGT TATATTGCAA AGGCCATTGG CCTCATGATG 240
 35 TATTGGCTAC ACTTCTGAAC AACCTCAAAG TTCAAGAAAG GCAGAACAGA GTTGTACCA 300
 CTGTAGCAAT AGCTATTGTT GCAGAAACAT GTTCACCTT TACAGTACTC CCTGCCTTAA 360
 TGAATGAATA CAGAGTTCCT GAACTGAATG TTCAAATGG AGTGTTAAAA TCGCTTTCCT 420
 40 TCTGTGTTGA ATATATTGGT GAAATGGGAA AAGACTACAT TTATGCCGTA ACACCGTTAC 480
 TTGAAGATGC TTTAATGGAT AGAGACCTTG TACACAGACA GACGGCTAGT GCAGTGGTAC 540
 45 AGCACATGTC ACTTGGGGTT TATGGATTTG GTTGTGAAGA TTCGCTGAAT CACTTGTTGA 600
 ACTATGTATG GCCCAATGTR TTTGAGACAT CTCCTCATGT AATTCAGGCA GTTATGGGAG 660
 CCCTAGAGGG CCTGAGAGTT GCTATTGGAC CATGTAGAAT GTTGCAATAT TGTTTACAGG 720
 50 GTCTGTTTCA CCCAGCCCGG AAAGTCAGAG ATGTATATTG GAAAATTTAC AACTCCATCT 780
 ACATTGGTTC CCAGGACGCT CTCATAGCAC ATTACCCAAG AATCTACCAA CGATGATAAG 840
 55 RACACCTATA TTCGTTATGA ACTTGACTAT ATCTTATAAT TTTATTGTTW ATTTKGTGKT 900
 TAATGCACAS TACTTCACAC CTTAAACTTG CTTTGATTG GTGATGTAAA CTTTAAACA 960
 60 TTGCAGATCA GTGTAGGACT GGTCCATAGG GGAAGAGCTA GGAANTCCAT AGGC 1014

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

5	TCGCAGCAGG GTGTGTCCAG ATGGTCAGTC TCTGGTGGCT AGCCTGTCCT GACAGGGGAG	60
15	AGTTAAGCTC CCGYTCTCCA CCGTGCCGGC TGGCCAGGTG GGCTGAGGGT GACCGAGAGA	120
	CCAGAACCTG CTTGCTGGAG CTTAGTGCTC AGAGCTGGGG AGGGAGGTTC CGCCGCTCCT	180
20	CTGCTGTCTAG CGCCGGCAGC CCCTCCCGGC TTCACTTCCT CCCGCAGCCC CTGCTACTGA	240
	GAAGCTCCGG GATCCAGCA GCCGCCACGC CCTGGCCTCA GCCTGCGGGG CTCCAGTCAG	300
25	GCCAACACCG ACGCGCANTG GGAGGAAGAC AGGACCCTTG ACATCTCCAT CTGCACAGAG	360
	GTCCTGGCTG GACCGAGCAG CCTCCTCCTC CTAGGATGAC CTCACCCTCC AGCTCTCCAG	420
	TTTTCAGGTT GGAGACATTA GATGGAGGCC AAGAAGATGG CTCTGAGGCG GACAGAGGAA	480
30	AGCTGGATTT TGGGAGCGGG CTGCCTCCCA TGGAGTCACA GTTCCAGGGC GAGGACGGGA	540
	AATTCGCCCC TCAGATAAGA GTCAACCTCA ACTACCGAAA GGAACAGGT GCCAGTCAGC	600
35	CGGATCCAAA CCGATTGAC CGAGATCGGC TCTTCAATGC GGTCTCCCGG GGTGTCCCCG	660
	AGGATCTGGC TGGACTTCCA GAGTACCTGA GCAAGACCAG CAAGTACCTC AECGACTEGG	720
	AATACACAGA GGGCTCCACA GGTAAGACGT GCCTGATGAA GGCTGTGCTG AACCTTAAGG	780
40	ACGGGGTCAA TGCTTGCATT CTGCCACTGC TGCAGATCGA CCGGGACTCT GGCAATCCTC	840
	AGCCCCCTGGT AAATGCCCCAG TGCACAGATG ACTATTACCG AGGCCACAGC GCTCTGCACA	900
45	TCGCCATTGA GAAGAGGAGW TTGCAGTGTG TGAAGCTCCT GGTGGAGAAT GGGGCCAATG	960
	TGCATGCCCG GGTCTGCGGC GCTTCTTCCA GAAGGGCCAA GGGACTTGCT TTTATTTCGG	1020
	TGAGCTACCC CTCTYTTTGG CCGCTTGAC CAAGCAGTGG GATGTGGTAA GCTACCTCCT	1080
50	GGAGAACCCA CACCAGCCCC CCAGCCTGCA GGCACTGACT CCCAGGGCAA CACAGTCCTG	1140
	CATGCCCTAG TGATGATCTC GGACAACTCA GCTGAGAACA TTGCACTGGT GACCAGCATG	1200
55	TATGATGGGC TCCTCCAAGC TGGGGCCCGC CTCTGCCCTA CCGTGCAGCT TGAGGACATC	1260
	CGCAACCTGC AGGATCTCAC GCCTCTGAAG CTGGCCGCCA AGGAGGGCAA GATCGAGATT	1320
	TTCAGGCACA TCCTGCAGCG GGAGTTTTCA GGAAGTGGCC ACCTTTCCCG AAAGTTCAAC	1380
60	GAGTGGTGCT ATGGGCCTGT CCGGGTGTGC CTGTATGACC TGGCTTCTGT GGACAGCTGT	1440

- 5 GAGGAGAACT CAGTGCTGGA GATCATTGCC TTTTCATGCA AGAGCCCGCA CCGACACCGA 1500
ATGGTCGTTT TGGAGCCCCT GAACAACTG CTGCAGGCGA AATGGGATCT GCTCATCCCC 1560
AAGTTCTTCT TAAACTTCCT GTGTAATCTG ATCTACATGT TCATCTTCAC CGCTGTGGCC 1620
TACCATCAGC CTACCCTGAA GAAGCAGGCC GCCCCTCACC TGAAAGCGGA GGTGGGAAAC 1680
10 TCCATGCTGC TGACGGGCCA CATCCTTATC CTGCTAGGGG GGATCTACCT CCTCGTGGGC 1740
CAGCTGTGGT ACTTCCTGGC GCGCCACGTG TTCATCTGGA TCTCGTTCAT AGACAGCTAC 1800
TTTGAAATCC TCTTCCTGTT CCARGCCCTG CTCACAGTGG TGTCCARGT GCTGTGTTTC 1860
15 CTGGSCATCG AGTGGTACCT GCCCCTGCTT GTGTCTGCGC TGGTGCTGGG CTGGCTGAAC 1920
CTGCTTTACT ATACACGTGG CTTCCAGCAC ACAGGCATCT ACAGTGTCAT GATCCAGAAG 1980
20 CCCTGGTGAG CCTGAGCCAG GANNTTGGCG CCCCGAAGCT CCTACAGGCC CCAATGCCAC 2040
AGAGTCAGTG CAGCCCATGG AGGGACAGGA KGACGAKGGC AACGGGGCCC AGTACAGGGG 2100
TATCCTGGAA GCCTCCTTGG AGCTCTTCAA ATTCAACATC GGCATGGGCG AGCTGGCCTT 2160
25 CCAGGARCAG CTGCACTTCC GCGGCATGGT GCTGCTGCTG CTGCTGGSCT ACGTGCTGCT 2220
CACCTACATC CTGCTGCTCA ACATGCTCAT CGCCCTCATG AGCGAGACCG TCAACAGTGT 2280
30 CGCCACTGAC AGCTGGAGCA TCTGGAAGCT GCAGAAAGCC ATCTCTGTCC TGGAGATGGA 2340
GAATGGCTAT TGGTGGTGCA GGAAGAAGCA GCGGGCAGGT GTGATGCTGA CCGTTGGCAC 2400
TAAGCCAGAT GGCAGCCCSG ATGAGCGCTG GTGCTTCAGG GTGGAGGAGG TGAAC TGGGC 2460
35 TTCATGGGAG CAGACGCTGC CTACGCTGTG TGAGGACCCG TCAGGGGCAG GTGTCCCTCG 2520
AACTCTCGAG AACCTGTGCC TGGCTTCCCC TCCCAAGGAG GATGAGGATG GTGCCTCTGA 2580
40 GGAAAACTAT GTGCCGTGCC AGCTCCTCCA GTCCAACTGA TGGCCAGAT GCAGCAGGAG 2640
GCCAGAGGAC AGAGCAGAGG ATCTTTCCAA CCACATCTGC TGGCTCTGGG GTCCCACTGA 2700
45 ATTCTGGTGG CAAATATATA TTTTCACTAA CTCAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
AAAAAAAAA AAAAAAGGC 2779

50

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1923 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

	ACCCGCTCCG CTCGCTCCG CTCGGCCCCG CGCCGCCCGT CAACATGATC CGCTGCGGCC	60
	TGGCCTGCGA GCGTGCCGC TGGATCCTGC CCCTGCTCCT ACTCAGCGCC ATCGCCTTCG	120
5	ACATCATCGC GCTGGCCGGC CGCGGCTGGT TGCAGTCTAG CGACCACGGC CAGACGTCCT	180
	CGCTGTGGTG GAAATGCTCC CAAGAGGGCG GCGGCAGCGG GTCCTACGAG GAGGGCTGTC	240
10	AGAGCCTCAT GGAGTACGCG TGGGGTAGAG CAGCGGCTGC CATGCTCTTC TGTGGCTTCA	300
	TCATCCTGGT GATCTGTTTC ATCCTCTCCT TCTTCGCCCT CTGTGGACCC CAGATGCTTG	360
	TCTTCCTGAG AGTGATTGGA GGTCTCCTTG CCTTGGCTGC TGTGTTCCAG ATCATCTCCC	420
15	TGGTAATTTA CCCCCTGAAG TACACCCAGA CCTTCACCCT TCATGCCAAC CSTGCTGTCA	480
	CTTACATCTA TAACTGGGCC TACGGCTTTG GGTGGGCAGC CACGATTATC CTGATYGGCT	540
20	GTGCCCTTCTT CTTCGTCTGC CTCCCCAACT ACGAAGATGA CCTTCTGGGC AATGCCAAGC	600
	CCAGGTACTT CTACACATCT GCCTAACTTG GGAATGAATG TGGGAGAAAA TCGCTGCTGC	660
	TGAGATGGAC TCCAGAAGAA GAAACTGTTT CTCCAGGCGA CTTTGAACCC ATTTTTTTGGC	720
25	AGTGTTTATA TTATTAAACT AGTCAAAAAT GCTAAAATAA TTTGGGAGAA AATATTTTTT	780
	AAGTAGTGTT ATAGTTTCAT GTTTATCTTT TATTATGTTT TGTGAAGTTG TGTCTTTTCA	840
30	CTAATTACCT ATACTATGCC AATATTTTCT TATATCTATC CATAACATTT ATACTACATT	900
	TGTAAGAGAA TATGCACGTG AACTTAACA CTTTATAAGG TAAAAATGAG GTTTCCAAGA	960
	TTTAATAATC TGATCAAGTT CTGTATTATT CCAAATAGAA TGGACTCGGT CTGTTAAGGG	1020
35	CTAAGGAGAA GAGGAAGATA AGGTTAAAAG TTGTTAATGA CCAACATTC TAAAAGAAAT	1080
	GCAAAAAAAA AGTTTATTTT CAAGCCTTCG AACTATTTAA GGAAAGCAA ATCATTTCCT	1140
40	AAATGCATAT CATTTGTGAG AATTCTCAT TAATATCTG AATCATTCAT TTCAGCTAAG	1200
	GCTTCATGTT GACTCGATAT GTCATCTAGG AAAGTACTAT TTCATGGTCC AAACCTGTTG	1260
	CCATAGTTGG TAAGGCTTTC CTTTAAGTGT GAAATATTTA GATGAAATTT TCTCTTTTAA	1320
45	AGTTCTTTAT AGGGTTAGGG TGTGGGAAAA TGCTATATTA ATAAATCTGT AGTGTTTTGT	1380
	GTATATATGT TCAGAACCAG AGTAGACTGG ATTGAAAGAT GGACTGGGTC TAATTTATCA	1440
50	TGACTGATAG ATCTGGTTAA GTTGIGTAGT AAAGCATTAG GAGGGTCATT CTGTGCACAA	1500
	AAGTGCCACT AAAACAGCCT CAGGAGAATA AATGACTTGC TTTTCTAAAT CTCAGGTTTA	1560
	TCTGGGCTCT ATCATATAGA CAGGCTTCTG ATAGTTTGCA ACTGTAAGCA GAAACCTACA	1620
55	TATAGTTAAA ATCCTGGTCT TTCTTGGTAA ACAGATTTTA AATGTCTGAT ATAAAACATG	1680
	CCACAGGAGA ATTCGGGGAT TTGAGTTTCT CTGAATAGCA TATATATGAT GCATCGGATA	1740
60	GGTCATTATG ATTTTTTACC ATTTGACTT ACATAATGAA AACCAATTCA TTTTAAATAT	1800

CAGATTATTA TTTTGTAAGT TGTGGAAAAA GCTAATTGTA GTTTTCATTA TGAAGTTTTC 1860
 CCAATAAACC AGGTATTCTA AAAAAAAAAA AAAAAAACTN GAGGGGGGGC CCGGTACCCA 1920
 -5 ATT 1923

10 (2) INFORMATION FOR SEQ ID NO: 193:.

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2346 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

20 AGGCTCAGGG GGACACTCTC AAAATTACAC AGCTTTTAAC AGGTGGCAGA ATTGGGGTTC 60
 AGACCCAGAT CTGGGTTCAA GTCATCATG GTGTGATTGC GGCATTCTT CCGCATCTG 120
 GGCCTTGCCA TCTCTCTCTC CGAGTGGACA TGGAGAGGAC GGGGGCCAG CAGCTGGATG 180
 25 GCTGCAGGGG ATCAAGTCTT CTCTGGGGCT GGGCACGTAN AAGAGCATGT GGCTGGTGGG 240
 CGGCATGCCT GGCTCCTCAC CTGGCAGTCT GCCTGCCCTG CTAACCGGCT GTCTCTTGTT 300
 30 CCCCTAGTGC CCTCGGCTAG CATGACCCGC CTGATGCGWT SCCGCACAGC CTCTGGTTCC 360
 AGCGTCATTC TCTGGATGGC ACCCGCAGCC GCTCCCACAC CAGCGAGGGC ACCCGAAGCC 420
 GCTCCCACAC CAGCGAGGGC ACCCGCAGCC GCTCGCACAC CAGCGAGGGG GCCCACCTGG 480
 35 ACATCACCCC CAACTCGGGT GCTGCTGGGA ACAGNGCCGG GCCCAAGTCC ATGGAGGTCT 540
 CCTGTAGGC GGCCTGCCCA GCTGCCGCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC 600
 40 CTCCCCGGCC CCTTTTCGCC CCCTGCCTGC CATACTGCGC CTAACCGGT ATTAATCCAA 660
 AGCTTATTTT GTAAGAGTGA GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC 720
 TCTCCAAAGG CGGGGTGGCG GTGGACAAA GGAAGGAAGC AAGCATCTCC GCATCGCATC 780
 45 CTCTTCCATT AACCAGTGGC CGGTGCCAC TCTCCTCCCC TCCCTCAGAG ACACCAAAC 840
 GCCAAAACA AGACGCGTAC AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC 900
 50 ATCCTGGTTC AAACGGGTGC CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCTCTTTT 960
 AACTGAGGAG AAGCTGATCC AGTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG 1020
 GGTAATAGTG ACATGCAGGC ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAAAGGTG 1080
 55 GGATTCATGT CGAGGCTAGA GGCATTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA 1140
 ACCGATTTT AAAGTTGGTG CATCTAGAAA GCTTTGAATG CAGAAGCAAA CAAGCTTGAT 1200
 60 TTTTCTAGCA TCCTCTTAAT GTGCAGCAAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG 1260

	ACAAAAATAT TTCAGCAAAC GTTGGGCATC ATGGTTTTTG AAGGCTTTAG TTCTGCTTTC	1320
5	TGCCTCTCCT CCACAGCCCC AACCTCCCAC CCCTGATACA TGAGCCAGTG ATTATTCTTG	1380
	TTCAGGGAGA AGATCATTTA GATTGTGTTT GCATTCTCTTA GAATGGAGGG CAACATTCCA	1440
	CAGCTGCCCT GGCTGTGATG AGTGTCTTG CAGGGGCCGG AGTAGGAGCA CTGGGGTGGG	1500
10	GGCGGAATTG GGGTTACTCG ATGTAAGGGA TTCCTTGTTG TTGTGTTGAG ATCCAGTGCA	1560
	GTTGTGATTT CTGTGGATCC CAGCTTGGTT CCAGGAATTT TGTGTGATTG GCTTAAATCC	1620
15	AGTTTTCAAT CTTGACAGC TGGGCTGGAA CGTGAACCTA GTAGCTGAAC CTGTCTGACC	1680
	CGGTCACGTT CTTGGATCCT CAGAACTCTT TGCTCTGTGC GGGGTGGGG TGGGAACTCA	1740
	CGTGGGGAGC GGTGGCTGAG AAAATGTAAG GATTCTGGAA TACATATTCC ATGGGACTTT	1800
20	CCTTCCCTCT CTGCTTCCT CTTTCTCTGC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC	1860
	CACTGACGTT TCTGGGCGGC CAGTGCGGCT GCCAGGTTCC TGTACTACTG CCTTGTACTT	1920
25	TTCATTTTGG CTCACCGTGG ATTTTCTCAT AGGAAGTTTG GTCAGAGTGA ATTGAATATT	1980
	GTAAGTCAGC CACTGGGACC CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG	2040
	TCCAGCCTTC CAGGTGGCGT GAGAGGCAAT GACTCGTTAC CTGCCGCCCA TCACCTTGGA	2100
30	GGCCTTCCCT GGCCTTGAGT AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGGA	2160
	TGGGAAACTA TTGTGCACAA GTCTTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA	2220
35	TTTCCAGACC AATAAATTTG TAACTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
	AAAAAAAAAA AAAAAAACT CGAGGGGGGC CCGTACCCAA TTCGCCGTAT ATGATCGTAA	2340
	ACAATC	2346

40

(2) INFORMATION FOR SEQ ID NO: 194:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

	TATCTGAACC ACCCTTTATT CTACATATGA TAGGCAGCAC TGAAATATCC TAACCCCTTA	60
55	AGCTCMAGGT GCCCTGTGGN ACGAGCAACT GGACTATAGC AGGGCTGGGC TCTGTCTTCC	120
	TGGTCATAGG CTCACTCTTT CCCCCAAATC TTCCTCTGGA GCTTTGCAGC CAAGGTGCTA	180
60	AAAGGAATAG GTAGGAGACC TCTTCTATCT AATCCTTAAA AGCATAATGT TGAACATTCA	240

	TTCAACAGCT GATGCCCTAT AACCCCTGCC TGGATTTCCTT CCTATTAGGC TATAAGAAGT	300
	AGCAAGATCT TTACATAATT CAGAGTGGTT TCATTGCCTT CCTACCCTCT CTAATGGCCC	360
- 5	CTCCATTAT TTAGCTAAAG CATCACACAG TGGCACTAGC ATTATACCAA GAGTATGAGA	420
	AATACAGTGC TTTATGGCTC TAACATTACT GCCTTCAGTA TCAAGGCTGC CTGGAGAAAAG	480
10	GATGGCAGCC TCAGGGCTTC CTTATGTCCT CCACCACAAG AGCTCCTTGA TGAAGGTCAT	540
	CTTTTCCCC TATCCTGTTT TCCCCCTCCC CGCTCCTAAT GGTACGTGGG TACCCAGGCT	600
	GGTTCCTGGG CTAGGTAGTG GGGACCAAGT TCATTACCTC CCTATCAGTT CTAGCATAGT	660
15	AAACTACGGT ACCAGTGTTA GTGGGAAGAG CTGGGTTTTC CTAGTATACC CACTGCATCC	720
	TACTCCTACC TGGTCAACCC GCTGCTTCCA GGTATGGGAC CTGCTAAGTG TGGAAATTACC	780
20	TGATAAGGGA GAGGGAAATA CAAGGAGGGC CTCTGGTGT TCTGGCCTCA GCCAGCTGCC	840
	CACAAGCCAT AAACCAATAA AACAAGAATA CTGAGTCAGT TTTTATCTG GGTTCCTCTC	900
	ATTCCCACTG CACTTGGTGC TGCTTTGGCT GACTGGGAAC ACCCCATAAC TACAGAGTCT	960
25	GACAGGAAGA CTGGAGACTG*TCCACTTCTA GCTCGGAAGT TACTGTGTAA ATAACTTTC	1020
	AGAACTGCTA CCATGAAGTG AAAATGCCAC ATTTTGCTTT ATAATTTCTA CCCATGTTGG	1080
30	GAAAACTGG CTTTTCCTCA GCCCTTTCCA GGGCATAAAA CTCAACCCCT TCGATAGCAA	1140
	GTCCCATCAG CCTATTATTT TTTTAAAGAA AACTTGCAGT TGTTTTCTT TTTACAGTTA	1200
	CTTCCTTCCT GCCCCAAAT TATAAACTCT AAGTGTAATA AAAAGTCTTA ACAACAGCTT	1260
35	CTTGCTTGTA AAAATATGTA TTATACATCT GTATTTTAA ATTCTGCTCC TGAAAAATGA	1320
	CTGTECCATT CTCCACTCAC TGCATTGGG GCCTTTCECA TTGGTCTGCA TGTCTTTTAT	1380
40	CATTGCAGGC CAGTGGACAG AGGGAGAAGG GAGAACAGGG GTCGCCAACA CTTGTGTTGC	1440
	TTTCTGACTG ATCCTGAACA AGAAAGAGTA AACTGAGGC GCTCGCTCCC ATGCACAAC	1500
	CTCCAAAACA CTTATCCTCC TGCAAGAGTG GGCTTTCCAG GGTCTTTACT GGAAGCAGT	1560
45	TAAGCCCCCT CCTCACCCCT TCCTTTTTTC TTTCTTTACT CCTTTGGCTT CAAAGGATTT	1620
	TGGAAAAGAA ACAATATGCT TTCACTCAT TTTCAATTTT TAAATTTGCA GGGGATACTG	1680
50	AAAAATACGG CAGGTGGCCT AAGGCTGCTG TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT	1740
	TACAAGATAA AAAACGAATC CCCTAAACAA AAAGAACAAT AGAACTGGTC TTCCATTTTG	1800
	CCACCTTTCC TGTTCATGAC AGCTACTAAC CTGGAGACAG TAACATTTCA TTAACCAAAG	1860
55	AAAGTGGGTC ACCTGACCTC TGAAGAGCTG AGTACTCAGG CCACTCCAAT CACCCTACAA	1920
	GATGCCAAGG AGGTCCCAGG AAGTCCAGCT CCTTAACTG ACGCTAGNCA ATAAACCTGG	1980
60	GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT CCATCTGTGA GGTGACAGGC AAGGATGAAA	2040

	GACAAAGAAG GAAAAGAGTA TCAAAGGCAG AAAGGAGATC ATTTAGTTGG GTCTGAAAGG	2100
	AAAAGTCTTT GCTATCCGAC ATGTACTGCT AGTACCTGTA AGCATTTTAG GTCCCAGAAT	2160
5	GGAAAAAATA ATCAGCTATT GGTAATATAA TAATGTCCTT TCCCTGGAGT CAGTTTMTTT	2220
	AAAAAGTTAA CTCTTAGTIT TTA CTGTGTTT AATTCTAAAA GAGAAGGGAG CTGAGGCCAT	2280
10	TCCCTGTAGG AGTAAAGATA AAAGGATAGG AAAAGATTCA AAGCTCTAAT AGAGTCACAG	2340
	CTTTCCAGG TATAAAACCT AAAATTAAGA AGTACAATAA GCAGAGGTGG AAAATGATCT	2400
	AGTTCCTGAT AGCTACCCAC AGAGCAAGTG ATTTATAAAT TTGAAATCCA AACTACTTTC	2460
15	TTAATATCAC TTGGTCTCC ATTTTCCCA GGACAGGAAA TATGTCCCCC CCTAACTTTC	2520
	TTGCTTCAA AATTAAATC CAGCATCCCA AGATCATTCT ACAAGTAATT TTGCACAGAC	2580
20	ATCTCTCAC CCCAGTGCCT GTCTGGAGCT CACCCAAGGT CACCAAACAA CTGGTTGTG	2640
	AACCNAACTG CCTAACCTT CTGGGGGAGG GGGATTAGCT AGACTAGGAG ACCAGAAGTG	2700
	AATGGGAAAG GGTGAGGACT TCACAATGTT GGCCTGTCAG AGCTTGATTA GAAGCCAAGA	2760
25	CAGTGGCAGC AAAGGAAGAC TTGGCCCAGG AAAAACCTGT GGGTTGTGCT AATTTCGTG	2820
	CAGAAATAG GGTGGACAGA AGCTTGTGGG GTGCATGGAG GAATTGGGAC CTGGTTATGT	2880
30	TGTTATTCTC GGACTGTGAA TTTTGGTGAT GTAAACAGA ATATTCTGTA AACCTAATGT	2940
	CTGTATAAAT AATGAGCGTT AACACAGTAA AATATTCAAT AAGAAGTCAA AAAAAAAAAA	3000
35	AAAAAACTCG AGGGGGGGCC CGGTACCCAA TTTNCCAAAT AGAGATNGTA TTAC	3054

(2) INFORMATION FOR SEQ ID NO: 195:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GGCAGAGCTC GTGGCCGNAA CTTTTCTGCT TCCTGGCTGC CACCTACTGG CTGGCCGCGG	60
50	CCCTGGCCTG GGCCTGCACC AGCCTGCGNG CGGGCTCCA CAGCAGCCCC CTTCCAAGCA	120
	CGGTCCCCAC ACCGCGCACC TTCTGCGGGA ACGTGCTCGC CGTGCCGGGG ACCATATGGA	180
55	CGGAAGGCTT TGTGCTCACC TACAAGCTGG GTGAGCAGG TGCCAGCAGC CTGTTGATCC	240
	TCTTGGCTCC TGCTGGAGCA CGAGCGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG	300
	TGTGGGTGCT GTGGTCTGCT CCATCGCTGG CTCCTCCCTG GGTGGGACCT TGCTGGCCAA	360
60	GCACTGGAAG CTGCTGCCTC TGTGAGGTCG GTGCTGCGCT TCCGCCTCGG GGGCCTAGCC	420

5 TGTCAGACTG CCTTGGTCTT CCACCTTGA CACCCTGGGG GCCAGCATGG ACGCTGGCAC 480
 AATCTTGAGA GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GARGCCTGGT 540
 CACCACAGTC ACCTTCACTG GGAATGATGC GCTGCAGCCA GCTGGCCCCC AGGGCCTTGC 600
 AGGCCACACA CTACAGCCTT CTGGCCACGC TGGAGCTGCT GGGGAAGCTG CTGCTGGGCA 660
 10 CTYTGGSCGG AGGGCCTGGC TGATGGGTG GGGCCACATC CCTGCTTCTT GCTCCTGCTC 720
 ATCCTCTCTG CCTTTCCCGT TCTGTACCTG GACCTAGCAC CCAGCACCTT TCTCTGAGCT 780
 GAGTGGCTGG AGTGGTCAAT AAAGCCACAT GTGCCTGTGG CCCAAAAAA AAAAAAAAAA 840
 15 AAAAAAAAAA AAAAAAAGT GAGGGGGGGC CCGGTACCCA AATCGCCGGA TATGATCGTA 900
 AACAATC 907

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(2) INFORMATION FOR SEQ ID NO: 196:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

GGCACGAGGA GGGACAGGGA GTGGGCAAGG GGAAGAAGCA GCTTATTTGA CTAACCAGCC 60
 35 CCTCTGTGGT CCACCAGCGT CTTGGCTTGG TGGGAGGGCT CTCAATCAGC AGGGCCCCAG 120
 KAGGGCAAGA AGAAGTGGGG CAAAGCCTGG GGCTCGGCCG CGGTGCGGGC AGCTTTGCMA 180
 TCTGGAGCCA CGCCTCCTCC AGGCCATGCT CCTTGAACCT GGAAATGTCA ACCGGAGCCC 240
 40 TTAACACCAG CCCTCCAGCA TCTAATAGAC TTGAATCTAC TCTAAACGAA TATTTAATCC 300
 AACCTCAACT ACATTGTAGC TCAGTCCAAC GACTAACCTT GAAATGGGGG TGTTCAGGCC 360
 45 TTCAGCGAGA TGGCCAAGCG GTCCCTGGG GGCTGTGGCA GCGGGCTTAT CCTTCTCTGT 420
 TGCCAACCTT GCCGTCCGAC CTCCTCCGCC CCCATGCGGT GACCCCGTCC GTGTCTGTGT 480
 CTGTCCATAC GTGTGAGTCC AGCTAAAAAG ACAAACAGA ACCCGTGGGC CCAGCTCGGA 540
 50 AGGTGCGTGG AGAAGGCTCC GACGTCTCCG AAGTGCAGCC CTTGGGATGG CATTCGTTG 600
 TGTGCCTTAT TCCTGGAGAA TCTGTATACG GCTCGCCTAT AAGAAATATA GCCTCTTCAT 660
 55 GCTGTATTAA AAGGACTTTT AAAAGCAAAA AAAAAAAAAA AAAAAGTCGA GGGGGGGCCC 720
 GGTACCCAAT TCGCCCAATA GTGAGTCGTA TTACAATTCA CTGGGCCGTC STTTTAACAA 780
 60 CGTCGTGAAC TGGGAAAACC CTGGCGTTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC 840

CTTTCGCCAG CTGGCGTTAA TAGCGAAAAA NGCCCGCACC CGAATCGCCC TTCCCAACAG 900
 TTGCGCAGC CCTGAATGGC GAAATGGCAA ATTGTAAGCG TTTAATATTT TKKTTAAAAT 960
 - 5 TCCNCGTTWA AWTTTTTGT TAAATCARCT CAATTTTTTTT AACCCAATAA GSCCGAAATC 1020
 CGGCAAATCC CCYTTATTAA TTCCAAAAAA ATAAACCSAA AAWGGGTTTG AATTTTTTKT 1080
 10 TTCCCAYTT TTGAAACAA AWTYCCCCCT TTTTAAAAAA GTTGAACCC CCAMCCYTCC 1140
 AAAGGGGAAA AAACSYYYYT YTG GGGGGNA ANGGGGCCCC CNTACTTTNA ACAYCCCCC 1200
 CCAAWCAATT TTTTGGGG GTCCCNAAAG GTCCCCCTAA AANCTTTTTT CGGAACCCNA 1260
 15 AGGGGANCCC CCCATTTAAA ATTTTNGGTN 1290

20 (2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

30 GGTGTGCCTG GATGGTCGTG TAGGTGAGTT TTACCAAGGA TTATGGTAAC AAATGAGTGA 60
 GACCTCTATG GAGAAAATAT TGAAGNNCAT TAAAGAAGAC CTCATANTAG GAGAGAATGT 120
 SCTTTGGAGG ATTTGTATTG AGCTTTTACA GTATTCATTT TTCAACTCAA GGCAATGGCT 180
 35 TTCTACACCA ACTCTAATCC ATAAACGGGT CTTATGACAT CTATGAAGTA GTAGCAAGAC 240
 ATGCTTAGTG TGTATTTCTC TCTTTGAGAC ACTGTAATTT CTACCAGAAA TTTCCAGAGC 300
 40 ATTATGTAGG TAGAAAAAAA TGCAAGCAAG CTGTTAAAGA TCTTGGATCC CATTATATAG 360
 TATGTATAGC TGAAATCTGT AATTCAATCA CTTTTCTCT TTTATCCTCT AACCAAAAAA 420
 TTGTTTAATT TTGCATCCCA AATGTTTTTA ATCTTTGTAT ATTTTTTAAA AAYCCTTTTC 480
 45 TCCTCATCAT TGCCTTTTTT GTGGTTGTAA ATAGACTTAC TTGCACTTTG AAGATGAGTT 540
 ACTCCTTGTC ATCTTACAAA TATGTGATAT GGTAATTTTC ATAACAGATG TCAGTTTGA 600
 50 ACCAAGAATT GGTGATTGTG TTATAAGAAA AAAACTGGCT TCATTTCTGT GAAATGCTC 660
 TTTGAAAATT TCTTTTACA CGTGTAAGCC AACTGAGATA CCGTGATGGT GTTGATTCT 720
 TTCAATGATG CTTACCATCT ATTTTAGCCA CTGAGCCTTT TATTATTGT CTATTTGTAA 780
 55 AGTTTATTG TCTTAACTCA TTTAATAAAT ATACTGTTA TCTGTTCTG AATGGGGACT 840
 GAACTTTTTG GATATTGATA TTGATTGAA AATATTTTGG AATTTTTTCT ACTTGAAATT 900
 60 TTAGAAATCT AATKGAAAAT TCTATAATGT ACTGAAAGTA WGGTTGTGTA CAGTGAKCAC 960

TCTCTAATAA TATGATGNCT TGCCCTAAAN GAGGNGGGAC ATGTCCCACT TTCCACCAG 1020

5

(2) INFORMATION FOR SEQ ID NO: 198:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AATTCGCGAA GCTGAGGGTT GTGTGCCNTC GGGCGAGCCA AGTCTTTTGA CCGGACCCTT 60
CCCGGCGCAG AAGANCTGAA GTTGATTTGA GAGCCTGTGT TTGGGGTTTRA GCCGAGCTGC 120
20 TCGGGGCTTY GTCGCCGGCC AGGACACAAG YTACTTGCAA CGGGGCGGCG CCTGGCTTAT 180
GATGTTCTCT AACCCAGGGG CGGCCTCTGC CCTCTACTCG TGCCAGGCC ACTTGCCAGG 240
25 CAGGAGCCCT CCCCAAGCCT TCAGGGCTGC TCGGAGTCAC CTGTTGGAAT GGAATAAAG 300
GACCCTTG TGGAACAGG TGCTCAAAC ACCCTGCTGC TGGCTGCCAG GCAGGCCCTC 360
TGAAGGGAA GGGGCAGGAC TCATCAGGAC CTCCCTGGAC CCTGCAGGGC AGGCAGTTGG 420
30 CCCGAGCCCA AGCATTTGGC TCTGCTTGCC CCAAGGGGAC AGGAAGCCTC TTGGGCCTCT 480
TCCCTTCCTG GACAAGGCC CCTGCCTTTG CCTCACATAA ACTG 524

35

(2) INFORMATION FOR SEQ ID NO: 199:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGATACAAG GAAGGGTGAT CATCATCTGT CACCATGCAA TTCCTGCTCA CAGCCTTTCT 60
50 GTTGGTGCCA CTCTGGCTC TTTGTGATGT CCCCATATCC CTAGGCTTCT CCCCTCCTA 120
GAAGGCTTC TTGATAGATT AGAAAATAAG AATGAGTGAC ATTTCTATG TGCATATAAG 180
AAGGAGCCAC AAGACATGTC TTTTAAATAA AAGGACAGTG TCCATCCTTT TAGCTGCCGA 240
55 ATAGAACCTT GGTCTCATCC TCCTGGAGCT AGGSCTTAAA ACAGCTTCTG TGTTCCTSAT 300
TKGTCTCART GTTTTGCCAA GGTTCCTATC GG 332

60

(2) INFORMATION FOR SEQ ID NO: 200:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

	CCAGGGAAGC CCCARGCCTG TCCTGAATTG ACATCAGTGC TTCCCTGAAC TGCCTCCCCC	60
15	ACCCCTGGGC ATTATCCAG GAAACTTATG TTTTCTAGAA GCTAAGCAGC TGCTGGGACT	120
	CAGGGACTGG TGCAGGTAGG CTGAGTGGCA GCTCAGTCCT AGAAGGTCTC TGAAGATCTG	180
	GACTGAGGAC CYTGCTACTC CCCAAGCCAG AGCCCATCAG CCAGGCCTGC TGTGAGCCAC	240
20	CTGCCTGTGG AGTGCTGAGC TCAACCAAAG GCTGGCAAGC TCTGGGCCCTC ATTTAAGGGA	300
	TTCTGATGAG CCGATGGGCC CTGGAGGCAG CCCATTAAAG CATCTGGCTC GTTTTGGAA	360
25	AAAAAAAAA AAAAAG	376

30

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40	CCAGTATAT TTCTATAACA TTTATTTTAG TGAACITATA ATGTTTCTTT GTATTAAATT	60
	ATTAGATTAT ATCTTTAGAT AATATTGTTA CTNAATTAGT AGGTAATATA TATTTTATTC	120
	AAAAATAAAT TGTGCATCTA ATGTCTACCA ATTAATGTAC TTGTAGATGT ATCTTATCTT	180
45	AACTTGAGTC TTTGCTGCCC CTAATGAGGT GTGAAGGACT CTTCTCCCCT GGGGAAGTTT	240
	TTCTTTTTCA GGAGGGAGGA GGGCTTTCCC AGGTAATGTG TCTAGAGTGT TGGGCAGAA	300
	AATCTGGGAC CACACCACAC CAGTTCTCTC CTTAATCCAC GTCAATTGCC TTCTATCCCA	360
	GCTATGTTTC CAGTGTCTCT TGGGTGTTTC CAAGAGCAAC AAGAAAYGAA TAAATCTCTG	420
	KTGAGTTGTT TATTTGTCTT TCACTTTGTT TTACACTGTA WTTTCTGAGT TTATGGGTGT	480
55	CTGTGAATTA AAAAGGAAAA GTRGAAATAA GTAAACTCA GGTGAAGGA AATATACATA	540
	AATAAGATAA AGCTGACCTG TAGATATARR CAGGTTATAA RAGCTTAGAG TTGTCTAAGT	600
60	TGRGTGCAA KTTTCCTCTG ATCTTTCTGA TGCCGARACA AAAAAGGCAG TCATGTTTGT	660

-5 WATGTGATTG GAATGGAACC CGARAAGAGA GCAYGCTGTG TTCTTGGGGA CAGGAAAGCT 720
TGYGTGCACC AAGTCTKAAC CACCACCTTC ATGGGACATA GRTTATGTGC TGGAACATAT 780
TTCACACCGG CCTGGCAGTA AACACTTGTA GTGTGTGCA GTGGAAACGG TCATCTTCCG 840
CTAAAGCAGG CGGTGTTGTG CAGCGGAAAT GGTCATCTGC TGCTAAAACA CAGCTTCCAT 900
10 CGTAATGTAT GCTCCTTACT CAAAGAGTGT GGTCCTCAAAC AGCCTTTGGG AGGTCCTCCT 960
TGATTCATGG ATGAAACCTG GAACATCTTG AGGACTGAGT TAACCATAGG TCCTTAAATA 1020
15 ACTCTCCACA CGTTTTTCTT AGTTTATCTC TACATGCAGG GTGTGCAGCA GCCTGTTCAA 1080
AGTCATATTT TCTGGGAAAT ATTTCCAGTG TTTATTTGCA CTTTAGCCCA CTCTGTGTAG 1140
CCTTATTTCT TCTAAACTCA CCATTAATCT GAATAATAGT CAAATTTAGG GG 1192

20

(2) INFORMATION FOR SEQ ID NO: 202:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

ATCTTGGGCT ATCTTTGACA GGGGATCTCT GCAAGTTGAT GCTTTCTACA AGTGAATATA 60
35 GTCAGTCCCC AAAGATGGAG AGCTTGAGTT CTCACAGAAT TGATGAAGAT GGAGAAAACA 120
CACAGATTGA GGATACGGAA CCCATGTCTC CAGTTCTCAA TTCTAAATTT GTTCCTGCTG 180
40 AAAATGATAG TATCCTGATG AATCCAGCAC AGGATGGTGA AGTACAAC TG AGTCAGAATG 240
ATGACAAAAC AAAGGGAGAT GATACAGACA CCMGGGATGA CATTAGTATT TTAGCCACTG 300
GTTGCAAGGG CAGAGAAGAA ACGGTAGCAG AAGATGTTTG TATTGATCTC ACTTGTGATT 360
45 CGGGGAGTCA GGCAGTTCCTC TCACCAGCTA CTCGATCTGA GGCACTTTCT AGTGTGTTAG 420
ATCAGGAGGA AGCTATGGAA ATTAAAGAAC ACCATCCAGA GGAGGGGTCT TCAGGGTCTG 480
AGGTGGAAGA AATCCCTGAG ACACCTTG TG AAAGTCAAGG AGAGGAACTC AAAGAAGAAA 540
50 ATATGGAGAG TGTTCGGTTG CACCTTTCTC TGA CTGAAAC TCAGTCCCA 589

55

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 base pairs
60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5 GGCACGAGCG CAAGCTGCTG GCCGCCATCA ACGCGTTCCG CCAGGTGCGG CTGAAACACC 60
GGAAGCTCCG GGAACAAGTG AACTCCATGG TGGACATCTC CAAGATGCAC ATGATCCTGT 120
10 ATGACCTGCA GCAGAATCTG AGCAGCTCAC ACCGGGCCCT GGAGAAACAG ATTGACACGC 180
TGGCGGGGAA GCTGGATGCC CTGACTGAGC TGCTTAGCAC TGCCCTGGGG CCGAGCAGCT 240
15 TCCAGAACCC AGCCAGCAGT CCAAGTAGCT GGACCCACGA GGAGGAACCA GGCTACTTTC 300
CCCAGTACTG AGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCAGCCTGAA CAAAGCACCT 360
CAAGTGCAAG GACCAAAGGG GGCCTGGCTT GGATGGGTG GCTTGCTGAT GGCTGCTGGA 420
20 GGGGACGCTG GCTAAAGTGG GGAGGCCTTG GCCCACCTGA GGCCCCAGGT GGGAACATGG 480
TCACCCAC TCTGCATACC CTCATCAAAA AACTCTCAC TATGCTGCTA TGGACGACCT 540
CCAGCTCTCA GTTACAAGTG CAGGCGACTG GAGGCAGGAC TCTTGGGTCC CTGGGAAAGA 600
25 GGGTACTAGG GGCCCGGATC CAGGATTCTG GGAGGCTTCA GTTACCGCTG GCCGAGCTGA 660
AGAACTGGGT ATGAGGCTGG GCGGGGCTG GAGGTGGCGC CCCCTGGTGG GACAACAAAG 720
30 AGGACACCAT TTTCCAGAG CTGCAGAGAG CACCTGGTGG GGAGGAAGAA GTGTAACTCA 780
CCAGCCTCTG CTCTTATCTT TGTAAATAAT GTTAAAGCCA GAAAAAAAAA AAAAAAAAAA 840
35 AAAAAA 847

(2) INFORMATION FOR SEQ ID NO: 204:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

50 ACAAACATAC TCGCAGGAAG GAGTCTCATG CTGCCCCGAG CATCAGCGCA ACNCNTGGCC 60
GCCATCAACG CGTTCGCCA GGTGCGGCTG AAACACCGGA AGCTCCGGGA ACAAGTGAAC 120
TCCATGGTGG ACATCTCCAA GATGCACATG ATCCTGTATG ACCTGCAGCA GAATCTGAGC 180
55 AGCTCACACC GGGCCCTGGA GAAACAGATT GACACGCTGG CGGGGAAGCT GGATGCCCTG 240
ACTGAGCTGC TTAGCACTGC CCTGGGGCCG AGGCAGCTTC CAGAACCCAG CCAGCAGTCC 300
60 AAGTAGCTGG ACCCACGNAG GAGGAACCAG GCTACTTTCC CCAGTACTGA GGTGGTGGAC 360

ATNCGTCTCT TGCCACTCCN TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC 420
 AAAGGGGGCC CTGGCTTGGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC 480
 -5 TAAAGTGGGK AGGCCCTGGC CCACCTGAGG CCCCAGGTGG GAACATGGTC ACCCCCACTC 540
 TGCATACCCT CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT 600
 TACAAGTGCA GGCGACTGGA GGCAGGACTC CTGGGTCCCT GGGAAAGAGG GTACTAGGGG 660
 10 CCCGATCCA GGATTCCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT 720
 GAGGCTGGGG CGGGGCGGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATTT 780
 15 TTCCAGAGCT GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT 840
 CTTATCTTTG TA 852

20

(2) INFORMATION FOR SEQ ID NO: 205:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GATTCCGCAC GAGGCTTGCT GGAGCAGGAG AAGTCTCTRG CCGGCTGGGC ACTGGTGCTG 60
 GCASGARCTG GCATTGGACT CATGGTGCTG CATGCAGAGA TGCTGTGGTT CGGGGGGTGC 120
 35 TCGGCTGTCA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 180
 CTGACCATCG GCTATGGTGA CGTGGTGCCG GGCACCATGT GGGGCAAGAT CGTYTGCCTG 240
 40 TGCACTGGAG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGGCCGTGGT GGCCCGGAAG 300
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACCTCA TGATGGATAT CCAGTATACC 360
 AAAGAGATGA AGGAGTCCGC TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 420
 45 ACTCGCAGGA AGGAGTCTCA TGCTGCCCGC AGGCATCAGC GCAANCTGCT GGCCGCCATC 480
 AACGCGTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 540
 50 GTGGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 600
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CCTGACTGAG 660
 CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCAGAAC CCAGCCAGCA GTCCAAGTAG 720
 55 CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 780
 CTGCCACTCC TGANCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC AAAGGGGGCC 840
 60 CTGGCTTGGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGC TAAAGTGGGK 900

AGGCCTTGGC CCACCTGAGG CCCAGGTGG GAACATGGTC ACCCCCACTC TGCATACCCCT 960
 CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT TACAAGTGCA 1020
 -5 GCGGACTGGA GGCAGGACTC YTGGGTCCCT GGGAAAGAGG GYACTAGGGG CCCGGATCCA 1080
 GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT GAGGCTGGGG 1140
 10 CGGGGCTGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATTT TTCCAGAGCT 1200
 GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACTCACC AGCCTCTGCT CTTATCTTTG 1260
 TAATAAATGT TAAAGCCAGA AAAAAATAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC 1320
 15 AGACCCAATC TCCCTATAGT AAGNCGCCNN ANAN 1354

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(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

30

TCCCCAGGTG CACAGCCAGG GCCCTCCTGT CTGCAGGAGA ATTCACAGCT GGTGTGGGAC 60
 TCAGCCCCTA GNCCATTCAA AGCCTTAATG TTGTAATCAT ATCTTACGTG TTGAAGACCT 120
 35 GACTGGAGAA ACAAATGTG CAATAACGYG AATTTTATCT TAGAGATCTG TGCAGCCTAT 180
 TTCTGTCACA AAAGTTATAT TGTCTAATAA GAGAAGTCTT AATGGCCTCT GTGAATAATG 240
 TAACTCCAGT TACACGGTGA CTTTAAATAG CATACAGTGA TTTGATGAAA GGACGTCAAA 300
 40 CAATGTGGCG ATGTCGTGGA AAGTTATCTT TCCCGCTCTT TGCTGTGGTC ATTGTGTCTT 360
 GCAGAAAGGA TGGCCCTGAT GCAGCAGCAG CGCCAGCTGT ANATAAAAAA TAATTCACAC 420
 45 TATCAGACTA GCAAGGCACT AGAACTGGAA AAGACCACAG AAAACAAAGA ATCCAACCCT 480
 TTCATCTTAC AGGTGAACAA ACTGTGATGA TGCACATGTA TGTGTTTGT AAGCTGTGAG 540
 CACCGTAACA AAATGTAAAT TTGCCATTAT TAGGAAGTGC TGGTGGCAGT GAAGAAGCAC 600
 50 CCAGGCCACT TGACTCCAG TCTGGTGCCC TGTCTACACC AGACAACACA GGAGCTGGGT 660
 CAGATTCCCC TCAGCTGCTT AACAAAGTTC CTCGAACAGA AAGTGCTTAC AAAGCTGCCT 720
 55 TCTCGGATAC TGAAAGGTCG AGTTTTCTGA ACTGCACTGA TTTATTGCA GTTGAAAAAA 780
 AAAAAAGCT ATTCCAAAGA TTTCAAGCTG TTCTGAGACA TCTTCTGATG GCTTTACTTC 840
 CTGAGAGGCA ATGTTTTTAC TTTATGCATA ATTCATGTGT GCCAAGGAAT AAAGTGAAGA 900
 60

	AACAGCACCT	TTTAATATAT	AGGTCTCTCT	GGAAGAGACC	TAAATTAGAA	AGAGAAAAC	960
	GTGACAATTT	TCATATCTC	ATTCTTAAAA	AACACTAATC	TTAACTAACA	AAAGTTCTTT	1020
5	TGAGAATAAG	TTACACACAA	TGGCCACAGC	AGTTTGTCTT	TAATAGTATA	GTGCCTATAC	1080
	TCATGTAATC	GGTTACTCAC	TACTGCCTTT	AAAAAAAAAA	ACCAGCATAT	TTATTGAAAA	1140
	CATGAGACAG	GATTATAGTG	CCTTAACCGA	TATATTTTGT	GACTTAAAAA	ATACATTTAA	1200
10	AACTGCTCTT	CTGCTCTAGT	ACCATGCTTA	GTGCAATGA	TTATTTCTAT	GTACAACTGA	1260
	TGCTTGTTCT	TATTTTAATA	AATTTATCAG	AGTGAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1320
15	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAGAA	NAAAAA	1378

20 (2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

30	AANCCACTGC	ANTTTAAACC	CCCTCCCTC	CAAGAAAGTT	CACAACCGGC	CATGGATGAC	60
	CCTCATTTTA	GATGGGCCNC	AATATTTAAG	ATGGACTGRG	GMCCCARAG	ACTGACCTT	120
	GAAAGGGGGA	CTCAGAAGAA	AGATCCTTGA	CATTGCCMAA	CATGCTGGGC	TTGTCCAACA	180
35	CAGTGATGCG	GCTCATCGAG	AARCGGGCTT	TCCMAGGACA	AGTACTTTAT	GATAGGTGGG	240
	ATGCTGCTGA	CCTGTGTGGT	CATGTTCTC	GTGGTGCACT	ACCTGACATG	AGCCAGCCAC	300
40	GCTCAGTGGC	TGAACAGCAT	TCCCACAGCC	TGCAAGTGTG	TGTGTGTGTG	AAAGAGAGAG	360
	GGGGCCCA	GGCCGCTTT	TGAAATGTTT	GCCTGTCTGA	ACTGTGAAGA	CACTTGGGAG	420
	TGATTGTGGT	CTAATTTCCA	ACCTGCTCTG	TTTTCTGTGA	CATCTTGGAG	GGGAGCTAG	480
45	TGCCAMCACC	ATGCGCGGTG	CTTAGGAAAT	GAAAGAAGTC	CCGGGTCTGT	CTCTCTCACT	540
	CTCGCTCTCA	MTGGGGGAGG	GAAAGAATGG	CTTTGGTGGC	TTTGTTCACA	CAGCTGATGC	600
50	GTGSCCTGGG	AAGGTGTCCA	CAGTGAGCCC	TGTGTGCAGG	ACTGTCCACN	ACGGTTCACA	660
	CCTGTGCACC	ATCAGGCCTT	TCTGGCTCCT	GATAGGGTGG	AGCAAAAGTG	GAAAGGAAAG	720
	GAAAGAGGCY	TTTTCTCACA	GCCATTATAT	TAAATAGTAG	GTGATTTCAC	ATCYTCGTGC	780
55	TCCTGGCCAC	CCTCCCTGT	GCCTCAGTGA	CATGTAGATG	ACTGACTGCC	AATACTTGTC	840
	ACCATTCCT	GGAAGCAGCT	ACCTAGGGGA	AACAAGATGT	AGTGCTATTG	CCGATAACAA	900
60	GTAAGATTTT	CCACACTACA	GCTGGGTGTT	TCTCTTTTCT	AAAGTGAGGC	CAGTGTATT	960

-5 TCCCGGGAGT GTTCAGTCTT GACCCTAGTC ACTGATTTT TCTAGTTGTT AATAGAGTGG 1020
TTGGGCTTTT AAGGTTTCAGA GACTGTGGGC TTGGGCACCT GCGCCCAGGG STTTTGTGGG 1080
GGCCTTTGCC CCTTAGRAAA GTAGCTTTTA GGGGCAAAGA TTTGTTGATT TTCCCCATTA 1140
CAGTCTTCAG CTCNAGGGTT TAAAAA 1166

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(2) INFORMATION FOR SEQ ID NO: 208:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TACTTCTAGG ATTATAAGGA ATTAACATTG AGATGACATT TCCATTGAG AAGGAAAATA 60
25 GTTGCTTTCA GTGCCTTTTA TTTGATTCTT GGAGAGAGCA GACTCGCACS AACATTCAAC 120
CCCAGCGCTG ATATGACAGT AATCCTCAGA GGCAGAGCCC AGCACAAAAC AGCAATGCTA 180
GAAAGTTACA ATTGGAAAGT TTCCTGCCAG CTCGGGAAT GACACTGCAA AGCTGATGCC 240
30 AGAAACTGCC AGRGTAATTC TCCTCATTAC TGCTCTACCC ACCCACTTTC AGCTCCCCAA 300
ATTAAGTAGT GCAGTTGACT AATTCTCTTT ACCTTTATCA TTTARGGTGA RGCATTGCAC 360
35 AAAAAGTCTC GACTTTGCCA TATAAGGGCT GTGGTTCTCT GTGGTCCCTT GGATAAGAGG 420
CATCACCATT ATCTGGAAC ATGCAGTAAA TGCAGATTNT TCATCTCTC CCCAGACCTC 480
CTGAGTTAGA AATTCACAAG TTCTCCAGGT GATCTCATAC ATGCTAAAGT TTGAGAACCA 540
40 TTGAGTAAAG TTAATGCATT AAGAAGAGAT TAGATAGGA TGGTGGCGTA TCTTCCTACA 600
GTTTCCTGT TAACAAGAAA GTCAGAGGTC AGTTGATCAG ACATTAGATT ATTTATTGCT 660
45 AAAACTAAAA AAAATTAAAA AAAACTGGAG GGGGGCC 697

50

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

60 CGTGAGTCAC CTCTCTATAG TGGGCGTGGC CGAGGCCGGG GTGACCCTGC CGAAGCCTCC 60

	GCTGCCAGAA ACCATGTTCA AGGTAATTAA AAGGTCOGTG GGGCCAGCCA GCCTGAGCTT	120
- 5	GCTCACCTTC AAAGTCTATG CAGCACCAA AAAGGACTCA CCTCCCAAAA ATTCCGTGAA	180
	GGTTGATGAG CTTTCACTCT ACTCAGTTCC TGAGGGTCAA TCGAAGTATG TGGAGGAGGC	240
	AAGGAGCCAG CTTGAAGAAA GCATCTCACA GCTCCGACAC TATTGCGAGC CATACACAAC	300
10	CTGGTGTGAG GAAACGTACT CCCAAACTAA GCCCAAGATG CAAAGTTTGG TTCAATGGGG	360
	GTTAGACAGC TATGACTATC TCCAAAATGC ACCTCCTGGA TTTTTCCTGA GACTTGGTGT	420
15	TATTGGTTTT GCTGGCCTTA TTGGACTCCT TTTGGCTAGA GGTTCAAAAA TAAAGAAGCT	480
	AGTGTATCCG CCTGGTTTCA TGGGATTAGC TGCCTCCCTC TATTATCCAC AACCAAGCCAT	540
	CGTGTTCGCC CAGGTCAGTG GGGAGAGATT ATATGACTGG GGTTCACGAG GATATATAGT	600
20	CATAGAAGAT TTGTGGAAGG AGAACTTTCA AAAGCCAGGA AATGTGAAGA ATTCACCTGG	660
	AACTAAGTAG AAAACTYCAT GYTCTGCCAT CTTAATCAGT TATRGGTAAA CATTGGAAAC	720
25	TCCATAGAAT AAATCAGTAT TTCTACAGAA AAATGGCATA GAAGTCAGTA TTGAATGTAT	780
	TAAATTGGCT TTCTTCTTCA GGAAAACTA GACCAGACCT CTGTTATCTT CTGTGAAATC	840
	ATCCTACAAG CAACTAACC TGGAATCCCT TCACCTAGAG ATAATGTACA AGCCTTAGAA	900
30	CTCCTCATTC TCATGTTGCT ATTTATGTAC CT	932

35 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

45	GTCATTCTTT AAATAAAAGC TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA	60
	AGATTCCCC TAGGGTTGAT ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTTCA	120
50	TTTAAAGCT TTGGCTATAT AGTCAGAAAT GTCCTAAATA ACAAATATT TTGTATTTAA	180
	TTTAGGGAAG ACTAAAGGA AGAAAAATGA AAATCAGTC TTTATGTAAG CTCCAAGGAT	240
	ATTAGGGCTT AAAGGCTTT TCTAGTTTGA TGAGAATTG TACTACTGAT TTTTATATAT	300
55	TCCTGTTTTT GAGATGAACA GATCTCTGGG GAAATTGTTG AGTTACAATG GCATTTCACT	360
	GTGATCCCTC TCAAGCTCAG ATCAGTTCTA TAACCCAATG ACAACCTGTC TCTTTGGTTT	420
60	ACTGTCTGT GAAATGTCAG CTCAAGTTTC CCAGAAGTCG TGTGTTTATG ATGAGTCAGA	480

GTGCTTTTCC TCGGTGGGAC AGTTGCTGGC CCTCTTAATT TTGGTGTATG TGCTTCCAAG 540
 TATCTAAACC TCCAGTCTGA TCTGTATATG CTATCCTAAC TGTTAATTGT ATTATTGATT 600
 -5 ATGTTGATTA TCTTGCTTGA AGGTTCATAC TTTTCAATTT GATAGAAATA AAGTTTTTTT 660
 C 661

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(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GAAACTGACA TTGTTAAACA CACTAAAACA GAAGTACTTA CCTCTTGAAG ATTTAATATA 60
 TAATGGTTGA CATGATACAT GTACATGAAT GGAATGACCA GATGCTTATG GTCTACATTT 120
 25 TCCTTTATCC TGTTAGTATT ACCTTCCTTA ATCTTTGTTC CTTAACATGC TAAATTCCTC 180
 TTCAGTGTTC ATTTTCTAGT GACAGAATGC TAACATTTCT TACACCCTGG CAGAAGGGAG 240
 30 AGAAATGTGT TTTGGGGTGG GTAACATAAT TTTTGAGTGA AATATCATAA GATGAGAATG 300
 GAAAGAGGGA GACACAAAGA GTTATAACAA AAAACAATG GTTTTTTTAG CCATTTGACT 360
 GGCTCTTTAA ATAGTCTACA AGACATTCAC GTTNAACATC ACTTTTAGTG AAATAAAATG 420
 35 TGCCATACTA GTATGTGCTT CAAAAGGGCA AATGTGCTTT AGTGCCCTAA GGCTAAATTT 480
 TGGTCATTTG ACATCAGAGA TGTGTAAAGT ATTGCACCTA ATACGCACCT ATTTCTCAAT 540
 40 AGTGNATTTT TTTTGGCTAG CATTTNCTTT ACCACTAACC TTGTTGGATA GC 592

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(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 938 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

55 TGGAGTGGCT TTCCAGCTGA ATGAATCCTA TGTCTCGCGT GCAGGTGGTT GGTTTTCAAT 60
 GTTCTTSCCT ATTTTTTTCC TATTGGCTCT TGGGAGTTTN CTTTGTTCGC TCCTGTGTTT 120
 60 GCCCAGCTTT AATAAAACCA GGCGCAAACA AAAACCATAG CATTCGTGAA CAATAGGGGG 180

	CCCACATTGG ACCCAGTATG TCACTTTAAT GGACTTCAAG AAAAAATCTG AATGGGAAAA	240
	TGACACTAGG AATGTATACT CCACACATTT TATGCCATAT AATGGTGTGT TTTCTTAATT	300
5	TTGTTTCTTG TGGCGAAATG TGGCTTTCAA ATTAAATGM CCTTTTCTTC TTKGAACTT	360
	TTTGTTKGA CTKGTATAAT TAAGGGTTTG GAAAGATTCA TAATTMTGAG AGAGGTTTGC	420
10	AACCAGGAGA TACAAAGAAG TCTCAGTAGT AATCTTGTTC ATGTGCTTTT ACAGCCAGCT	480
	ACATTTAAGR ATGTATTAGT TACAGAAATT ATATGTCTGT GTATGTGTCT CTA CTCAATA	540
	AAGTACATGC CTCCACATAA TGCGGTGCTG TCCATCTCGG CAAATACTGG CCAAGTCCCT	600
15	TTATGACAGG CACACAGAAA CCATAGCATG GTCTGGCTTT CAGAAAATGC CTCTCATCTT	660
	TCCTGGAACC TTATTTTGCT AAATGTCTGT TTTCTTGTGA TTGTTGTAC CTCACAGCAC	720
20	CATTGTGACC ATGGTGATGC CTCATTGCA TGATATGTAC CTGTGTTTA ATGTGAAATA	780
	CATTTTCATT GAAGAGTCTG ATGACTTGCT AGCGTTTAT TTTTCTGTA AGCTCAATGT	840
	GCTGAAACCA AACCAGGCTT TTA AAAACCT GTGTAGAAGA AAACCAAAA ATCCTGTGTG	900
25	GGTGTCTTT CCCTGTCAA CTCATTAAAA ATTCTTT	938

30 (2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

40	ACCTGCCCG GAGAGTGGTG GCATCTRARA GGCTGGTCGT GGACTGTGGT TGGGGGAGGT	60
	GGGAGCTGTT TTAACCGTGT GCCCCCTCTC CTGTGCKGC GTGGCATCC CCCGGGCAG	120
	TGGAACGCGG GCGCTCCTCC AGCTTCCGAG TCCAGCCAGC CTGGGCGCGG GCGCGCCCC	180
45	CGAGACACCC GAGGAGTCCG TTCTCCCTG GTTACGTGGA CTGTGGAGCT GGTCTCTGT	240
	GGCTCAGCGC CGTGCGGAGG TTGAAGCGTA CCTGCGGAGG TCGCACCAGG GCGGTGAGGA	300
50	GGAGGAGGAA GGGCATGAGC CGAGCTTGAG GAATCCGTGY TCCAACTCT AACTCAAGG	360
	RTGCMCTGCG CAACTCTGGT GCGATGGGC TGGGGCAGAT GTCCTTGAG TTCTACCAGA	420
	AGAAGAAGTC TCGCTGGCCA TTCTCAGACG AGTGCATCCC ATGGGAAGTG TGGACGGTCA	480
55	AGGTGCATGT GGTAGCCCTG GCCACGGAGC AGGAGCGGCA GATCTGCCG GAGAAGGTGG	540
	GTGAGAACT CTGCGAGAAG ATCATCAACA TCGTGAGGT GATGAATCGG CATGAGTACT	600
60	TGCCCAAGAT GCCCACACAG TCGGAGGTGG ATAACGTGTT TGACACAGGC TTGCGGGACG	660

TGCAGCCCTA CCTGTACAAG ATCTCCTTCC AGATCACTGA TGCCCTGGGC ACCTCAGTCA 720
 CCACCACCAT GCGCAGGCTC ATCAAAGACA CCCTTGCCCT CTGAGCGTCG CTGGATCTCT 780
 -5 GGGAGCTCCT TGATGGCTCC CAGACCTTGG CTTTGGGAA TTGCACTTTT GGGCCTTTGG 840
 GCTCTGGAAC CTGCTCTGGG TCATTGGTGA GACTTGGAAG GGGCAGCCCC CGCTGGCTTC 900
 10 TTGGTTTTGT GGTTGCCAGC CTCAGGTCAT CCTTTTAATC TTTGCTGACG GTTCAGTCCT 960
 GCCTCTACTG TCTCTCCATA GCCCTGGTGG GGTCCCCCTT CTTTCTCCAC TGTACAGAAG 1020
 AGCCACCACT GGGATGGGGA ATAAAGTTGA GAACATGAGT TTGGGCTGAA AAAAAAAAAA 1079
 15

(2) INFORMATION FOR SEQ ID NO: 214:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TGAAGCAGGC GCTCTTGGCT CGGCGCGGCC CGCTGCAATC CGTGGAGGAA CGCGCCGCCG 60
 30 AGCCACCATC ATGCCTGGGC ACTTACAGGA AGGCTTCGGC TCGTGGTCA CCAACCGATT 120
 CGACCAGTTA TTTGACGACG AATCGGACCC CTTCCAGGTG CTGAAGGCAG CAGAGAACAA 180
 35 GAAAAAAGAA GCCGGCGGGG GCGGCGTTGG GGGCCCTGGG GCCAAGAGCG CATCAGGGCC 240
 GCGGCCCAGA CCAACTCCAA CGCGGCAGGC AAACAGCTGC GCAAGGAGTC CCAGAAAGAC 300
 CGCAAGAACC CGCTGCCCCC CAGCGTTGGC GTGGTTGACA AGAAAGAGGA GACGCAGCCG 360
 40 CCCGTGGCGC TTTAAGAAAG AAGGAATAAG ACGAGTTGGA AGAAGACCTG ATCAACAAC 420
 TCAGGGTGAA GGGAAAATAA TTGATAGAAG ACCAGAAAGG CGACCACCTC GTGAACGAAG 480
 45 ATTCGAAAAG CCACTTGAAG AAAAGGGTGA AGGAGGCGAA TTTTCAGTTG ATAGACCGAT 540
 TATTGACCGA CCTATTGAGG GTCGTGGTGG TCTTGGAAGA GGTGAGGGG GCCGTGGACG 600
 TGAATGGGC CGAGGAGATG GATTTGATTC TCGTGGCAA CGTGAATTTG ATAGGCATAG 660
 50 TGAAGTGAT AGATCTTCTT TTTACATTA CAGTGGCCTG AAGCACGAGG ACAAACGTGG 720
 AGGTAGCGGA TCTCACAAC TGGGAACTGT CAAAGACGAA TTAAC TACT TGGATCAATC 780
 55 AAATGTGACT GAGGAAACAC CTGAAGGTGA AGAACATCAT CCAGTGGCAG AACTGAAAA 840
 TAAGGAGAAT GAAGTTGAAG AGGTAAAAGA GGAGGGTCCA AAAGAGATGA CTTTGGATGA 900
 GTGAAGGCT ATTCAAATA AGGACCGGGC AAAAGTAGAA TTTAATATCC GAAAACCAA 960
 60

	TGAAGGTGCT GATGGGCAGT GGAAGAAGGG ATTTGTTCTT CATAAATCAA AGAGTGAAGA	1020
	GGCTCATGCT GAAGATTCGG TTATGGACCA TCATTTCCGG AAGCCAGCAA ATGATATAAC	1080
-5	GTCTCAGCTG GAGATCAATT TTGGAGACCT TGGCCGCCCA GGACGTGGCG GCAGGGGAGG	1140
	ACGAGGTGGA CGTGGGCGTG GTGGGCGCCC AAACCGTGGC AGCAGGACCG ACAAGTCAAG	1200
10	TGCTTCTGCT CCTGATGTGG ATGACCCAGA GGCATTCCCA GCTCTGGCTT AACTGGATGC	1260
	CATAAGACAA CCCTGGTTCC TTTGTGAACC CTTCTGTTCA AAGCTTTTGC ATGCTTAAGG	1320
	ATTCCAAACG ACTAAGAAAT TAAAAAATAA AAGACTGTCA TTCATACCAT TCACACCTAA	1380
15	AGACTGAATT TTATCTGTTT TAAAAATGAA CTTCTCCCGC TACACAGAAG TAACAAATAT	1440
	GGTAGTCAGT TTTGTATTTA GAAATGTATT GGTAGCAGGG ATGTTTTTCAT AATTTTCAGA	1500
20	GATTATGCAT TCTTCATGAA TACTTTTGTA TTGCTGCTTG CAAATATGCA TTTCCAAACT	1560
	TGAAATATAG GTGTGAACAG TGTGTACCAG TTTAAAGCTT TCACTTCATT TGTGTTTTTT	1620
	AATTAAGGAT TTAGAAGTTC CCCCAATTAC AAACCTGGTT TAAATATTGG ACATACTGGT	1680
25	TTTAATACCT GCTTTGCATA TTCACACATG GTCAACTGGG ACATGTTAAA CTTTGATTTG	1740
	TCAAATTTTA TGCTGTGTGG AATACTAACT ATATGTATTT TAACTTAGTT TTAATATTTT	1800
30	CATTTTTGGG GAAAAATCTT TTTTCACTTC TCATGATAGC TGTATATAT ATATGCTAAA	1860
	TCTTTATATA CAGAAATATC AGTACTTGAA CAAATTCAAA GCACATTTGG TTTATTAACC	1920
	CTTGCTCCTT GCATGGCTCA TTAGGTTCAA ATTATACTG APTTACATTT TCAGCTATAT	1980
35	TTACTTTTTA AATGCTTGAG TTTCCCATTT TAAAATCTAA ACTAGACATC TTAATTGGTG	2040
	AAAGTTGTTT AAAC TACTTA TTGTTGGTAG GCACATCGTG TCAAGTGAAG TAGTTTTATA	2100
40	GGTATGGGTT TTTTCTCCCC CTTCAACAGG GTGGGTGGAA TAAGTTGATT TGGCCAATGT	2160
	GTAATATTTA AACTGTCTCG TAAATAAGT GTCTGGCCAT TTGGTATGAT TTCTGTGTGT	2220
	GAAAGGTCCC AAAATCAAAA TGGTACATCC ATAATCAGCC ACCATTTAAC CCTTCCTTGT	2280
45	TCTAAAACAA AAACCAAAGG GCGCTGGTTG GTAGGGTGAG GTGGGGGAGT ATTTTAATTT	2340
	TTGGAATTTG GGAAGCAGAC AGCTTTACTT TGTAAGGTTG GAACAGCAGC ACTATACATG	2400
50	AAATATAAAC CAAAAACCTT TACTGTTTCT AAATTTCTTA GATTGCTATT ATTTGGTTGT	2460
	AAGTTGAGTA TTCCACAGAA AGTGGTAATT ATCTCTTCTC TCTTCCTCCA TTAGAAAATT	2520
	AGGTAAATAA TGGATTCCTA TAATGGGAGC ATCACCATT ATTAAAACAC ACATAGAATG	2580
55	ATGAATTAAA AAAGTTTCTT AGGATTGTCT TTTATTCTGC CACATTTATT GATAAACAGT	2640
	GAAGGAATTT TAAAAAATT TTTAAGAATT GTTGTGTCAG TCATTTTAG AAATGTTCTA	2700
60	CCTGTATATG GTAATGTCCA GTTTTAAAAA TATTGGACAT CTTCAATCTT AACATTTCT	2760

	ATTAGCTGA TTGGTTCTCA CATATACTTC TAAAAGAAAC TTTTATGTTA TAAGAGTTAC	2820
	TTTTGGATA AGATTTATTA ATCTCAGTTA CCTACTATTC TGACATTTTA GGAAGGAGGT	2880
- 5	AATGTTTTTT AATGATGGAT AAACCTGTGC TGGTGTTTTG GATCTTATGA TGCTGAGCAT	2940
	GTTCTGCACT GGTGCTAATG TCTAATATAA TTTTATATTT ACACACATAC GTGCTACCCA	3000
10	GAGATTAATT TAGTCCATAT GAACTATTGA CCCATTGTTC ATTGAGACAG CAACATACGC	3060
	ACTCCTAAAT CAGTGTGTTT AGACTTTTCA AGTATCTAAC TCATTTCCAA ACATGTACCA	3120
	TGTTTTATAA ACCTCTTGAT TTCCAGCAAC ATACTATAGA AAACACCTGC TACTCAAAAC	3180
15	ACAACTTCTC AGTGTCAATC ATTGCTGTGC TGAGAGACAA CATAGCAATA TCTGGTATGT	3240
	TGCAAGCTTT CAAGATAGCC TGAACCTAAA AAGTGGTGC ATTAGTTGTA TCTGATGGAT	3300
20	ATAAATTTGC CTCCTAGTTC ACTTTGTGTC AAGAGCTAAA ACTGTGAACC TAACTTTCTC	3360
	TTATGGTGG GTAATAACTG AAAATAAAGA TTTATTTTCA TGCTCACTTC TTAAAAGTCA	3420
	TAAAAACAAT CAAATAGGRT CATGTTTATT GTCATGTGTT TCCTGGKTTT TGACCTGTGT	3480
25	GCACCCCCCT GTGTGTTTAT AATTTTAAA TTGAATTTTA TATGGGGTTT TTATTTGCTA	3540
	AAAACCAGGC TGTGTAATCA CATTTGGGAA GGGTACTTAT CTTAATGACT AATGACTTAA	3600
30	TTGGGAAAGT TGAATTCTTG TAAAATACAA AATCCAAGGA CTCTTGGA TTTAATCTAA	3660
	TTGTCACTTC NTTAGGCAGA TNCACTTTTT TGGATAATGG AAAGTTAAGC ATACCGAATG	3720
	CTACTTTTGG TTGACAAACG GGCCTAATAG TCCGGGGGA AATCCCTAAC NGGTAAGGNT	3780
35	CCCAAGTATG G	3791

40 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

50	CAGTGCTCGC TCCTGCTCGG GCGCTGCGG CCCC GGCGT CGCCATGACC AGTGAGCTGG	60
	ACATCTTCGT GGGGAACAGA CCCTTATCGA CGAGGACGTG TATCGCCTCT GGCTCGATGG	120
55	TTACTCGGTG ACCGACGCGG TGGCCCTGCG GGTGCGCTCG GGAATCCTGG AGCAGACTGG	180
	CGCCACGGCA GCGGTGCTNC AGAGCGACAC CATGGACCAT TACCGCACCT TCCACATGCT	240
	CGAGCGGCTG CTGCATGCGC CGCCCAAGCT ACTGCACCAG YTCATCTTCC AGATTCCGCC	300
60	CTCCCGGCAG GCACTACTCA TCGAGAGGTA CTATGCCTTT RATGAGGCCT TTGTTCCGGA	360

	GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC CAAGAAAGAC CTGGATGACA TCAGCACCAA	420
-5	AACAGGCATC ACCCTCAAGA GCTGCCGGAG ACAGTTTGAC AACTTTAAAC GGGTCTTCAA	480
	GGTGGTAGAG GAAATGCGGG GCTCCCTGGT GGACAATATT CAGCAACACT TCCTCCTCTC	540
	TGACCGGTTG GCCAGGGAAT ATGCAGCCAT CGTCTTCTTT GCTAACAACC GCTTTGAGAC	600
10	AGGGAAGAAA AAAGTGCAGT ATCTGAGCTT CGGTGACTTT GCCTTCTGCG CTGAGCTCAT	660
	GATCCAAAAC TGGACCCTTG GAGCCGTCGA CTCACAGATG GATGACATGG ACATGGACTT	720
15	AGACAAGGAA TTTCTCCAGG ACTTGAAGGA GCTCAAGGTG CTAGTGGCTG ACAAGGACCT	780
	TCTGGACCTG CACAAGAGCC TGGTGTGCAC TGCTCTCCGG GGAAAGCTGG GCGTCTTCTC	840
	TGAGATGGAA GCCAACTTCA AGAACCTGTC CCGGGGGCTG GTGAACGTGG CCGCCAAGCT	900
20	GACCCACAAT AAAGATGTCA GAGACCTGTT TGTGGACCTC GTGGAGAAGT TTGTGGAACC	960
	CTGCCGCTCC GACCACTGGC CACTCAGCGA CGTGCGGTTC TTCTGAATC AGTATTCAGC	1020
25	GTCTGTCCAC TCCCTCGATG GCTTCCGACA CCAGGCCTCT GGGACCGCTA CATGGGCACC	1080
	CTCCGCGGCT GCCTCCTGCG CCTGTATCAT GACTGAGGTG CCTCCCAACG CTCCGCCAC	1140
	GCTGACAATA AAGTTGCTCT GAGTTTGGAG ACTGGTCCTC GCTCCGGGGA GCAAGTGGG	1200
30	GGCGTGCAGA TGTGCCTGTG TCTGTCTCTG AGCACCTGGT GTCCGTGTAC AAGGATGGAT	1260
	GTGTNCNGTG GCTCCTTGGG AACTGAGACA TATCTCAGGG AATGGTGTCT GTGCTCAGCC	1320
35	CATCCACCAG AAGA	1334

(2) INFORMATION FOR SEQ ID NO: 216:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

50	GTGGCGGGGA TGCTGCGAGG GGGTCTCTG CCCCAGGCGG GCCGGCTGCC TACCTCCAG	60
	ACTGTCCGCT ATGGCTCCAA GGCTGTTACC CGCCACCGTC GTGTGATGCA CTTTCAGCGG	120
	CAGAAGCTGA TGGCTGTGAC TGAATATATC CCCCCGAAAC CAGCCATCCA CCCATCATGC	180
55	CTGCCATCTC CTCCAGCCC CCCACAGGAG GAGATAGGCC TCATCAGGCT TCTCCGCCGG	240
	GAGATAGCAG CAGTTTTCCTA GGACAACCGA ATGATAGCCG TCTGCCAGAA TGTGGCTCTG	300
60	AGTGCAGAGG ACAAGCTTCT TATGCGACAC CAGCTGCGGA AACACAAGAT CCTGATGAAG	360

	RTCTTCCCA ACCAGGTCCT GAAGCCCTTC CTGGAGGATT CCAAGTACCA AAATCTGCTG	420
	CCCCTTTTGT TGGGACACAA CATGCTGCTG GTCAGTGAAG AGCCCAAGGT CAAGGAGATG	480
-5	GTACGGATCT TAAGGACTGT GCCATTCTCTG CCGCTGCTAG GTGGCTGCAT TGATGACACC	540
	ATCCTCAGCA GGCAGGGCTT TATCAACTAC TCCAAGCTCC CCAGCCTGCC CCTGGTGCAG	600
10	GGGAGCTTG TAGGAGGCCT CACCTGCCTC ACAGCCCAGA CCCACTCCCT GCTCCAGCAC	660
	CAGCCCCTCC AGCTGACCAC CTTGTTGGAC CAGTACATCA GAGAGCAACG CGAGAAGGAT	720
	TCTGTCATGT CGGCCAATGG GAAGCCAGAT CCTGACACTG TTCCGGACTC GTAGCCAGCC	780
15	TGTTTAGCCA GCCCTGCGCA TAAATACACT CTGCGTTATT GGCTGTGCTC TCCTCAATGG	840
	GACATGTGGA AGAACTTGGG GTCGGGGAGT GTGTTTGTC CTTGGTTTTT ACTAGTAATG	900
20	ATATTGTGAG GTATAGGGCC ACTTGGAGAT GCAGAGGATT CCATTTCAGA TGTCAGTCAC	960
	CGGCTTCGTC CTTAGTTTTT CCAACTTGGG ACGTGATAGG AGCAAAGTCT CTCCATTCTC	1020
	CAGGTCCAAG GCAGAGATCC TGAAAAGATA GGGCTATTGT CCCCTGCCTC CTTGGTCACT	1080
25	GCCTCTTGCT GCACGGGCTC CTGAGCCACC CCCTTGGGGC ACAACCTGCC ACTGCCACAG	1140
	TAGCTCAACC AAGCAGTTGT GCTGAGAATG GCACCTGGTG AGAGCCTGCT GTGTGCCAGG	1200
30	CTTTGTGCTG AGTGCTGTAC ATGTATTAGT TCCTTTACTG CTGACCACAT TGTACCCATT	1260
	TCACAGAGAA GGAGCAGAGA AATTAAAGTGG CTTGCTCAAG GTCATGCAGT TAGTAAGTGG	1320
	CAGAACAGGG ACTTGAACCA AGCCCTCTGC TCTGAAGACC GCGTCCTGAA TTTCTTCACT	1380
35	AGAGCTTCCT CATCAGGTTA CCCAGAAGTG GGTCCCATCC ACCATCCAGG TGTGCTTGGA	1440
	TGTTAGTTCT CCACCCCTGA GGTGTACGCT GTGAAAAGTT TGGGAGCACT GCTTTATAAT	1500
40	AAAATGAAAT A	1511

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

55	AGGCCTTACT TTTCTCCCA CAAAGGAGTC GCAGCCACGC TAGCTCTGAC TTGCCACTGT	60
	GACAAAGTTC ACGTAGCAGG TCTAGGCAAA GACTGGGCAA TTGAGCAGAG GAGACGGACC	120
	TGTGAGTCTG ACCRYGAGSC GGRCCCTTC ACCTTGGCTG GGCTGGTCCT GGTCCCTAGG	180
60	TTTTGTCAGG TTGTCCTTGT TTGGATCCCT CAACTAGGTG ATAAGCACTG GAGGGGGATG	240

ACCCGCCTTG GACGTGTTTC TTAAACCTCA TCCATATAAT AGGGCCGTGG GATGGTTGTA 300
 GAGGTAAAGC AGGATGATGG TGTTTTAAGA CCAGAGCTTG GGACCAGGGC TCCTACACCT 360
 -5 AATTTTCTCT CCTGGTAGCT GAACAAAGGT CTAAATTAGC TTAACAAAAG AACAGGCTGC 420
 CGTCAGCCAG AGTTCTGAAG GCCATGCTTT CAGTTTCCCT TGTGACAAT TGCTCTCCAG 480
 10 TTCTATGAA AGCACAGAGC CTTAGGGGGC CTGGCCACAG AACACAACCA TCTTAGGCCT 540
 GAGCTGTGAA CAGCAGGGGG TTGTGTGTCT GTTCTGTTTC TCTGCTTGCC GAACTTTCTC 600
 AATAAACCTT ATTTCTTATT TTATATTTAC GTNGGTGCTG GG 642
 15

(2) INFORMATION FOR SEQ ID NO: 218:
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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GGTCCCACTG TTCCATTTTA TGCTAATAGA TTCCATTCTA GGGCCAGCC GTCTCTTGAC 60
 30 TGATGGTGTT CCCTTTAACC CTTGGCATGT ATAATAGAAT TTTGGTGAAT GAAAGAACCC 120
 AAATAGGCCA GATAGTCCCC CCAGGCCCTG ATATCCATAA AAGGCTTGGG AATGCATTAT 180
 35 GTAATGTGCC TTAGTCTTTT TGTGTTTTTA GAAAAAAAAA ACAAGATGGG CTCAGATGGA 240
 -----TGCCTACGTA-AAAATGGTTC-CTAGCTGTGT-CTCATAACT-TTTCTTTGAA-TTGAGTAGTG-----300-----
 AAAGGAAGGA GGAGGAAAGG AAATTAAATG TCCTTCTAGT ATTCTCTGGA CTCAAGTCTG 360
 40 ACATATGRGA TAATAACCTA TATTGAAATG CCAAGAATTG TATCTGAAAC AAGRGAACAG 420
 TTTGACACAT TTATCATGCC TTCATATTAC ATATTAAGTG AAACCAATTA ATAAACATAT 480
 45 GAAATATCCA TTGCACAAGG CAAAGGCACC TAAACCTTTT GTTCTTTTTT CTACATAGCA 540
 GAAATGATT TTTTTTTTAT TTTTTTAGGG GAACCTATAT AATTATGACC CAGTGATGTC 600
 TTTTGGTGAC TTAAGCTTAT GAATTCAGGT TACAATTGAG TTGATTCTAG ATGGTTACTA 660
 50 CCTTGAAAAG GATGTTGGTG CCTTATGTGA CACGAGCCAG AGCCTGCTGG GAATAAACAA 720
 AGCAGATTCA TGCCAACACC AACTCGTAGC TTTAGTGCCA GATGGGAGTG GTCACAGACT 780
 55 CCCAAAATGT GGGGCTTTGG ATTTCCACAC CATCCACGT GTGTGTCATC TTCCTCTTTC 840
 ACACTCTTGA TGATAATTTG AAAATGRTGA AATCACCTCT GAATTTGCCT ATAGCATGAG 900
 CACATTCTTA TGACAACATA ACAAATAGTT CATAATGTGA ATATTAGAAA CTGTTACAGC 960
 60

CTGCAGTTAC CATAATTTTC CATGTTTGTG GAATTGATAT TGAAATAGCA GGGCTAAGGA 1020
 ATTACTGGCA AGTTTTAGCC TGTGGGTAAT ACCTTAGGGT TATTTAAATA TTTGTAATTT 1080
 - 5 TATTTAAATG TTCATGAATG TTTGAAAGGA ACAAATTAT CAGGGATGGC TCTTTGCCAT 1140
 GGGTCTTATT TTCACCCTCT TTTCTGTAAG AAAAAAGAAC AATGTCTTAA TGTATTTTAA 1200
 10 AAGTTTTTGG TATAGTTTCT AATTCOAATT TTAATAAAG T 1241

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

25 TGTATATGTG ACCTAAAACA TACACACATG CACACACACA TACATATCCA TTCATTCAAT 60
 CATTCAAGTG GTGTTTCCAG TGTCTGTGTG TCACTGTTTA TGCAGTTTCC ATTTCCCAGT 120
 GAATTATGAG TGGAGGGCAA CTTTCTAAC CAGATTGTCT TTTCAGAACA AAGACCKGGG 180
 30 RATTGAGGAA GAGTTTGAA AGAGGGAGAG GCAAGGAAAG AGAGCTTTAA ATTGAAAGGT 240
 TAATTTCCCTA AGAGGAACCT GGGCTGAATG ACTACAGTGT TATACCCTCC AATCTTTGCA 300
 GGTGGGCATG GAACACTGCT TGTATCACTC TGTGCACGGT ATAAATCCAT ATATCCACAA 360
 35 AAACACACAT CCATCCATCA ACATATACAT GGTTTGGGAT GAGCAGGTCA ATAGTTTTGA 420
 GAGGGAGTTT GTTCCTTTTT TTTTCTCATT ATACTCTTAA ATTGTTGTCA GTTATCAAAC 480
 40 AAACAAACAG AAAAATTGTT TGGGAAAAAC CTTCATACG CCTTTTCTAT CMAGTGCTTT 540
 AAAATATAGA CTAAATACAC ACATCCTGCC AGTTTTTCT TACAGTGACA GTATCCTTAC 600
 CTGCCATTTA ATATTAGCCT CGTATTTTTT TCACGTATAT TTACCTGTGA CTTGTATTTG 660
 45 TTATTTAAAC AGGAAAAAAA ACATTCAAAA AAAGAAAAAT TAACTGTAGC GCTTCATTAT 720
 ACTATTATAT TATTATTATT ATTGTGACAT TTTGGAATAC TGTGAAGTTT TATCTCTTGC 780
 50 ATATACTTTA TACGGAAGTA TTACGCCTTA AAAATACGAA AATAAATTTT ACAAGGTTTC 840
 TGTTTTGTGT GGAAGAGTAA TTGATGTTGC TAAGAATGAT GTTTGTTTTT TTGGGGTTTT 900
 TGTGTGTTTT TTTTAAATG TTACCAGCAC TTTTGTGTA AGTTTCACTT TCCGAGGTAT 960
 55 TGTACAAGTT CACACTGTTT GTGAAGTTTG AATATGAAGG AATAATTAAA AAAAAAAAAA 1020
 AAACCNCGGG GGGGGCCCCG TCCCATTTGGN CCCAAGGGGG CGTTACGGG GTCACGGCCG 1080

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TGAATTGAGG GCTTAAAGAT AACATATGG GRTTGGAGTT GTGTGTCCAT AGGGTTTCAC 60
TGCCTATTTG ATTTGAGTTT ATCCCTATTA ATTTTTTACA GTGAAATTTT ATTAAAGTAT 120
AATGTACATA TATTTTCAGT GGATTTTGCT CTGAAGGTTT TCCAGTGGTC TGACTACGAG 180
ATAGTGCGGC TTCAGCTGTG GGATATTGCA GGGCAGGAGC GCTTCACCTC TATGACACGA 240
TTGTATTATC GGGATGCCTC TGCCTGTGTT ATTATGTTTG ACGTTACCAA TGCCACTACC 300
TTCAGCAACA GCCAGAGGTG GAAACAGGAC CTAGACAGCA AGCTCACACT ACCCAATGGA 360
GAGCCGGTGC CCTGCCTGCT CTTGGCCAAC AAGTGTGATC TGTCCCCTTG GGCAGTGAGC 420
CGGGASCAGA TTGACCGGTT CAGTAAAGAG AACGGTTTCA CAGGTTGGAC AGAAACATCA 480
GTCAAGGAGA ACAAAAATAT TAATGAGGCT ATGAGAGTCC TCATTGAAAA GATGATGAGA 540
AATTCCACAG AAGATATCAT GTCTTTGTCC ACCCAAGGGG ACTACATCAA TCTACAAACC 600
AAGTCCTCCA GCTGGTCCTG CTGCTAGTAG TGTTTGGYTT ATTTTCCATC CCAGTTCTGG 660
GAGGTCTTTT AAGTCTCTTC CCTTTGGTTG CCCACCTGAC MATTTTATTA AGTACATTTG 720
AATTGTCTCC-TGACTACTGT-CCAGTAAGGA-GGCECATGT-CACTTAGAAA-AGACACCTGG-780
AACCCAKGTG CATTTCTGCA TCTCCTGGAT TAGCCTTTSA CATGTTGCTG RCTCACATTA 840
GTGCCAGTTA GTGCCTTCGG TGTAAGATCT TCTCATCAGC CCTCAATTTG TGATCCGGAA 900
TTTTGTGAGA AGGATKAGAA ATCAGCACCT GCGTTTTAGA GATCATAATT CTCACCTACT 960
TCTGAGCTTA TTTTTCATT TGATATTCAT TGATATCATG ACTTCCAATT GAGAGGAAAA 1020
TGAGATCAAA TGTCATTTCC CAAATTTCTT GTAGGCCGTT GTTTCAGATT CTTTCTGTCT 1080
TGGAATGTAA ACATCTGATT CTGGAATGCA GAAGGAGGGG TCTGGGCATC TGTGGATTTT 1140
TGGCTACTAG AAGTGTCCCA GAAGTCACTG TATTTTGTAA ACTTCTAACG TCATAATTAA 1200
GTTTCTCTTG TCTTGGGCAT CAAGANTAGT TCCAATTTTT TGGGCCGGGG CAGGGTGG 1258

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	CACAATATAT GAAATAGTAC CCTCTAAAAA AGAGAAAAAA AAAATCAGGC GGTCAAACCTT	60
10	AGAGCAACAT TGTCTTATTA AAGCATAGTT TATTTCACTA GAAAAAATTT AATATCAAGG	120
	ACTATTACAT ACTTCATTAC TAGGAAGTTC TTTTAAAAAT GACACTTAAA ACAATCACTG	180
15	AAAACCTGAT CCACATCACA CCCTGTTTAT TTTCCCTTAAA CATCTTGGAA GCCTAAGCTT	240
	CTGAGAATCA TGTGGCAAGT GTGATGGGCA GTAAAATACC AGAGAAGATG TTTAGTAGCA	300
	ATTAAAGGCT GTTGCACCT TTAAGGACCA GCTGGGCTGT AGTGATTCCCT GGGGCCAGAG	360
20	TGGCATTATG TTTTACAAA ATAATGACAT ATGTCACATG TTGTCATGTT TGTTCGCTTG	420
	TTGAATTTTT GAACAGCCAG TTGACCAATC ATAGAAAGTA TTACTTTCTT TCATATGGTT	480
25	TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG AATATCTATG GCCACAGCAG CATACCAGTT	540
	TCCATCCTAA TAGGAATGAA ATTAATTTTG TATCTACTGA TAACAGAATC TGGGTCACAT	600
	GAAAAAAAT CATTTTATCC GTCTTTTAAG TATATGTTTA AAATAATAAT TTATGTGTCT	660
30	GCATATTGCA GAACAGCTCT GAGAGCAACA GTTTCCCATT AACTCTTTCT GACCAATAGT	720
	GCTGGCACCG TTGCTTCCTC TTTGGGAAGA GGAAAGGGTG TGTGAACATG GCTAACAATC	780
35	TTCAAATACC CAAATTGTGA TAGCATAAAT AAAGTATTTA TTTTATGCCT CAGTATATTA	840
	TTATTTAATT TTTTAGGTAA TGCCTATCTC TTGGTCTATT AAGGAAAGAA GCAATCAGTA	900
	GAGAATTCAG GATAGTTTTG TTTAAATTCT TGCAGATTAC ATGTTTTTAC AGTGGCCTGC	960
40	TATTGAGGAA AGGTATTCTT CYATACAAC TGTTTTAACC TTTGAGAACA TTGACAGAAA	1020
	TTATGCAATG GTTGTGTGAG ATACGGACTT GATGGTGCTG TTTAATCAGT TTGCTTCCAA	1080
45	AGTGGCCTAC TCAAGAGGCC CTAAGACTGG TAGAAATTAA AAGGATTTCA AAAACTTTCT	1140
	ATTCTTTCTT TAAACCTACC AGCAAAC TAGTGTGATA GCAATGAATG GTATGATGAA	1200
	GAAAGTTTGA CCAAATTTGT TTTTGTGTG TTGTTGTGT TTTGAATTTG AAATCATCTT	1260
50	TATTCCTTTT AAGAATGTTT ATGTATGAGT GTGAAGATGC TAGCGAACCT ATGCTCAGAT	1320
	ATTCATCGTA AGTCTCCCTT CACCTGTTAC AGAGTTTCAG ATCGGTCAC TATAGTATGT	1380
55	ATTTCTTTAG TAAGAATGTG TTAATAATTAC AATGATCTTT TAAAAAGATG ATGCAGTTCT	1440
	GTATTTATTG TGCTGTGTCT GGTCTAAGT GGAGCCAATT AAACAAGTTT CATATGTATT	1500
	TTCCAGTGT TGAATCTCAC ACACGTACT TTGAAAATTT CCTTCCATCC TGAATAACGA	1560
60	ATAGAAGAGG CCATATATAT TGCCTCCTTA TCCTTGAGAT TTCCTACCT TTATGTTAAA	1620

AGTTGTGTAT AATTGTTAAA ATCTGTGAAA GAATAAAAAG TGGATTTAA. TTAAAAAAA 1680
AAAAAAA AAA 1693

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(2) INFORMATION FOR SEQ ID NO: 222:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

20

ACGCGTGGGT CGACCCACGC GTCCGCGACN TGGCGTGGTG GGAAGGGAG AAGGATTTGT 60

AAACCCCGGA GCGAGGTTCT GCTTACCCGA GGCCGCTGCT GTGCGGAGAC CCCCAGGTGA 120

AGCCACCGTC ATCATGTCTG ACCAGGAGGC AAAACCTTCA ACTGAGGACT TGGGGGATAA 180

25

GAAGGAAGGT GAATATATTA AACTCAAAGT CATTGGACAG GATAGCAGTG AGATTCACCT 240

CAAAGTGAAA ATGACAACAC ATCTCAAGAA ACTCAAAGAA TCATACTGTC AAAGACAGGG 300

30

TGTTCCAATG AATTCACCTCA GGTTCCTCTT TGAGGGTCAG AGAATTGCTG ATAATCATAC 360

TCCAAAAGAA CTGGGAATGG AGGAAGAAGA TGTGATTGAA GTTATCAGG AACAAACGGG 420

GGGTCATTCA ACAGTTTAGA TATCTTTTTT ATTTTTCCTC TTTCCCTCA ATCCTTTTTT 480

35

ATTTTAAAA ATAGTCTCTT TGTAAATGTG TGTTCAAAC GGAATTGAAA ACTGGCACCC 540

CATCTCTTTG AACATCTGG TAATTTGAAT TCTAGTGCTC ATTATTCATT ATTGTTTGT 600

40

TTCAATTGTG TGATTTTGG TGATCAAGCC TCAGTCCCCT TCATATTACC CTCTCCTTTT 660

TAAAAATTAC GTGTGCACAG AGAGGTCACC TTTTTCAGGA CATTGCATTT TCAGGCTTGT 720

GGTGATAAAT AAGATCGACC AATGCAAGTG TTCATAATGA CTTTCCAATT GGCCCTGATG 780

45

TTCTAGCATG TGATTACTTC ACTCTGGAC TGTGACTTTC AGTGGGAGAT GGAAGTTTTT 840

CAGAGAACTG AACTGTGGAA AAATGACCTT TCCTTAACTT GAAGCTACTT TTAAATTTG 900

50

AGGGTCTGGA CCAAAGAAG AGGAATATCA GGTGAAAGTC AAGATGACAG ATAAGGTGAG 960

AGTAATGACT AACTCCAAAG ATGGCTTCAC TGAAGAAAAG GCATTTTAAG ATTTTAAAA 1020

AATCTGTGCA GAAGATCCCA GAAAAGTTCT AATTTTCATT AGCAATTAAT AAAGCTATAC 1080

55

ATGCAGAAAT GAATACAACA GAACACTGCT CTTTTTGATT TTATTTGTAC TTTTGGCCT 1140

GGGATATGGG TTTTAAATGG ACATTGTCTG TACCAGCTTC ATTAAATAA ACAATA 1196

60

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- 5 - (A) LENGTH: 1791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

10 TCAGGGAGGT GGCAGGAAAG GCTTGAACA GCTGCCGAG TGACGGAGCG GCGGCCCCGC 60
CCGGTTGCGC TGGAGGTGGA AGCTTCCAGG TAGCGGCCCG CAGAGCCTGA CCCAGGCTCT 120
15 GGACATCCTG AGCCCAAGTC CCCACACTC AGTGCACTGA TGAGTGGGA AGTGAAGGTG 180
ACAGGGCAGA ACCAGGAGCA ATTTCTGCTC CTAGCCAAGT CGGCCAAGGG GGCAGCGCTG 240
20 GCCACACTCA TCCATCAGGT GCTGGAGGCC CCTGGTGTCT ACGTGTCTGG AGAACTGCTG 300
GACATGCCCA ATGTTAGAGA GCTGGCTGAG AGTGACTTTG CCTCTACCTT CCGGCTGCTC 360
ACAGTGTCTG CTTATGGGAC ATACGCTGAC TACTTAGCTG AAGCCCGGAA TCTTCTCCA 420
25 CTAACAGAGG CTCAGAAGAA TAAGCTTGA CACCTCTCAG TTGTACCCCT GGCTGCTAAA 480
GTAAAGTGTA TCCCATATGC AGTGTGCTG GAGGTCTTGC CCTGCGTAAT GTGCGGCAGC 540
30 TGGAAGACCT TGTGATTGAG GCTGTGTATG CTGACGTGCT TCGTGGCTCC CTGGACCAGC 600
GCAACCAGCG GCTCGAGGTT GACTACAGCA TCGGGCGGGA CATCCAGCGC CAGGACCTCA 660
GTGCCATTGC CCGAACCCTG CAGGAATGGT GTGTGGGCTG TRAGGTCTGT CTGTCAGGCA 720
35 TTGAGGAGCA GGTGAGCCGT GCCAACCAAC ACAAGGAGCA GCAGCTGGGC CTGAAGCAGC 780
AGATTGAGAG TGAGGTTGCC AACCTTAAAA AAACCATTAA AGTTACGACG GCAGCAGCAG 840
40 CCGCAGCCAC ATCTCAGGAC CCTGAGCAAC ACCTGACTGA GCTGAGGGAA CCAGCTCCTG 900
GCACCAACCA GCGCCASCCA GCAAGAAAGC CTCAAAGGGC AAGGGGCTCC GAGGGAGCGC 960
CAAGATTGGG TCCAAGTCGA ATTGAAAGRA CTGTCGTTTC CTCCCTGGGG ATGTGGGGTC 1020
45 CCAGCTGCCT GCCTGCCTCT TAGGAGTCCT CAGAGAGCCT TCTGTGCCCC TGGCCAGCTG 1080
ATAATCCTAG GTTCATGACC CTTACCTCC CCTAACCCCA AACATAGATC ACACCTTCTC 1140
50 TAGGGAGGAG KCAAATGTAG GTCATGTTTT TGTGTTGTTT TTCTGTTTTT TGTGACTTCA 1200
TGTGTTCCAT TGCTCCCCGC TGCCATGCTC TCTCCCTTGT TTCCTTAAGA GCTCAGCATC 1260
TGTCCCTGTT CATTACATGT CATTGAGTAG GTGGGTAGCC CTGATGGGGG TCGCTCTGTC 1320
55 TGGAGCATAA CCCACAGGCG TTTTCTCTGC CACCCCATCC CTGCATGCCT GATCCCCAGT 1380
TCCTATACCC TACCCCTGAC CTATTGAGCA GCCTCTGAAG AGCCATAGGG CCCCCACCTT 1440
60 TACTCACACC CTGAGAATTC TGGGAGCCAG TCTGCCATGC CAGGAGTCAC TGGACATGTT 1500

CATCCTAGAA TCCTGTCACA CTACAGTCAT TTCTTTTCCT CTCTCTGGCC CTGGGTCTC 1560
 5 GGAATGCTG CTGCTTCAAC CCCAGAGCCT AAGAATGGCA GCCGTTTCTT AACATGTTGA 1620
 GAGATGATTC TTTCTTGGCC CTGGCCATCT CGGGAAGCTT GATGGCAATC CTGGAAGGGT 1680
 TTAATCTCCT TTTGTGAGTT TGGTGGGGAA GGAAGGGTA TATAGATTGT ATTAAAAAA 1740
 10 AAAAGGTATA TATGCATATA TCTATATATA ATATGACGCA GAAATAAATC T 1791

15 (2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2517 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

25 AACTAGTGG ATCCAAAGAA TTCGGCACAG CGGCACAGCA TTGTGAGCT TTTCTGTGTG 60
 TGTGGGGCCC TCAAGCGAGC TCGACTGGTC CATCCTGGGG TAGCGASGTG GTGTTTGTGA 120
 AAAAGGACGA TGCCATCACC GCATAYAAGA AGTACAACAA CCGGTGTCTG GACGGGCAGC 180
 30 CGATGAAGTG CAACCTTCAC ATGAATGGGA ATGTTATCAC CTCAGACCAG CCCATCCTGC 240
 TCGGGCTGAG TGACAGCCCA TCAATGAAAA AGGAGAGCGA GCTGCCTCGC AGGGTGAAC 300
 35 CTGCCTCCTC CTCCAACCCC CCTGCCGAAG TGGACCCTGA CACCATCCTG AAGGCACTCT 360
 -----TCAAGTCTC AGGGGCTCT KTGACGAGC AGCCCAAGCA WTTCAAAATC AAGCTTTGAG----- 420
 CAGGGGAGTR AGGCAGCCAG AAGTGGGGGC AGAGGAGGGT GGCTCTGTTT CCCCAAGGCA 480
 40 AAGCTTATGA CCAATGGGCC ATCGGACTGG AGACCCTGA TTGTGGGAAG GGTGCCAGG 540
 GATAAAGAGC TTCCTCACTG GATGGGACCC GCCTTTCTGT GTTGTGTTCT GCCCTGTGCT 600
 45 CTTCTCTCTA CGTTAACGTT TCCTGTAGTA TGTTCCTTCA TCTCATCGCC AAGGTAGGCT 660
 TGTGTTTMTM AGTGTGTGCC TCCCCGAGCC TCAGCCCCAA GCTGATTTCT TATCTGAAA 720
 TGGTACACTG AATCTCTTGG GTGGCTTTCT TGTGGCCCCA TGGGATGCAG CGTGGGGGCT 780
 50 GTCTGAAGGA CCCTGCTTTT TCCAGGGGCC GAGGGGCTGC CTTTCCTTTG TGTGTATTAA 840
 GCTTTTCAAA CAATGGAGGG GATGGAGAGC CCTGGTGTCC TGACGGGAGC CAGGTGCGCC 900
 55 TGAGAGCTGT GCCGCTCCTC TGTCTTGTC A GTGGAGGTGC CTGGGTGGGG AGCAGGTCTC 960
 AGGCCTCTTG TCCTCTCCCC AGTGGCTCCA GGCCTCACTA GTGGCAAGGG CAGGATGAGG 1020
 CTGCACCGCT GGGAAGAGTC TATCTAAGCT CTTGGCTTGG AGTCCCGTGT CGTCTCCRCC 1080
 60

	CAGAGGAAGT TCTCCAGAGT TCACCTTTCC CTTTTCCTTG AGTGTGCTG AATGCCCCAC	1140
	CCCAGCTCTC TTTCCCTTCT GGGTGTCTTT GCTGGGAGGG GGCTGTGTTG TGAGCCCTCC	1200
5	CGGTTCTCAC CTCGCTGGC ACTTAACCAC ACCCTGGTTT TGTGTAGCCG CCAGCTCTCT	1260
	TCTGGTTGGG CCTTTGAAAG GCTCAGCCTC CCATTGTGCA GTGCTTGGGT TTGGAGCTTA	1320
10	TTTGAATGGA AGAGGTCAGT TTGTTCTGG CTCTCCATTT CTGGCCTCAG TTGTCTACAG	1380
	GACAGTGGTC AGGGATGCCT GGAGGCATAT ATCCAGCTGC CACCAAGGGG CACTGTTTGT	1440
	TCCACTTAT GTGAGTGACC CCATCCATCC ATGACCAGAG GATTATTTTC CTGCCTTGGC	1500
15	AGAGGAGGAG GAGTCAAGGG AGCAGGGCAG CTCTACCAGG CAAGGTGTTT CCCCAGCATA	1560
	GGCGCAGACA GTTGGGACGA AACTTCAGAG CCCAGGCAGT CCCTGAATGA CCAGGCCAGT	1620
20	GTTGTCACTG AGTGGTCCCC TGCTGGTTGG GAGTGAAGAG AATCCAGGCT GGCAGAGCTG	1680
	GAGCCAGTTG GGGAGCACGG TTCTGGGAGC TCTGCAAAAT CAGTAGCAAG TGCTGGAAAA	1740
	GGCACATGCC GAAGATACTC AAGAGCTCCC AAGATTTGCT TGAGGCTAGC CCAGTGAAAA	1800
25	AAACCAGAGA CTCATGTTTC CAGGGGTCAG TCTGTCAGGC AGGAAGGACC CAGGATTTGA	1860
	ACCCAGCTTC AGTGTGCAGG CTCTGAGGCT GCCCAGGACG GGAAAGTCCA AGGAAGGGGC	1920
30	CTGGTGGTGC TCCACTTGCA GTTCTTTAAA GAATGCTGCT TTTTATTCTC CTAACCTTTT	1980
	CAAGTGGGTG CAGACTTCTC GTTAGCAGCT GGAAGACATT CCTCCACAC TTTTCCCTTC	2040
	CTGGCCCCAAG AGAGCATCCA GAAGGCAGTA GGACCTGGTT TTTCAGGTAC TGGGAGCCGG	2100
35	GGGCTCACTG CTTGCACTGT GCTTAGGGTA GGGATGGTAA ATATCCTCCC TGCATGGCTT	2160
	TATCCTCCCT CTCATCCCAA AGCAGGTATC TTCTGGTTGT CACAGAGTTT CATTGAGTCC	2220
40	AGCTGCAGCC ACGTGGCCAT CTGGAGCTGG TGCTATAGGT GACCATCTGG TACATTGAGG	2280
	GGACCTGTTT GCCTCCTCCA CTCTATAAGC AGTCATCTTG GGAGACCGGG AGGAGAAGGT	2340
	GGTGGGCTAG TCCTGTGTCC TCCTCCACTT CCCATGCCTC TATGTTACCC ATCTGTGTCT	2400
45	CCTGTGCAGA AGGAGAGGAA GGGGCATTAA GAGATGAAGG GTGATTATGT ATTACTTATC	2460
	CATTTCTGAA TAAACATTTG TTATTCCTAA AAAAAAAAAA AAAAAACTCG AGGGGGG	2517

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(2) INFORMATION FOR SEQ ID NO: 225:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

	TTGTANCTAA TCGAGGATG ATTCTAATGA CAGAGTCTTT CAACACTTTG CACATGATGT	60
5	ATCACGAAGC TACAGCTTGC CATGTGACTG GAGATTTAGT AGAACTTCTG TCAATATTTT	120
	TTTCGGTTTT GAAGTCTACA CGCCCTTATC TTCAGAGAAA AGATGTGAAA CAAGCATTAA	180
	TCCAGTGGCA GGAGCGAATT GAATTTGCCC ATAAACTGTT AACTCTTCTT AATTCCTATA	240
10	GTCCTCCAGA ACTTAGAAAT GCCTGTATAG ATGTCCTCAA GGAACITGTA CTMTTGAGTC	300
	CCCATGATTT TYTTCATACT CTGGTTCCCT TTCTACAACA CAACCATTGT ACTTACCATC	360
15	ACAGTAATAT ACCAATGTCT CTTGGACCTT ATTTCCCTTG TCRAGAAAAT ATCAAGCTAA	420
	TAGGAGGGAA AAGCAATATT CGGCCTCCGC GCCCTGAACT CAATATGTGC CTCTTGCCCA	480
	CAATGGTGGA AACCAGTAAG GGCAAAGATG ACGTTTATGA TCGTATGCTG CTAGACTACT	540
20	TCPTTCTTA TCATCAGTTC ATCCATCTAT TATGCCGAGT TGCAATCAAC TGTGAAAAAT	600
	TTACTGAAAC ATTAGTTAAG CTGAGTGTC TAGTTGCCTA TGAAGGTTTG CCACTTCATC	660
	TTGCACTGTT CCCCAACTT TGGACTGAGC TATGCCAGAC TCAGTCTGCT ATGTCAAAAA	720
25	ACTGCATCAA GCTTTTGTGT GAAGATCCTG TTTCGCAGA ATATATTAAA TGTATCCTAA	780
	TGGATGAAAG AACTTTTTTA AACAACAACA TTGTCTACAC GTTCATGACA CATTTCTTC	840
30	TAAAGGTTCA AAGTCAAGTG TTTTCTGAAG CAAACTGTGC CAATTTGATC AGCACTCTTA	900
	TTACAACTT GATAAGCCAG TATCAGAACC TACAGTCTGA TTTCTCCAAC CGAGTTGAAA	960
35	TTTCCAAAGC AAGTGCTTCT TTAAATGGGG ACCTGAGGGC ACTCGCTTTG CTCTGTGACG	1020
	TACACACTCC CAAACAGTTA AACCCAGCTC TAATTCCAAC TCTGCAAGAG CTTTAAAGCA	1080
<hr/>		
	AATGCAGGAC TTGTCTGCAA CAGAGAACT CACTCCAAGA GCAAGAAGCC AAAGAAAGAA	1140
40	AAACTAAAGA TGATGAAGGA GCAACTCCCA TTAAGAGGCG GCGTGTAGC AGTGATGAGG	1200
	AGCACACTGT AGACAGCTGC ATCAGTGACA TGAAAACAGA AACCAGGGAG GTCCTGACCC	1260
45	CAACGAGCAC TTCTGACAAT GAGACCAGAG ACTCCTCAAT TATTGATCCA GGAAGTGGC	1320
	AAGATCTTCC TTCCCTGAA AATAGTCTG TTAAGAATA CCGAATGGAA GTTCCATCTT	1380
	CGTTTTGAGA AGACATGTCA AATATCAGGT CACAGCATGC AGAAGAACAG TCCAACAATG	1440
50	GTAGATATGA CGATTGTAAA GAATTTAAAG ACCTCCACTG TTCCAAGGAT TCTACCCTAG	1500
	CCGAGGAAGA ATCTGAGTTC CCTTCTACTT CTATCTCTGC AGTTCTGTCT GACTTAGCTG	1560
55	ACTTGAGAAG CTGTGATGGC CAAGCTTTGC CCTCCAGGA CCCTGAGGTT GCTTTATCTC	1620
	TCAGTTGTGG CCATTCCAGA GGAATCTTTA GTCATATGCA GCAACATGAC ATTTTAGATA	1680
	CCCTGTGTAG GACCATTGAA TCTACAATCC ATGTCGTAC AAGGGATATC TGGCAAAGGA	1740
60	AACCAAGCTG CTTCTTGACA TTAGGTGTAG CATGTCTACT TTTAAGTCCC TCACCCCAA	1800

5 CCCCCATGCT GTTGTATATA GTTTTGCTTA TTTGTTTTTG TGCTTCAGTT TGTCCAGTGC 1860
 TCTCTGCTTG AATGGCAAGA TAGATTATA GGCTTAATTC TTGGTCAGGC AGAACTCCAG 1920
 ATGAAAAAAA CTTGCATCTT CAGTATACTT CCTAAAGGGC AATCAGATAA TGGATATGTT 1980
 TTATGTAATT AAGAGTTCAC TTTAGTGGCT TTCATTTAAT ATGGCTGTCT GGGAAGAACA 2040
 10 GGGTTGCCTA GCCCTGTACA ATGTAATTTA AACTTACAGC ATTTTTACTG TGTATGATAT 2100
 GGTGTCCTCT GTGCCAGTTT TGTACCTTAT AGAGGCAGAT TGCCCTCCGAT CGCTGTGGTT 2160
 CTTATTATCA AAATTAAGTT TACTTGTATA CGGAACAACC ACAAGAAATT TGATTCTGTA 2220
 15 AAGAATCCTC TTTAGCTGTG GCCTGGCAGT ATATAAATGG TGCTTTATTT AACAGAATAC 2280
 CTGTGGAGGA AATAAGCAC ACTTGATGTA AAAATAATTG TTTTATTTTT ATTGACATGA 2340
 20 CTGATTGATT GCTATTCTGT GCACTNAATT AAAGTGATTG TGATGACTTA AAAAAAAAAA 2400
 AAAAAAAAAA AAAAAAAAAA AAAA 2424

25

(2) INFORMATION FOR SEQ ID NO: 226:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ATATAGGACG GATAATCTGT TTACATTCTG TTCTTCTCGA TGCACTCACA AGCGGGTAAC 60
 TAGGTGACAA GAAAACAAAG ATCTTATTCA AAAGAGGTCT TACAGCAACC CAACGTCTCA 120
 40 TCTTCCATA GTAAAGATGA CGGCGCCTTG AGGTAAGCTA CAGGCAACAC CACTTCCGCG 180
 TTTCTCTTGC GCCCTGGTCC AAGATGGCGG ATGAAGCCAC GCGACGTGTT GTGTCTGAGA 240
 45 TCCCGGTGCT GAAGACTAAC GCCGGACCCC GAGATCGTGA GTTGTGGGTG CAGCGACTGA 300
 AGGAGGAATA TCAGTCCCTT ATCCGGTATG TGGAGAACAA CAAGAATGCT GACAACGATT 360
 GGTTCGACT GGAGTCCAAC AAGGAAGGAA CTCGGTGGTT TGGAAAATGC TGGTATATCC 420
 50 ATGACCTCCT GAAATATGAG TTTGACATCG AGTTTGACAT TCCTATCACA TATCCTACTA 480
 CTGCCCCAGA AATTGCAGTT CCTGAGCTGG ATGGAAAGAC AGCAAAGATG TACAGGGGTG 540
 55 GCAAATATG CCTGACGGAT CATTTCAAAC CTTTGTGGGC CAGGAATGTG CCCAAATTG 600
 GACTAGCTCA TCTCATGGCT CTGGGGCTGG GTCCATGGCT GGCAGTGGAA ATCCCTGATC 660
 TGATTGAGAA GGGCGTCATC CAACACAAAG AGAAATGCAA CCAATGAAGA ATCAAGCCAC 720
 60

5 TGAGGCAGGG CAGAGGGACC TTTGATAGGC TACGATACTA TTTTCCTGTG CATCACACTT 780
 AACTCATCTA ACTGCTTCCC CGGACACCCT CCACCTCTAG TTGTTACTAA GTAGCTGCAG 840
 TAGGCATTGC TGGGGAAGAA ACAAACACAC ACCAAACAGT ACTGCTACTT AGTTTCTAAG 900
 GCTGCACAGG GAAGGGAAAG ACTGGGCTTT GGACAATCTA GAGGTAATTT ATATCCGCCC 960
 10 CCAGGTGGAG CAACATGCGA TTCTGGAGGC ACGGGGGTAA CTGAAAGTGA GTACATATAG 1020
 TCTTTCTGGT TTCTGGAGAT AACCCATCAA TAAAAGCTGC TTCCTCTGGG TAAAAAAAAG 1080

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(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

TTGCATTAC AATTACTGGG AGGCAGGCAG GGCAGTTGC ATGCTGGGGG TGGCTGCATG 60
 GSCTGCCASC TCTCCTGGGT TTGAAGGATG CGGTACASCT GCTTCAGCTG AGCAACGATG 120
 30 TTATCCTTGA TGTCTGGGGT TGAGATCTGC AGGCGGACAC TGCCACTATC AAAGGATCGT 180
 GTGAAATCAC CAGAAAACAT CTCGTAGATC ATCCGAGCCA CTACTGGAAT GACCTGAACC 240
 35 AAGATGAGTT TCCTTTCCAA TGGTTTCCCA TCTGGCCATT CTTCCCCAAA GCATAAGTAG 300
 ATCTCAAACG GTGGCTGCTT CTCTATCTGT CCTTTCTGGT GGGCAATGAG ATCGCTAAGG 360

AATGTTTCCA GACAAATAG CTTGACCTTC TTTTGTCTCT CAATCAGGTT GGGAGCAACA 420
 40 AGTGATGGGG CACATGGCCC AGACCAGTAC ACCTTGCACT GGCACAGYCT GATGGCATAA 480
 ATGGCATGAC CGCTGACCTC CAGGATCAGT CCTCTGTCCA TGACGTCCAG CAGCTTGCTA 540
 GTGAACAGCT TCTGCTTCTC ATTGGTAATA TGCTCAGGAC CTGGGAATTT GACCTGCTCC 600
 45 AGNCTGACGG GACCAAAGAG CTCCTCCTGG TCAGGCATGG GACCCAGGTC CCCATAGAAG 660
 AGTCGGCAGC CCTGAGGGTT GCTCACGGTC ATGGTCCTGC CCGTACTCCT TCCCACGGTA 720
 50 CTGAAACTTG ATGTCCAGGT CAGTCATTGG GAGAGAGCTG ATCCACAGTT CTGGAGAGCT 780
 ATAGAAGGRC TGTATAGGTG CCTGGGGWAC TTCCATCTCC AGGGGTCAG TTTTGGGCCA 840
 CACTGCCTCC GGSCTGCAGT TGCCCACACT GCAATTGCCC AACTGGCTG GCGCCATGGG 900
 55 AGAACCATTG ATGTTTCAGGA AGGGGAAGGT GTCCTGGATG GGAACATGGT GCTGCGACTG 960
 ATCCAGCTCA TCTTCCTCAT CTTCTTCATC CACATCATTA TCCTTCTCAT CCCAGGGAGC 1020
 60 AGACCCTGTG GATCCTGGGT TAATGATCGA SCCCTGGGGC TGAGGGATGT CACACACTTG 1080

5 ATATATCTTC ACTGGGTTCA TGGGCACCTC CCTTGGTGCC ATCCATACAT CCAGGTTGAA 1140
 TTCTCTGCTC TTATTGAGAG CACAGCGCAG CTGGGCCTTC CATTAGCTG GGTCAGGGTC 1200
 ATCCACCCCT TCCTGGTACT TCCCTGTCTC TACAGCCCAG GCCTTAAAAA TGGTATTTTC 1260
 CTCTTCTTGT TGAGGGCTAT GCCGGGTGGC ATGTTTCCAG GGAATCTGGA AGCGTTTAGA 1320
 10 GTCCCTGTGT AGCCAG 1336

15 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

25 TCAGCTGGTC CCTTCCTTGT GTCCTGGGGG ACCTGCTGGC GGCCTCTTCC TGGGAGCCAT 60
 GACCTCAGAC CCCACCCACA CTCCAGATCG AGACCCCTGC CTCCCCCGG CAAATGTCCT 120
 CCCGCTGCCT TGCAGCCTGC ACTTTCACACA TGCTCACCCC CAGCACAGTC CCACTGGCCC 180
 30 CTCAMCTCCC CTTCCCTGAG CTCCTTCCCA AGGACTCCTG GTCACTGCCT GCTGTGCAKT 240
 CAGAGGCCCA GGGTCCAGCA GCCCGSGGG AACGGGTGCT GCCTSTTCCT CCAGTTAGCT 300
 35 CCAGYTCAGG TCTGAGACCC GTGYTGAGTA AAGGTCTGAG CAMCGACCGT GCCCTCTGCC 360
 CAGGGCTGGG TCCTGAGCAG CTGGTTTTCC TGCAGGAAGG TTGGAGCAAG CAAAGTCCTT 420
 CTCTGCCCTC AGGGTCAGCT GCCCAGACTG GGGCGGATGC AGAGAGGCAG GTGGGCTGTG 480
 40 GCTGGACTGG TCCGGAGCTG GCTTCCTTAC CAGAAAAGCC TCAGCCTTCC TCTGGAAGCA 540
 TCCCCCGTTC TGGGCAAGGG GGAAGGGCTC CTTTAAGGGG TGTGCTTTCC CAGTGGGGAG 600
 45 CAGTCTGGCC CTGCCCCCTA CTAAAGCCTC TGCTCTCAGC ACTTTCCTCC AAGTCCTTGT 660
 AACTTGCTTG AAGGTGGGTT CTGGCTGCCA GCCAGTCCCT GGACAACTC TCCTGCCCCT 720
 TTTAAATTTC ACTCATTTTG TATAAACCCA GCAGGCTGGT GTTTACTTAG CCCTGTAGCT 780
 50 TTTTTCATTT TTTCTTTCCG TCTTCTTCTT TGAGTTCACG GTTCAATATT GCCTCCTCGC 840
 CCTGGTGAGG GGAGGTGCTG CTTTCTGCCC CCACCTGCCG GCTGGTTCCA GCAGCGCTGG 900
 55 NGCCCAGCTG GGGGGCCGGG ATGGGGGCTT CTCTCTCTGG GAGGGGTGCA GGTGCCCTCC 960
 CCAGGCTGGG AGGGTTCCTT CCCTAGCTCC CCATCTGCCC CCGCTGGTGA GAGTTGGGCT 1020
 TCTTGGTCTT GGAATCCCT GGCATTGGGA ACAGAGCATT TCCAGCATTT GTTGTGTGTTG 1080
 60

	TTTTACTCAC CTAACCCTTA GAAAATGAAT GTTAGAAGGT GCCTGCCGAG GCGGGACAGA	1140
	GTGTTTGCTC GCGCTGGAGA AGGCTCTGCT CAGCCCTGAG AGTCCCTTCC TGCCCCACCG	1200
5	ATACTGGCAC TTTAAAAAGG AAGCTGACCG CACAGTGTC AGACGAATTG GCCCCAGAA	1260
	GATGGGGAGT TCTGTCCTGC CCTTCTGTGT CTGCGTGACC TCACCCAGCC TAGGAGGGAG	1320
10	GTGCATTCAG GGTAGATTG CCTCTCATTC AAAGTCTGG GCCTTTGGGY GGAAAACAGC	1380
	CAGCTTTGGC GCTGTTGGGG AGACTCCTCC AGACCAGGAA CCCCAGAAGG AGACAGAGCC	1440
	TGCCACATCC TCCCACGCCA GGCCCTGGGC CAGGGTGATT GGA CTGAGAA TTTGGCCACA	1500
15	ACCAAATTGA TGCTGGCTGG AACCAGAGGC CAGAAAGCCT GGCTTGTCC CCATGTGGGA	1560
	GGCCTGTCT CAGCCCTCTT GTCCCTTGA GCTCAGTGAA TCCCACCAG GTGCCACAG	1620
20	CTCCTGGACT TCAAATTCTA TATATTGAGA GAGTTGGAGA GTATATCAGA GATATTTTTG	1680
	GAAAGGAGTT GGTCTATGCA ATGTCAGTTT GGAATCTTCT TGAAAGTTTA ATGTTTTTAT	1740
	TAGGAGATTT AAAGAAAATA AAGGTCTACA ATATCTTTAG GTTTTTTTTT TTTCTGTTT	1800
25	ACCGCACAAA CTGACCACAT GGCATGTCTA TCAGGATGGA GGGTGTCAT GTTCTCTCT	1860
	GTCTTTAGGG AGGTGATAAG GAGATGGSCG RAGGGGTGTT TTTTCTTTG ACTCCCCTCC	1920
30	TTTCTAACAG AATGTTGCCA CCACTGCTTG AGTGGGCTGT GTTGTTCCT CTGTCCCAGC	1980
	TTCTGTGTA GAAAATAACA TTGTTAGGGG AACTCAGGCT AGTGTGAGC TCTTGGTTTG	2040
	GGG	2043
35		

(2) INFORMATION FOR SEQ ID NO: 229:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

	TAAAAAGAAG CGGAGAATC TGGGCGTCGC TCTAGAGATC GATGGGCTAG AGGAGAAGCT	60
50	GTCCCAGTGT CGGAGAGACC TGGAGGCCGT GAACTCCAGA CTCCACAGCC GGGAGCTGAG	120
	CCCAGAGGCC AGGAGGTCCC TGGAGAAGGA GAAAACAGC CTAATGAACA AAGCCTCCAA	180
55	CTACGAGAAG GAACTGAAGT TTCTTCGGCA AGAGAACCGG AAGAACATGC TGCTCTCTGT	240
	GGCCATCTTT ATCCTCCTGA CGCTCGTCTA TGCCTACTGG ACCATGTGAG CCTGGCACTT	300
	CCCCACAACC AGCACAGGCT TCCACTTGGC CCCTTGGTCA GGATCAAGCA GGCACCTCAA	360
60	GCCTCAATAG GACCAAGGTG CTGGGGTGTT CCCCTCCCAA CCTAGTGTTT AAGCATGGCT	420

TCCTGGCGGC CCAGGCCTTG CCTCCCTGGC CTGCTGGGGG GTTCCGGGTC TCCAGAAGGA 480
CATGGTGCTG GTCCCTCCCT TAGCCCAAGG GAGAGGCAWT AAAGACACAA AGCTGGAAAT 540

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(2) INFORMATION FOR SEQ ID NO: 230:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

20

AATGTGAAA TATTAGAATA TTGTTACTAT TTGACCCAAC TCAAAATCTC CATGGGAAAA 60

TACCTGTCGA TACCCACAGT ATTGTGAAA ATAATCAGAT GCAGTATCAC AGCTGTGTCA 120

GA CTCTAGTA CCAGTTGGGC AATCAAGGCA CAGCTAAAAA TTGAAAACAA AGATCTGGAC 180

25

AACAAAACAG CCAAAGGTGG GGGTCAAGAA GCTCTGACGT GTACCTAGCT GTAGAATGCT 240

ATGCACACGT GCCAGGTGTA GTGTGCATAT CCAGGAAAAA CTGCAGAGAG CCCAGTCTT 300

30

CAMCTCTGGT TGACCATGAG CTCTGTGTAA GCAGGAAGTG AAGGCTAAGG CAGATTTAAG 360

CTCTGAAAGC ATTCCACAAC ATACACACAA ATCGTGCAAA GCATTAAGGA AATCTTGTTA 420

CTGCTAAGTG TTGCTGACCC AGGAACAA 448

35

(2) INFORMATION FOR SEQ ID NO: 231:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

50

GTATGCTGCC CCAAACCAAT ATGTGTGGCT GCCTTTWACC TGA CTCTCC AACATGTAGC 60

CCCAAGAGGA GGCCTCTAGA CTRAGGGAGG GGCTGGTGAC CCAGGTGTGG TGGGGCTGCA 120

TGARACTACC AGAGAGACAG ACATTCTGGA ACTCACCTG GGGGATCCAG TGGATCTGCC 180

55

TATGGTCTGG TCCACCCAG ACCTGTGAGA TGTTCCTCAT GAGGATGCAC TTGTGCTTCT 240

GCAAGTATTG CTGCAGCTTC ATAGTGA CTCCAGCAC CAGCAATACA GYTAGCTACC 300

TGTGGCCTTG GATCTCAGCC AGCATGGCTG GGAGAGGGAG CARCTGGGCA TGTACCCTAA 360

60

ATGCTGTTAC CAGGAAGGA CTCCAGAGT GAAGACAAGT AGGGACT 407

5 (2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

15 GTATTTGATT TCAGGCTGCT AAATGGGCTC ATTTAGCATT CATTCTTGA TGTAGACATT 60
AAAAAAAAA CTGAATAGCA TTCTTTCCAG GNTAACTAAT AAAGCAGACA TGCTAAGCCT 120
ATAAATACAT CAGCACTGCA GCACACGTTT AAGGTTGCCA CGGACAAGGA TCACACAATA 180
20 GAGAACTG TAGTTCGGTC TGCTCACAAG ACCCAGAACA TTGATCAGTT TTTGTTGTTG 240
GTTTATTATT TTTCTGTAA AAAATGTGA AAAGTTTGT TTAGCTAGAT GATATTTTAA 300
25 TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACACTT AACACACATA CCTTATGTTT 360
TGTTTGT TGTTTTACAC TCAGTATAAA TCAGGAGAAG TTAGCCAACC ATCTAGCATT 420
TAGAATCCTC TTTTTTATTG TCTCTAAGG ATATGGATGT TCCCATAACA GCAACAAAAC 480
30 AGCAACAAA ACATTTTATA AATATCACTT GATAGACTGT AAGCACCTGC TTAACCTTGT 540
GTNCCAAATA TTTAGTGTGT ATATATATAT ATATATACAC ACACACACAC ATATATATTC 600
35 AACAAATAA GCAAATATA ACATGCATTT CACATTTTGT CTTCCCTGT TACGATTTTA 660
ATAGCAGAAC TGTATGACAA GTTTAGGTGA TCCTAGCATA TGTTAAATTC AAATTAATGT 720
AAAACAGATT AACACAACA AAGAACTGT CTATTTGAGT GAAGTCATGC TTTCTATTAT 780
40 AATAACTTGG CTTCGGTTAT CCATCAAATG CACACTTATA CTGTTATCTG 830

45

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

55 CCAGAAGAAA GACCAATCTA GAATATGGAA CTCTAATCAC TTCTAGTATT TCAACTTCCT 60
AGCAGAAATG AACTTGGCCC TAGACCTAGG GGATAAGCAA TGTTCTTTAT GTAGCCAATG 120
60 CTACGGAAAC AAAAGAGGTG AAAGAGACCC TTTTATTATA CTTAATGTAC ATATATTGAC 180

	TTTTTGAGCA AGAATGCCAG AAATAGCCTT CATTTCTACC CTGCAAATA ATCCAGATCT	240
5	GCTTTCTAAA ATGRANTCAG TTTCTAAAGT GAAACATGCA ATATTTATGC TCTGACTGAC	300
	TCCTGAATTG GARGAGGAAG RACTTCTGTT TACAGAAAAC YGTATTGTTA TATATGTCAG	360
	GCTGTGTATT GTGACTATCA GCATTCTGGT GCAAATGAAC TTTTCTCCAT CATCGACTGT	420
10	GGAAAATTGA TACTTTTAAA GCATATTCTT CTATGAGCAC AGGTCCTCCT AGTGAAACTT	480
	AATTTGACAA AGGGTGTCAT ATGCTTTCCT AACCTGAWTT GTATTAACAT TCACAGAGCC	540
15	TACATTTTCT CATTAGGGTT RTGATGCTCA GTATCTTTCC AAGTGCCAGG CAGRGCTTNC	600
	CTTTTCTGAT CAAACATACC ATTTTGTGTA TTTCACAACT ATAGACAGTC ACTTCTGCAG	660
	TCCCAATTTA AAAATGCAGA ACTGCTTTAT CCAAGAATGC TGAAAAATAC TGTCTATCC	720
20	AGGTTTCCTA AACTATAAAA GCAGATTTTG CTMTTGMTTG TTAATCATAG GCATGGCCGA	780
	GCATTGTGGA TTAGCCTGAG GCTTAAAATC AGATGCATGT CTGGTAAGAT GACCACTGTC	840
25	TCACTATCAA GAGCCTGCAG AGCCATTTTC CAGACCTGTG ATTGCCCAGA ACACATAGTC	900
	CCCACGTTTC TAATTTGGAG CAAATCTAAA AG	932

30

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 2786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

40

TTAGCAGGGT GAGCTGTTAA AACAGCACAC ATCTCTCATC CCTCTTCCT TTATTCCTCC 60

CTGGGTTTCA GAAAGGAAGG ATATATGGGG ACCACCTCCC CCTTCTTTGA TCCCAGCATC 120

45

TCAGTCCCCC TCCCAACCCT CCATATGGCT CTCAATGGTG CTCACTTGCT TGGAAGCAGG 180

CTCCCAATAG GGAGGGGSCT GCCCTCTACA GTCTCTTTGA CTGTAAGACA GGGCTCTGTA 240

50

TCAGTGAGAC GATGAGAAAA GTCCCAGGCT AATGGCAGAA ATTTGCACTT TGAACATGTG 300

TGTTTTTGTG TTGTGGAACC TGAGATTCCT TATTTATTAA CAGGAAGTCT GATTTTTTTT 360

TTTTGGAGTC TTTGTTGCTA TATTTTGTGG GGCTGGGAGA GAGAGATTAG ATTATTTTGA 420

55

CATGGGATCC CTTCATAAC AGGTACTTTG AAGGCAAGAC ATAGGGTTGA AGAAGCACAA 480

CCAGCCTCTG AAATCATAGC TCTCCAGTGG CTTTTAAAGA AAGCTGGTCC TCAGCACTAA 540

60

CAAAATCACT ACAATAGCCT AGTGCTTTTT TGGAAGCCTT TTTAGGGAAG AATGTTAGGT 600

	TCATGGTAAC TAGTATGCTC TTTGAGATTT TTACAGTGTT GAAACTTAAG AATTTTGAGA	660
	GGGTGAGGAG GGTGTTTCAG AATCTAAATT ACAGATAGAT GATTGTTTCT TGTGAATTTG	720
5	TTTCTTTTCC TTTTTFITG TCCCTACCAT TTCCTTACAT TTCCCTTGGG GCCCATCTCT	780
	GGCTCCTTGC TTTTGTTC TTGCTTTGCT TTATCAGTTC ATTCCAGCTC CCTGTTAGTG	840
10	AAGGACACTG CTGTTAGTGA AGGAACAAAG TCTATGAGTC CTAAAATTTT AAGTCAAAGA	900
	AAACTGCTCT GTTTCCCTT TAGTAACACT TCTGAAGAGG AAAAATTCA ATAGCCAAAG	960
	TTAATAATCC TATATAATAA TTGCTTTGGC TTTCACCTAA AATTCTGGGC ATCACAATTT	1020
15	CCTTGGGATA GAGGTTGTGT TGGGAATAG ATTGCTTATT GCTGTTCACT GGAGAGAAAA	1080
	GGTAGTGTTT TTGTACAAGG TCATACCGCC AGAAGCCCCA AATCCTATTT TGGCTCATCT	1140
20	TCAGGTAAAG AGTAATTCCT ATCCTGTGTG CCTCAGAAGC TAGAATCGAA GGCTTACCCT	1200
	ATTCATTGTT TATTGTCAGA AATGCATGAT GGCTCTTGGG AAGAATGACG TTTTGCTGGA	1260
	AAAAAAAAA AGAACAGTTT GTGTTTCACA AACATGGCTT ATCAATTTTT TCAAAGAATT	1320
25	CTTTTTTCCC AAAAAGAGGA GTAACAAAAT GTCATTTCTG AAAGAGGCTT ACTTTATACC	1380
	AACTAGTGTC AGCATTTGGG ATGCCAGGGA ACAGAGAGTG AGACACCTAC AATCACCAGT	1440
30	CTCAAATGCG CTATTGTTTC TTTCAGAGT GTTGCAGATT TGCCATTTCT CCATAATATG	1500
	GGGATAGAAA ATGGAATAAA GATAGAAGGG ATGTAGAATA TGCTTTCTCG CCAACATGGT	1560
	TTGGAGTCGA CTTTGGTATA TTGACTAGAT TTGAAAATAC AAGATTGATT AGATGAATCT	1620
35	ACAAAAAAGT TGTCTCTCTC TCAGGTCCCT TTTACACTTT TTGACTAACT AGCATCTATA	1680
	TTCCACACTT AGCTTTTTTG TCACACTTAT CCTTGTCTC CGTAAATTTT AATTGCAGTG	1740
40	GTTAGTCATC AGATATTTTA GCCACCTACA CAAAAGCAAA CTGCATTTTT AAAAATCTTT	1800
	CTGAGATGGG AGAAAATGTA TTCTCCTTTC CTATACCGCT CTCCCAACAA AAAAACAAT	1860
	AGTTAGTTCT ACTAATTAGA AACTTGCTGT ACTTTTTCTT TTCTTTTAGG GGTCAGGAC	1920
45	CCTCTTTATA GCTACCATT GCCTACAATA AATTATTGCA GCAGTTTGCA ATACTAAAAT	1980
	ATTTTTTATA GACTTTATAT TTTTCCTTTT GATAAAGGGA TGCTGCATAG TAGAGTTGGT	2040
50	GTAATTAAAC TATCTCAGCC GTTTCCTTGC TTTCCCTTCT GCTCCATATG CCTCATGTG	2100
	CTTCCAGGGA GCTCTTTTAA TCTTAAAGTT CTACATTTCA TGCTCTTAGT CAAATTCTGT	2160
	TACCTTTTAA ATAACCTCTC CCACTGCATA TTTCCATCTT GAATTGGTGG TTCTAAATTC	2220
55	TGAAACTGTA GTTGAGATAC AGCTATTTAA TATTTCTGGG AGATGTGCAT CCCTCTTCTT	2280
	KGTGGTTGCC CAAGGTTGTT TTGCGTAACT GAGACTCCTT GATATGCTTC AGAGAATTTA	2340
60	GGCAAACACT GGCCATGGCC GTGGGAGTAC TGGGAGTAAA ATAAAAATAT CGAGGTATAG	2400

ACTAGCATCC ACATAGAGCA CTTGAACCTC CTTTGTACCT GTTTGGGGAA AAAGTATAAT 2460
 GAGTGTACTA CCAATCTAAC TAAGATTATT ATAGTCTGGT TGTMTGAAAT ACCATTTTTT 2520
 5 TCTCCTTTTG TGTMTTCCC ACTTTCCAAT GTACTCAAGA AAATTGAACA AATGTAATGG 2580
 ATCAATTTAA AATATTTTAT TTCTTAAAAG CCTTTTTTGC CTGTTGTAAT GTGCAGGACC 2640
 CTTCTCCTTT CATGGGAGAG ACAGGTAGTT ACCTGAATAT AGGTIGAAAA GGTTATGTAA 2700
 10 AAAGAAATTA TAATAAAGG GATACTTTGC TTTTCAAATC TTTGTTTTCT CTTATTCTAG 2760
 GTAAGGCATA TTAAAAATAA ATATGT 2786

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(2) INFORMATION FOR SEQ ID NO: 235:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

GGGTGCAGGA ATTCGGCACG AGAGAATGTT TGATTTTCTT TCCTATTTTA AGGATCTTCT 60
 30 CTCTTGTTGA TGTGAAAAC TTACCTTAGT GAAGATGTGT TTCAACATGC TGTGTCCTT 120
 TACCTGCATA ATCAGAGCTA TGCATCTATT CAAAGTGATG ATCTGTGGGA TAGTTTAAAT 180
 GAGGTCACAA ACCAAACACT AGATGTAAAG AGAATGATGA AAACCTGGAC CCTGCAGAAA 240
 35 GGATTTCTTT TAGTGACTGT TCAAAGAAA GGAAAGGAAC TTTTATACA ACAAGAGAGA 300
 TTCTTTTAA ATATGAAGCC TGAAATTCAG CCTTCAGATA CAAGGTACAT GCCCTCTTTC 360
 40 TTTTCATGCC ATCTCTTTTG CACTCTCAGG TGGAATATT TTTAAGTGTT TTATAATCAT 420
 AAGTTCTTGT GAAACCTAAC AAGATTATCC CTTCTTAA 458

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(2) INFORMATION FOR SEQ ID NO: 236:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AGGATGAAGA GGAAATTATC TCTTGGATTG CTCTCCAGGA AATCCTTCTC TATACTTTAA 60
 AAGCTCTTGT TCTTTTCTAG GARTCCAATG TGCTGATTGC TGCTAACAGT CAGGGTACAA 120
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TTAAGGTGCT AGAATTGGTA TGAAGGGTTA ACTCAAGTCA AATTGTACTT GATCCTGCTG 180
 AAATACATCT GCAGCTGACA ATGAGAGARG AAACAGAAAA TGTCATGTGA TGTCTCTCCC 240
 5 CAAAGTCATC ATGGGTTTTG GATTTGTTTT GAATATTTTT TCTTTTTTTC TTKTCCCTCC 300
 TTTATGAGCC TTTGGGACAT TGGGAATACC CAGCCAACTC TCCACCATCA ATGTAACTCC 360
 10 ATGGACATTG CTGCTCTTGG TGGTGTATC TAATTTTTGT GATAGGGAAA CAAATTCCTT 420
 TGAATAAAAA TAAATAACWA AACAATAAAA GTTTATTGAG CCACAGTTGA GCTTGGAAG 480
 TTTTGTCAA ATGCNGCAAG AGATAACTCT TTTTANGAAG TAGCATATGT GAACTATAAT 540
 15 GTAACAGTGA ATAATTTGTA AAGTTCGTAT TTCCCAACCT CTTTGGAAT T 591

20 (2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1286 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

30 TCTTTTAAAG GTACAGCAGG GAAGAACTGG AAAGAACTG CCCTTCCATC 60
 TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTCAAG ACTGGGCTTC CACCGAGCAG 120
 35 GAGATTACCT GGGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 180
 CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 240
 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA 300
 40 CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 360
 TCCACCACCG GGTTCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 420
 45 AGAAAGTGGA CATTCCTCTG GTTATGATAG TSGTCTGCA CGTGCAATTTC CATATGGCAA 480
 TCGATGAAG AACGATACAG ATACAGGGAA TATGCAGAAA GAGGTTATGA GCGTCACAGA 540
 GCAAGTCGAG AAAANGAAGA ACGACATAGA GAAAGACGAC ACAGGGAGAA AGAGGAAACC 600
 50 AGACATAAGT CTTCTCGAAG TAATAGTAGA CGTCGCCATG AAAGTGAAGA AGGAGATAGT 660
 CACAGGAGAC ACAAACACAA AAAATCTAAA AGAAGCAAAG AAGGAAAAGA AGCGGGCAGT 720
 55 GAGCCTGCC CTGAACAGGA GAGCACCAGG GCTACACCTG CAGAATAGGC ATGGTTTGG 780
 CCTTTGTGT ATATTAGTAC CAGAAGTAGA TACTATAAAT CTTGTTATTT TTCTGGATAA 840
 TGTTAAGAA ATTTACCTTA AATCTGTTC TGTGTGTAG TATGAAAAGT TAACTTTTTT 900
 60 TCCAAATAA AAGAGTGAAT TTTTCATGTT AAGTTAAAA TCTTGTCTT GTACTATTC 960

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AAAAATAAAA AGACAGCAAT GACTTTATAT CCAAGAAAGG AATGTGAATG AGTCACTTAA 1020
 CAGGGAATCT AAAGAGCTGT GTTAGCTGTG TACATACACA GATTATCTGA GAAAAGGTCA 1080
 AGGGTTCCAC TTGGGCCACA GTTTTTTTGT TAATCAAACA CCACTCTCTT AAGRGGCTGC 1140
 ATCACAAARG GCAACCAARG GGCCCTCTT ARGGCTTTGA GGATTAAAC TAGTCTTTAT 1200
 CCATTACTGC TGTGGACACT CTGGCTTRG TATWTTTAGG GGGGNTCCTT ACCTTTTTTT 1260
 GGTTTTCCNC ACCTTTTGG TTGGGC 1286

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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ATGGCAGCGC AGAAGGACCA GCAGAAAGAT GCCGAGGCGG AAGGGCTGAG CGGCACGACC 60
 CTGCTGCCGA AGCTGATTCC CTCGGGTGCA GGCCGGGAGT GGCTGGAGCG GCGCCGCGCG 120
 ACCATCCGGC CCTGGAGCAC CTTCTGTGGAC CAGCAGCGCT TCTCACGGCC CCGCAACCTG 180
 GGAGAGCTGT GCCAGCGCCT CGTACGCAAC GTGGAGTACT ACCAGAGCAA CTATGTGTTC 240
 GTGTTCTTGG GCCTCATCCT GTACTGTGTG GTGACGTCCC CTATGTGTCT GGTGGCTCTG 300
 GCTGTCTTTT TCGGCGCTG TTAACATTCT CTATCTGCGC ACCTTGGAGT CCAAGCTTGT 360
 CCTCTTTGGC CGAAAGGTGA GCCCAGCGCA TCATATGCTC TGGCTGGAGG CATCTCCTTC 420
 CCTTCTTCTT GGCTGGCTGG TCGGGGCTCG GCCGTCTTCT GGGTGCTGGG AGCCACCCTG 480
 GTGGTCATCG GCTCCACGCG TGCCTTCCAC CAGATTGAGG CTGTGGACGG GGAGGAGCTG 540
 CAGATGGAAC CCGTGTGAGG TGCTTCTTGG GACCTGCCGG CCTCCCGGGC CAGCTGCCCC 600
 ACCCCTGCCC ATGCCTGTCC TGCACGGTCT GCTGCTCGGG CCCACAGCGC CGTCCCATCA 660
 CAAGCCCGGG GAGGGATCCC GCCTTTGAAA ATAAAGCTGT TATGGGTGTC ATTCAAAAAA 720
 AAAAAAAAAA AAAA 734

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5 CGGGGTCTTC AGGGTACCGG GCTGGTTACA GCAGCTCTAC CCCTCACGAC GCARACATGG 60
CAGCGCAGAA GGACCAGCAG AAAGATGCCG AGGCGGAAGG GCTGAGCGGC ACGACCTGTC 120
10 TGCCGAAGCT GATTCCCTCC GGTGCAGGCC GGGAGTGGCT GGAGCGGCGC CGCGCGACCA 180
TCCGGCCCTG GAGCACCTTC GTGGACCAGC AGCGCTTCTC ACGGCCCCGC AACCTGGGAG 240
AGCTGTGCCA GCGCCTCGTA CGCAACGTGG AGTACTACCA GAGCAACTAT GTGTTCTGTG 300
15 TCCTGGGCCT CATCCTGTAC TGTGTGGTGA CGTCCCCTAT GTTGCTGGTG GCTCTGGCTG 360
TCTTTPTCGG CGCCTGTTAC ATTCTCTATC TGCGCACCTT GGAGTCCAAG CTTGTGCTCT 420
20 TTGGCCGAGA GGTGAGCCCA GCGCATCAGT ATGCTCTGGC TGGAGGCATC TCCTTCCCTT 480
TCTTCTGGCT GGCTGGTGCG GGCTCGGCCG TCTTCTGGGT GCTGGGAGCC ACCCTGGTGG 540
TCATCGGCTC CCACGCTGCC TTCCACCAGA TTGAGGCTGT GGACGGGGAG GAGCTGCAGA 600
25 TGAACCCGT GTGAGGTGTC TTCTGGGACC TGCCGGCCTC CCGGGCCAGC TGCCCCACCC 660
CTGCCCATGC CTGTCTGCA CGGCTCTGCT GCTCGGGCCC ACAGCGCCGT CCCATCACAA 720
30 GCCCCGGGAG GGATCCCGCC TTTGAAAATA AAGCTGTTAT GGGTGTCAAT CAGGAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA 809
35

(2) INFORMATION FOR SEQ ID NO: 240:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TOGACCCACG CGTCCGGCAA CATGGCGGCT GCCGTGGTGC AGCGCCCGGG CTGAGCGACA 60
GCAAGTGCAG CGGGCTCCTA CCCCGGGTGA GGGGTGGCCT CCGCGTGGA TCGTGCCCTC 120
50 TTCAGCCCGC TCCTGTCCCC GACATCACGT GTATTCCGCA CGTCCCCTCC GCGCTGTGTG 180
TCTACTGAGA CGGGGAGGCG TGACAGGGCC CGGGTCCCTT CTCAGTGGTG CTCTGTGCTT 240
55 CAGGGCAAGC TCCCCGTCTC CGGGCGCACT TCCCTCGCCT GTGTTGGTTC CATCCTCCTT 300
TCTCCAGCCT CCTCCCCTCG CAGGCGGATG AMCCGGACGA CGGGCCAGTG CCTGGCACCC 360
CGGGGTGTC ARGGTCCAMG GGAACCCGA AGTCCGAGGA GCCCGARGTC CCGAACCAGG 420
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	ARGGGCTGCA GCGCATCAMC GGCCTGTCTC CCGGCCGTTT GGCTCTCATA GTGGCGGTGC	480
	TGTGCTACAT CAATCTCCTG AACTACATGG ACCGCTTCAC CGTGGCTGGC GTCCTTCCCG	540
5	ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG ACCGTGTTC	600
	TCTCCAGTTA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG TACAATCGGA	660
10	AGTATCTCAT GTGCGGGGGC ATTGCCCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA	720
	TCCCGGAGA GCATTTCTGG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTCGGGGAGG	780
	CCAGTTATT CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTGGCC GACCAGCGGA	840
15	CCGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG GCTACATTGC	900
	AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG TGACACCGGG	960
20	TCTAGGAGTG GTGGCCGTTT TGCTGTCTGT CCTGGTAGTG CGGGAGCCGC CAAGGGGAGC	1020
	CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACCC TCGTGGTGGG CAGATCTGAG	1080
	GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG CTGTGGCCTT	1140
25	TGTCACGGGC TCCCTGGCTC TGTGGGCTCC GGCATTCCCTG CTGCGTTCCC GCGTGGTCC	1200
	TGGGGAGACC CCACCTGGCC TTCCCGGAGA CTCTCTGCTT TCCTCTGACA GTCTCATCTT	1260
30	TGGAATCATC ACCTGCCTGA CCGGAGTCTT GGTGTGGGC CTGGGTGTGG AGATCAGCCG	1320
	CCGGCTCCGC CACTCCAACC CCCGGGCTGA TCCCTGGTC TGTGCCACTG GCCTCTGGG	1380
	CTCTGCACCC TTCTCTTCC TGTCCCTTGC CTGCGCCCGT GGTAGCATCG TGGCCACTTA	1440
35	TATTTTATC TTCATTGGAG AGACCCTCCT GTCCATGAAC TGGGCCATCG TGGCCGACAT	1500
	TCTGTGTAC GTGGTGATCC CTACCEGAGC CTCCACCGCC GAGGCTTCC AGATCTGCT	1560
40	GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCCTGATCT CTGACCGCCT	1620
	GCGCCGAAC TGGCCCCCT CTTCTTGTG CGAGTCCGG GCTCTGCAGT TCTCGCTCAT	1680
	GCTCTGCGCG TTTGTGGGG CACTGGGCGG CGCACTTTCC TGGGCACCGC CATCTTCATT	1740
45	GAGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGGTCC	1800
	ACAGACGACC GGATGTGGT GCGCCAGCGG GGCCGCTCCA CCCGCGTGCC CGTGGCCAGT	1860
50	GTGCTCATCT GAGARGCTGC CGCTCACCTA CCTGCACATC TGCCACAGCT GGCCCTGGGC	1920
	CCACCCACG AAGGGCCTGG GCCTAACCCC TTGGCTGGC CCAGCTTCCA GAGGGACCT	1980
	GGGCGGTGTG CCAGCTCCCA GACACTACMT GGGTAGCTCA GGGGAGGAGG TGGGGGTCCA	2040
55	GGAGGGGGAT CCCTCTCCAC AGGGGAGCC CCAAGGGCTC GGTGCTATTT GTAACGGAAT	2100
	AAAATTTGTA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG CCTCTGATCT	2160
60	TGCACCCCGT CTTACCCCCA GGGCTCCTGA AGACTGTGGG T	2201

(2) INFORMATION FOR SEQ ID NO: 241:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

15	GTCCTTCCCG ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG	60
	ACCGTGTTCA TCTCCAGTTA CATGGTGTGT GCACCTGTGT TTGGCTACCT GGGTGACAGG	120
	TACAATCGGA AGTATCTCAT GTGCGGGGGC ATTGCCTTCT GGTCCCTGGT GAACTGAGGG	180
20	TCATSCPTCA TCCCGGAGA GCATTTCTGG CTGCTCTCC TGACCCGGG CCTGGTGGGG	240
	GTGCGGGAGG CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTGGCC	300
	GACCAGCGGA SCGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGG AGTGGTCTGG	360
25	GCTACATTGC AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG	420
	TGACACCGGG TCTAGGAGTG GTGGCCGTC TGCTGCTGTT CCTGGTAGTG CGGGAGCCGC	480
30	CAAGGGGAGC CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGGG	540
	CAGATYTGAG GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG	600
	CTGTGGCCTT TGTACGGGC TCCCTGGCTC TGTGGGCTCC GGCATTCTG CTGCGTTCCT	660
35	GCGTGGTCTT TGGGAGAGC CCACCCCTGCC TTCCCGAGA CTCCTGCTCT TCCTCTGACA	720
	GTCTCATCTT TGGACTCATC ACCTGCCTGA CCGGAGTCTT GGGTGTGGG CTGGGTGTGG	780
40	AGATCAGCCG CCGYTCCGC CACTCCAACC CCCGGGCTGA TCCCTGGTC TGTGCCACTG	840
	GCCTCCTGGG CTCTGCACCC TTCCTCTTCC TGTCCCTTGC CTGCGCCCGT GGTAGCATCG	900
	TGGCCACTTA TATTTTCATC TTCATTGGAG AGACCTCTCT GTCCATGAAC TGGGCCATCG	960
45	TGGCCGACAT TCTGCTGTAC GTGGTGATCC CTACCCGACG CTCCACCGCC GAGGCCTTCC	1020
	AGATCGTGCT GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCCTGATCT	1080
50	CTGACCGCCT GCGCCGAAC TGGCCCCCTT CCTTCTTGTG CGAGTTCCGG GCTCTGCAGT	1140
	TCTCGCTCAT GCTCTGCGCG TTTGTGGGG CACTGGGCGG CGCACTTTCC TGGGCACCGN	1200
	CATCTTCATT GAGGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA	1260
55	AGCAGGGTCC ACAGACGACC GGATTTGGGT GCGCCAGCGG GCGCGCTCCA CCCGCGTGCC	1320
	CGTGGCCAGT GTGCTCATCT GAGAGGCTGC CGCTCACCTA CCTGCACATC TGCCACAGCT	1380
60	KGCCCTGGGC CCACCCACG AAGGGCCTGG GCCTAACCCC TTGGCCTGGC CCAGCTTCCA	1440

5 GAGGGACCCCT GGGCCGTGTG CCAGCTCCCA GACACTACMT GGGTAGCTCA GGGGAGGAGG 1500
 TGGGGGTCCA GGAGGGGGAT CCTCTCCAC AGGGGNCACC CCAAGGGCTC GGTGCTATTT 1560
 GTAACGGAAT AAAATTTGTA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG 1620
 CCTCTGATCT TGCACCCCGT CTTACCCCCA GGGCTCCTGA A 1661
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(2) INFORMATION FOR SEQ ID NO: 242:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

NGACAGAAAA GCAGAAGATG AGACTCTGTT CATTCACTTT TCCTAGGCCC ATCCTGTGGT 60
 25 CATCTTTCCC CCTCCCATCA TACCTCCTCC TTCTTGGAGC CTCTGCCGGC TTGGCTGTAA 120
 TGGTGGCACT TACCTGGATA TTTCAGTGGG AGGATGAAAG GCGAGACTCA CCCTACGCGG 180
 TGGGACAGAT GGGGAGAGGA AAAAGGCAGA GATNGCCAGG AGAGGGGTGC AGGACAAACC 240
 30 AGAGAGGTTG GGTACGGGA AAAGTGTTNG GAGAAAGTGG GGTGCAGGCC CTGCAGGCCG 300
 GTTTAGCCAG CAGCTGCCGC CTCCCCGGGC CCTTGGCATC CAACTTCGCA GACAGGGTAC 360
 35 CAGCCTCCTG GTGTGTATCA TAGGATTTGT TCACATAGTG TTATGCATGA TCTTCGTAAG 420
 GTTAAGAAGC CGTGGTGGTG CACCATGACA TCCAACCCGT ATATATAAAG ATAAATATAT 480
 ATATATATGT ATGTAAATTA TAGCACTGAG GGCCCTGCTG CCCTGCTGGA CCAAGCAAAA 540
 40 CTAAGCCMTT TGGTTTGGGT ATTATGTTTC GTTTTGTAT TTGTTGTTT TTGTGGCTTG 600
 TCTTATGTCG TGATAGCACA AGTGCCAGTC GGATTGCTCT GTATTACAGA ATAGTGTITT 660
 45 TAATTCATCA ATGTTCTAGT TAATGTCTAC CTCAGCACCT CCTCTTAGCC TAATTTTAGG 720
 AGGTGCCCCA ATTTTGTTC TTCAATTTTA CTGGTTACTT TTTTGTACAA ATCAATCTCT 780
 TTCTCTCTTT CTCTCCTCCC CACCTCTCAC CCTTGCCCTC TCCATCTCCC TCTCCCGCCC 840
 50 TCCCCTCCTC CCTCTGGCTC CCCGTCATC TTCTGTCCAC TCCATTCTCT CTCCCTCTCT 900
 CCTGCCTCCT GCTGCCCCCT CCCAGCCCA CTTSCCCGAG TTGTGCTTGC CGCTCCTTAT 960
 55 CTGTTCTAGT TCCGAAGCAG TTTCACTCGA AGTTGTGCAG TCCTGGTTGC AGCTTTCCGC 1020
 ATCTGCCTTC GTTTCGTGTA GATTGACGCG TTTCTTTGTA ATTTCACTGT TTCTGACAAG 1080
 ATTTAAAAAA AAAAAAAGGA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG GCCCGGTACC 1140
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CAATTG

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(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

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AACCCACGGC TGCTGCGGCA GGGCGTGGAG GGCAGAGGGC CGCGGAGGCG CAGTTGCAAA 60

CATGGCTCAG AGCAGAGACG GCGGAAACCC GTTCGCGGAG CCCAGCGAGC TTGACAACCC 120

20

CTTTCAGCCA CCACCAGCCT ATGAGCCTCC AGCCCCTGCC CCATTGCCTC CACCCTCAGC 180

TCCCTCCTTG CAGCCCTCGA GAAAGCTCAG CCCACAGAA CCTAAGAACT ATGGCTCATA 240

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CAGCACTCAG GCCTCAGCTG CAGCAGCCAC AGCTGAGCTG CTGAAGAAAC AGGAGGAGCT 300

CAACCGGAAG GCAGAGGAGT TGGACCGAAG GAGNCGAGAG CTGCAGCATG CTGCCCTGGG 360

RGGCACAGCT ACTCGACAGA ACAATTGGCC CCCTCTACCT TCTTTTGTGTC CAGTTCAGCC 420

30

CTGCTTTTTC CAGGACATCT CCATGGAGAT CCCCCAAGAA TTTCAGAAGA CTGTATCCAC 480

CATGTACTAC CTCTGGATGT GCAGCAGGST GGCTCTTCTC CTGAACTTCC TCGCCTGCCT 540

35

GGCCAGCTTC TGTGTGGAAA CCAACAATGG CGCAGGCTTT GGGCTTTCTA TCCTCTGGGT 600

CCTCCTTTTC ACTCCCTGCT CCTTTGTCTG CTGGTACCGC CCCATGTATA AGGCTTTCCG 660

GAGTGACAGT TCATTCAATT TCTTCGTTTT CTCTTTCATT TTCTTCGTCC AGGATGTGCT 720

40

CTTTGTCTC CAGGCCATTG GTATCCCAGG TTGGGGATTC AGTGGCTGGA TCTCTGCTCT 780

GGTGGTGCCG AAGGCAACAC AGCAGTATCC GTGCTCATGC TGCTGGTCGC CCTGCTCTTC 840

45

ACTGGCATTG CTGTGCTAGG AATTGTCATG CTGAAACGGA TCCACTCCTT ATACCGCCGC 900

ACAGGTGCCA GCTTTCAGAA GGCCAGCAA GAATTTGCTG CTGGTGTCTT CTCCAACCCT 960

GCGGTGCGAA CCGCARCTG CCAATGCAGC CGCTGGGGCT GCTGAAAATG CCTTCCGGGC 1020

50

CCCGTGACCC CTGACTGGGA TGCCCTGGCC CTGCTACTTG AGGGAGCTGA CTAGCTCCC 1080

GTCCCTAAGG TCTCTGGGAC TTGGAGAGAC ATCACTAACT GATGGCTCCT CCGTAGTGCT 1140

55

CCCAATCCTA TGGCCATGAC TGCTGAACCT GACAGGCGTG TGGGGAGTTC ACTGTGACCT 1200

AGTCCCCCA TCAGGCCACA CTGCTGCCAC CTCTCACACG CCCCACCCA GCTTCCCTCT 1260

GCTGTGCCAC GGCTGTTGCT TCGGTTATTT AAATAAAAAG AAAGTGAAC TGGAAAAAAA 1320

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AAAAAAAAA AAAAAAAG GGGGNCNC 1350

5 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

15 TCCCAGAGGC CGGGGGGTTT CAGCTCTGCC TGTAGCAGAG CCCTGAGGAG GAGGAGGAAG 60
 AGGATGTGCT GAAATACGTC CGGGAGATCT TTTTCAGCTA GGGCATAAAC TGTGCACTGA 120
 20 ACTGTCTGCC GAGAGCAGCT GGAGGACAGC TGAGCTTCCA CTGGTGCTGC TGGGCCGMCC 180
 GCCTGTGGGA ATGGGGCTCT CTGTGCTCCT ACCTTTGTGC CTTCTTGGGC CTGGCAGATT 240
 CACCTCAGGC CAGAAGCCCC TGGACACTCC GGGCCTTGGG GTGCCGTTCT GAGTGTGCGG 300
 25 AAGGCAGGAC TCAAAATGAG ATCCCATTTG ACTCCCTCTG TATGTACTGT GCCCTCTCCT 360
 GGCTCTTGAG GCTCTGGAGT CCCAATTGTC TGTGTTAGTC AGTGACCAGG TTCCAGGGAA 420
 30 AATRATGTCA TGTGGTGGTC CAACTTACTG GAACCAAAGA GACAGTACTT TGCAAAGAAA 480
 AGGATCACTG CCAGGTGCAC TGGAAATGCT ACAGTTTAGT CCGCATGATC TCTCCTGAAG 540
 GAGGAAGCCT GTTTCAAAAA TAGTTTCCAT CATGAGTCTA TCAATGAGCT CCCACCTCTC 600
 35 CAGCCAGCCT AGAAAGCAAA CGAGCTGCCC ACAGTTCTCT GCCCTGTCTG GGAGGTTGAG 660

 GCCACAGTGT ATAGACTGGT AAGCCAGACA GGCCTCCTCC CGCAAGCTGC TACCTTGCTT ----- 720
 40 TCACCTGTAC CTTGGTCCCC GGGCAGCTAG CTATAAGCA AGAGGGACAG GAGCCCAGAA 780
 GAGACACTGA GGACAAGAGA TCACACCAGA GTACATGTCT CTGCCTCTGT TTTCACTGTG 840
 GCTTTGGACA GGAATATATG AATAAATCAC TGCCATACAG GTTTTCCAAT ACACAAGTGC 900
 45 TAGAAAATAC ACACAATTCC CCAATGCGTA AGTTGTGCTA ATGTCTTTCC AAGTTCTGGG 960
 TTGGGAAGTG GAGGGTGGCA GCGTTTGTTC GTGCGCAACC GTCCAGTCTT GTTCACAGCG 1020
 50 AGGATTTGGA GTCCTCCAGG GTCTCATCAT GGGAGTGATT TGTCAGCGGA CGCCTCTGCC 1080
 CTGTCTGGCT TCAGGTCCAG GGAAGCTTTG AAGCAGTCAA GCCTTGCTCT TGTACCCCAT 1140
 GTGTCTGTGC TTTGTTGAGT CACTCAGAGA TCACTCCTGG ACCTCTGGGG TTGGAGTTCC 1200
 55 AGTGATGGCT TATGGCGGCC CACTCACTAT GGTGGGCTGA GTGGAAGCTC CTTAACCATG 1260
 TCCCCAGAGA CACTGAGGTG CTCGCTCTTT TAATGTCCTC GTTGTGTTCC GTAAGTTCTT 1320
 60 TGCTAGGTTT CATTTTGGCA TTTGGCAAAT CAGCCTGGAA GTCTGGCCCC ATGACAGCAA 1380

TCACTCCCTC CCCACCCTCC TGAAGCTAGA GGAAGATTTG CTCAGATCCA TTAATTAAAG 1440
 CAGGAATTGG TGTGACAATG AGCTGCATGG TTTAGGGAGT CTTTGGGAGC CTTGGAAGTC 1500
 5 CTGAAGGACA AACAATCTTG TACTAAGAA 1529

10 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1537 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

20 GTGCGAGGTC CCCGCCAGCC CCCAGCGGCC TTCCCGGCCC GGGGCGCTCC CAGAGCAAAC 60
 GAGGCCCTTG AGAGCTCCAC CTAGTTCACA GGATAAAATC CCACAGCAGA ACTCGGAGTC 120
 25 AGCAATGGCT AAGCCCCAGG TGGTTGTAGC TCCTGTATTA ATGTCTAAGC TGTCTGTGAA 180
 TGCCCTTGAA TTTTACCCTT CAGGTTATTC TTCCAGTTAC ACAGAATCCT ATGAGGATGG 240
 TTGTGAGGAT TATCCTACTC TATCAGAATA TGTTCAGGAT TTTTGAATC ATCTTACAGA 300
 30 GCAGCCTGGC AGTTTTGAAA CTGAAATTGA ACAGTTTGCA GAGACCCTGA ATGGTTGTGT 360
 TACAACAGAT GATGCTTTGC AAGAACTTGT GGAATCATC TATCAACAGG CCACATCTAT 420
 35 CCCAAATTTT TCTTATATGG GAGCTCGCCT GTGTAATTAC CTGTCCCATC ATCTGACAAT 480
 TAGCCACAG AGTGGCAACT TCCGCCAATT GCTACTTCAA AGATGTCGGA CTGAATATGA 540
 AGTTAAAGAT CAAGCTGCAA AAGGGGATGA AGTTACTCGA AAACGATTTC ATGCATTTGT 600
 40 ACTCTTTCTG GGAGAACTTT ATCTTAACCT GGAGATCAAG GGAACAAATG GACAGGTTAC 660
 AAGAGCAGAT ATTCTTCAGG TTGGTCTTCG AGAATTGCTG AATGCCCTGT TTTCTAATCC 720
 TATGGATGAC AATTTAATTT GTGCAGTAAA ATTGTTAAAG TTGACAGGAT CAGTTTGGGA 780
 45 AGATGCTTGG AAGGAAAAAG GAAAGATGGA TATGGAAGAA ATTATTGAGA GAATTGAAAA 840
 CGTTGTCTTA GATGCAAACT GCAGTAGAGA TGTAAAACAG ATGCTCTTGA AGCTTGTAGA 900
 50 ACTCCGGTCA AGTAACTGGG GCAGAGTCCA TGCAACTTCA ACATATAGAG AAGCAACACC 960
 AGAAAATGAT CCTAACTACT TTATGAATGA ACCAACATTT TATACATCTG ATGGTGTTC 1020
 TTTCACTGCA GCTGATCCAG ATTACCAAGA GAAATACCAA GAATTACTTG AAAGAGAGGA 1080
 55 CTTTTTTCCA GATTATGAAG AAAATGGAAC AGATTTATCC GGGGCTGGTG ATCCATACTT 1140
 GGATGATATT GATGATGAGA TGGACCCAGA GATAGAAGAA GCTTATGAAA AGTTTTGTTT 1200
 60 GGAATCAGAG CGTAAGCGAA AACAGTAAAG TTAAATTTCA GCATATCAGT TTTATAAAGC 1260

AGTTTAGGTA TGGTGATTTA GCAGAACACA AGAGAGCAAG AAAATGTGTC ACATCTATAC 1320
 CAAATTRAGG ATGTTGAGTT ATGTTACTAA TGTATGCAAC TTAAATTTTG TTAAACACTA 1380
 5 TCTGCCAAAA TAAACTTTAT TCCCTATAAC TTAAATGTG TATATATATA TAATAGTTTA 1440
 TTATGTACAG TTAATTCTAC TGTTTTGGCT GCAATAAAAT CGATTTTGAA ATAAAWRAAA 1500
 10 AAAAAAAAAA AAGGNGGCC GCTCTAGAGG ANCCAAG 1537

15 (2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

25 TGCAGGATTT GGCCAGGACC CSCCGCGGTG GCGGTGCTA TCGCTTCGCA GAACCTACTC 60
 AGGCAGCCAG CTGAGAAGAG TTGAGGGAAA GTGCTGCTGC TGGGTCTGCA GACGCGATGG 120
 ATAACGTGCA GCCGAAAATA AAACATCGCC CCTTCTGCTT CAGTGTGAAA GGCCACGTGA 180
 30 AGATGCTGCG GCTGGATATT ATCAACTCAC TGGTAACAAC AGTATTCATG CTCATCGTAT 240
 CTGTGTTGGC ACTGATACCA GAAACCACAA CATTGACAGT TGGTGGAGGG GTGTTTGCAC 300
 35 TTGTGACAGC AGTATGCTGT CTGCCCAGC GGGCCCTTAT TTACCGGAAG CTTCTGTTCA 360
 ATCCCAGCGG TCCTTACCAG AAAAAGCCTG TGCATGAAAA AAAAGAAGTT TTGTAATTTT 420
 ATATTACTTT TTAGTTTGAT ACTAAGTATT AAACATATTT CTGKATTATT CCAAAAAAAAA 480
 40 AAAAAAAAAA AAAAAAATT TGGTGG 506

45

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 GTCTTTCTTT TNCTGTTTGG AGTTGGTGAG TGAGTGAATA GGGTAACATG GGCCTTCAGG 60
 ATGACCCCTT GGAAGTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG 120
 60 GCCCCTGTGA GGGCCAGCTC TGGAAAAACC TGGGAGTTGA TGCCGGAGGY TGGGAAGAAC 180

	TCTGCTCGAG GGCAGGGTGC CCTGGAACAC TGGTAGTTCT GGGGCTGGGA GGGAGAGGGG	240
5	CTCCGGCTTT CTCTGAAATG AACACTGCTC TTCAGCAGTT CAAGTACTTG TTCTCAAAAC	300
	ATTTTCTAAT TGATTGGTAG GTTTTCATAA GCATTGTTTC TTTAAGGCAT GGAAAGGGAA	360
	GAATGCTCAA GCAAGTCATG TTTGTTTTCA GTGGGATGGG CCCGCGTTCT CACTGCTGGG	420
10	GGCTTCCCCT TGCATGTGGC ACCTTTGTGC AGGGCCACCA GGCAGACTCT TCCCACCTTC	480
	TCCCCTGAA GCACCAAGGG GCTTGAACCG TAATTTGGCT AATCAGAGGC ATTTTTTTTG	540
15	TCCTAGTATC TTTCACACTT GTCCAACCGT CTTATTTTTT TAAAAGTTCT GTTGCTTGTA	600
	TTAACACGAA ACTAGAGAGA AATAGTTTCT GAAGCCAGTT TATTGTGAAG ATCCCAAGG	660
	GGAGGTTCCG TAGAGAAAAA TAGTAAGCTG GTTTAGAAAC TGACGAGGGC AAACAGCCAG	720
20	GACGCATTGG AGAGGAATTT GCCAAAGATC TACCCTGAGA TAACGCCTGT CCAGTGTCTT	780
	CACCACGTGA ATAACCAGCG CTCCAAAGTG TTTTCTGCT TTGAAAAAAA AAATTCCACA	840
25	AGCTTTTAAA GGTGCATTTA AGAATCCATG TGACTTTAGA ATGGAAGTGC CGGCCCTGGC	900
	AACTGTCACG TGTGCTAGAA GGTTCGATGC CTCTGGAATG CATGTGATAC TCATCTCCAT	960
	TTTGTTTCCT TGATTGCATT TTTGTCTTT TAGCAGATCT GTCCCTGTGG GTGGTGTCTA	1020
30	AGAAGTCGGA CACCTTGGTT TTTGTGTTAG ATTGAGCTGG GCAGCTGCAA TCAGCTTCTT	1080
	TATATGCAAA TTAGGCACGA CCCATCTGTG GTTCCCTGGT TGGTGGCTAA TGAAGTGAGG	1140
35	GGAGGGAGGG ATGTCACCCC AAAAGTAGGC CCTCCCATTG GCTTTGGCCA GGCCAGACAC	1200
	TTACATCGT TTACATGGT CTGTGTAATT TTAAAGTTTA TGTGTATAAA GCGAAGCTGT	1260
	TTCTGTGAAA CTGTATATTT TGTAAATAAA TATATTGCTA CTTTGAGAWR AAAAAAAAAA	1320
40	AAAAACTCGA GGGGGGCCCG GTACCCAA	1348

45 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

55	GTGCCGAATC GGCAGAGCGG CACGAGCGC CACGAGAGCA GCGGAGTAA AGGGACTTGA	60
	GCGAGCCAGT TGCCGATTA TTCTATTTCC CCTCCCTCTC TCCGCCCCG TATCTCTTTT	120
60	CACCCTTCTC CCACCCTCGC TCGGTASCA TGGCGGAGCG TCGGCGGCCA CTCAGTCCCA	180

	TTCCATCTCC TCGTCGTCCT TCGGAGCCGA GCCGTCCGCG CCCGGCGGCG GCGGGAGCCC	240
	AGGAGCCTGC CCCGCCCTGG GGACGAAGAG CTGCAGCTCC TCCTGTGCGG TGCACGATCT	300
5	GATTTTCTGG AGAGATGTGA AGAAGACTGG GTTTGTCTTT GGCACCACGC TGATCATGCT	360
	GCTTTCCTG GCAGCTTTCA GTGTCATCAG TGTGGTTTCT TACCTCATCC TGGCTCTTCT	420
10	CTCTGTCACC ATCAGCTTCA GGATCTACAA GTCCGTCATC CAAGCTGTAC AGAAGTCAGA	480
	AGAAGGCCAT CCATTCAAAG CCTACCTGGA CGTAGACATT ACTCTGTCCT CAGAAGCTTT	540
	CCATAATTAC ATGAATGCTG CCATGGTGCA CATCAACAGG GCCCTGAAAC TCATTATTCG	600
15	TCTCTTCTG GTAGAAGATC TGGTTGACTC CTTGAAGCTG GCTGTCTTCA TGTGGCTGAT	660
	GACCTATGTT GGTGCTGTTT TTAACGGAAT CACCCTTCTA ATTCTTGCTG AACTGCTCAT	720
20	TTTCAGTGTC CCGATTGTCT ATGAGAAGTA CAAGACCCAG ATTGATCACT ATGTTGGCAT	780
	CGCCCGAGAT CAGACCAAGT CAATTGTTGA AAAGATCCAA GCAAACTCC CTGGAATCGC	840
	CAAAAAAAG GCAGAATAAG TACATGGAAA CCAGAAATGC AACAGTTACT AAAACACCAT	900
25	TTAATAGTTA TAACGTCGTT ACTTGTAATA TGAAGGAAA TACTCAGTGT CAGCTTGAGC	960
	CTGCATTCCA AGCTTTTTTT TTAATTGGT GTTTCTCCC ATCCTTTCCC TTTAACCCTC	1020
30	AGTATCAAGC AAAAAATTG ATGGACTGAT AAAAGAACTA TCTTAGAACT CAGAAGAAGA	1080
	AAGAATCAAA TTCATAGGAT AAGTCAATAC CTTAATGGTG GTAGAGCCTT TACCTGTAGC	1140
	TTGAAAGGGG AAAGATTGGA GGTAAGAGAG AAAATGAAAG AACACCTCTG GGTCTTCTG	1200
35	TCCAGTTTC AGCACTAGTC TTAAGTCACT ATCCATTATA GTTTTGCCCT TAAGAAGTCA	1260
	-----TGATTAACTT ATGAAAAAAT TATTTGGGGA CAGGAGTGTG ATACCTTCCT TGGTTTTTTT-----	1320
40	TTGCAGCCCT CAAATCCTAT CTTCTGCCCC CACAATGTGA GCAGCTACCC CTGATACTCC	1380
	TTTTCTTTAA TGATTTAACT ATCAACTTGA TAAATAACTT ATAGGTGATA GTGATAATTC	1440
	CTGATTCCAA GAATGCCATC TGATAAAAAA GAATAGAAAT GGAAAGTGGG ACTGAGAGGG	1500
45	AGTCAGCAGG CATGCTGCGG TGGCGGTCAC TCCCTCTGCC ACTATCCCCA GGAAGGAAA	1560
	RGCTCCGCCA TTTGGGAAAG TGGTTTCTAC GTCACGTGAC ACCGGTTCTG AGCATTAGTT	1620
50	TGAGAACTCG TTCCCGAATG TGCTTTCCTC CCTCTCCCT GCCCACCTCA AGTTTAATAA	1680
	ATAAGGTTGT ACTTTTCTTA CTATAAAATA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA	1740
55	CCCAAATCGC CGGATATGAT CGTAAA	1766

(2) INFORMATION FOR SEQ ID NO: 249:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2664 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

	AGTGTCTCTCG GAGCAGGCGG AGTAAAGGGA CTTGAGCGAG CCAGTTGCCG GATTATTCTA	60
10	TTTCCCCTCC CTCTCTCCCG CCCCGTATCT CTTTTCACCC TTCTCCCACC CTCGCTCGCG	120
	TASCATGGCG GAGCGTCGGC GGCCACTCAG TCCCATTCCA TCTCCTCGTC GTCCTTCGGA	180
15	GCCGAGCCGT CCGCGCCCGG CGGCGGCGGG AGCCCAGGAG CCTGCCCCGC CCTGGGGACG	240
	AAGAGCTGCA GCTCCTCCTG TCGGCTGCAC GATCTGATTT TCTGGAGAGA TGTGAAGAAG	300
	ACTGGGTTTG TCTTTGGCAC CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCAGTGTC	360
20	ATCAGTGTGG TTTCTTACCT CATCCTGGCT CTTCTCTCTG TCACCATCAG CTTCAGGATC	420
	TACAAGTCCG TCATCCAAGC TGTACAGAAG TCAGAAGAAG GCCATCCATT CAAAGCCTAC	480
25	CTGGACGTAG ACATTACTCT GTCTCAGAA GCTTTCCATA ATTACATGAA TGCTGCCATG	540
	GTGCACATCA ACAGGGCCCT GAAACTCATT ATTCTCTCTT TTCTGGTAGA AGATCTGGTT	600
	GACTCCTTGA AGCTGGCTGT CTTTATGTGG CTGATGACCT ATGTTGGTGC TGTTTTTAAC	660
30	GGAATCACCC TTCTAATTCT TGCTGAACTG CTCATTTTCA GTGTCCGAT TGTCTATGAG	720
	AAGTACAAGA CCCAGATTGA TCACTATGTT GGCATCGCCC GAGATCAGAC CAAGTCAATT	780
35	GTTGAAAAGA TCCAAGCAAA ACTCCCTGGA ATCGCCAAA AAAAGGCAGA ATAAGTACAT	840
	GGAAACCAGA AATGCAACAG TTAATAAAAC ACCATTTAAT AGTTATAACG TCGTTACTTG	900
	TACTATGAAG GAAAATACTC AGTGTCTAGCT TGAGCCTGCA TTCCAAGCTT TTTTTTTAAT	960
40	TTGGTGTTTT CTCCCATCCT TTCCCTTTAA CCCTCAGTAT CAAGCACAAA AATTGATGGA	1020
	CTGATAAAAG AACTATCTTA GAACTCAGAA GAAGAAAGAA TCAAATTCAT AGGATAAGTC	1080
45	AATACCTTAA TGGTGGTAGA GCCTTTACCT GTAGCTTGAA AGGGGAAAGA TTGGAGGTAA	1140
	GAGAGAAAAT GAAAGAACAC CTCTGGGTCC TTCTGTCCAG TTTTCAGCAC TAGTCTTACT	1200
	CAGCTATCCA TTATAGTTTT GCCCTPAAGA AGTCATGATT AACTTATGAA AAAATTATTT	1260
50	GGGGACAGGA GTGTGATACC TTCTTTGGTT TTTTMTTGCA GCCCTCAAAT CCTATCTTCC	1320
	TGCCCCACAA TGTGAGCAGC TACCCCTGAT ACTCCTTTTC TTAAATGATT TAACTATCAA	1380
55	CTTGATAAAT AACTTATAGG TGATAGTGAT AATTCCTGAT TCCAAGAATG CCATCTGATA	1440
	AAAAAGAATA GAAATGGAAA GTGGGACTGA GAGGGAGTCA GCAGGCATGC TCGGTTGGCG	1500
	GTCACCTCCT CTGCCACTAT CCCAGGGAA GGAAARGCTC CGCCATTGGG GAAAGTGTTT	1560
60	TCTACGTCAC TGGACACCGG TTCTGAGCAT TAGTTTGAGA ACTCGTTCCC GAATGTGCTT	1620

	TCCTCCCTCT CCCCTGCCCA CCTCAAGTTT AATAAATAAG GTTGTACTTT TCTTACTATA	1680
5	AAATAAATGT CTGTAAC TGC TGTGCACTGC TGTAACTTG TTAGAGAAAA AAATAACCTG	1740
	CATGTGGGCT CTCAGTTAT TGAGTTTTTG TGATCCTATC TCAGTCTGGG GGGGAACATT	1800
	CTCAAGAGGT GAAATACAGA AAGCCTTTTT TTCTTGATCT TTTCCCGAGA TTCAAATCTC	1860
10	CGATTCCCAT TTGGGGGCAA GTTTTTTTCT TCACCTTCAA TATGAGAATT CAGCGAACTT	1920
	GAAAGAAAA TCATCTGIGA GTTCCTTCAG GTTCTCACTC ATAGTCATGA TCCTTCAGAG	1980
15	GGAATATGCA CTGGCGAGTT TAAAGTAAGG GCTATGATAT TTGATGGTCC CAAAGTACGG	2040
	CAGCTGCAAA AAGTAGTGGA AGGAAATTGT CTACGTGTCT TGGAAAAATT AGTTAGGAAT	2100
	TTGGATGGGT AAAAGGTACC CTTGCCCTTAC TCCATCTTAT TTTCTTAGCC CCCTTTGAGT	2160
20	GTMTTAACTG GTTTCATGTC CTAGTAGGAA GTGCATTCTC CATCCTCATC CTCTGCCCTC	2220
	CCAGGAAGTC AGTGATTGTC TTTTGGGCT TCCCCTCCAA AGGACCTTCT GCAGTGAAG	2280
25	TGCCACATCC AGTTCCTTTC TTTTGTGCT GCTGTGTTTA GATAATTGAA GAGATCTTTG	2340
	TGCCACACAG GATTTTTTTT TTTTPTAAGA AAAACCTATA GATGAAAAAT TACTAATGAA	2400
	ACTGTGTGTA CGTGTCTGTG CGTGCAACAT AAAAATACAG TAGCACCTAA GGAGCTTGAA	2460
30	TCTTGGTTCC TGTAAATTT CAAATTGATG TGGTATTAAT AAAAAAAAAA AAAACAMAAA	2520
	AAAAAAAAAA AAAAGGGCGG CCGCTCTAGA GGATCCAAGC TTACGTACGC GTGCATGCGA	2580
35	CGTCCATAGC TCTTTCTATA GGGGTCCCCC AAATTCATT CANGGGCCG TCGGTTTTAN	2640
	AAAGGTCGTG ANTGGGGGAA ANCC	2664

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(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

50

CGTGGGAGTG AGGTACCAGA TTCAGCCCAT TTGGCCCGA CGCCTCTKTT CTCGGAATCC 60

GGGTGCTGCG GATTGAGGTC CCGGTTCTTA ACGGTGGGAT CCGTGTCTC GGGATGAGAT 120

55

TTGGCGTTTC CTCGGGGCTT TGGTGGGATC GGTGTCTCA GGATGAGATT TAGGGTTTCC 180

TCGGGGCTTT CGGGATCTTC ACCTAATATC CGGACTGCAA GATGGAGGAA GCGGGGAACC 240

60

TAGGAGGCCT GATTAARATG GTCCATCTAC TGGTCTTGTC AGGTGCCTGG GGCATGCAAA 300

	TGTGGGTGAC CTTCGTCTCA GGCTTCCTGC TTTCCTGAAG CCTTCCCCGA CATACCTTCG	360
	GACTAGTGCA GAGCAAACTC TTCCCCTTCT ACTTCCACAT CTCCATGGGC TGTGCCTTCA	420
5	TCAACCTCTG CATCTTGGCT TCACAGCATG CTTGGGCTCA GCTCACATTC TGGGAGGCCA	480
	GCCAGCTTTA CCTGCTGTTC CTGAGCCTTA CGCTGGCCAC TGTCAACGCC CGCTGGCTGG	540
10	AACCCCGCAC CACAGCTGCC ATGTGGGCCC TGCAAACCGT GGAGAAGGAG CGAGGCCTGG	600
	GTGGGGAGGT ACCAGGCAGC CACCAGGGTC CCGATCCCTA CCGCCAGCTG CGAGAGAAGG	660
	ACCCCAAGTA CAGTGCTCTC CGCCAGAATT TCTTCGGCTA CCATGGGCTG TCCTCTCTTT	720
15	GCAATCTGGG CTGCGTCTG AGCAATGGGC TCTGTCTCGC TGGCCTTGCC CTGGAAATAA	780
	GGAGCCTCTA GCATGGGCCC TGCATGCTAA TAAATGCTTC TTCAGAAAAA AAAAAAAAAA	840
20	AAACTCGAGG GGGGCCCGGT ACCCA	865

25 (2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2082 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

35	TGGGGGGGN AATGGGTGTC TGGCTCANGG ATTGCCNAAT CTGGAAATTC TCCATAACTT	60
	GCTAGCTTGT TTTTTTTTTT TTTTTTTTACA CCCCCCGCC CCACCCCGG ACTTGCACAA	120
	TGTTCAATGA TCTCAGCAGA GTTCTTCATG TGAAACGTTG ATCACCTTTG AAGCCTGCAT	180
40	CATTACATA TTTTTTCTTC TTCTTCCCCT TCAGTTCATG AACTGGTGTT CATTTTCTGT	240
	GTGTGTGTGT GTTTTATTTT GTTTGGATTT TTTTTTTTAA TTTTACTTTT AGAGCTTGCT	300
45	GTGTTGCCCA CCTTTTTTCC AACCTCCACC CTCACTCCTT CTCAACCCAT CTCTTCCGAG	360
	ATGAAAGAAA AAAAAAAGCA AAGTTTTTTT TTCTTCTCCT GAGTTCTTCA TGTGAGATTG	420
	AGCTTGCAAA GGAAAAAAA ATGTGAAATG TTATAGACTT GCAGCGTGCC GAGTTCCATC	480
50	GGGTTTTTTT TTTAGCATTG TTATGCTAAA ATAGAGAAAA AAATGCTCAT GAACCTTCCA	540
	CAATCAAGCC TGCATCAACC TTCTGGGTGT GACTTGTGAG TTTTGGCCTT GTGATGCCAA	600
55	ATCTGAGAGT TTAGTCTGCC ATTAAAAAAA CTCATTCTCA TCTCATGCAT TATTATGCTT	660
	GCTACTTGT CTTAGCAACA ATGAACTATA ACTGTTTCAA AGACTTTATG GAAAAGAGAC	720
	ATTATATTAA TAAAAAAA AAGCCTGCAT GCTGGACATG TATGGTATAA TTATTTTTTC	780
60	CTTTTTTTTT CCTTTTGGCT TGGAAATGGA CGTTCGAAGA CTTATAGCAT GGCATTCATA	840

CTTTGTGTTT ATTGCCTCAT GACTTTTTTGT AGTTTAGAAC AAAACAGTGC AACCGTAGAG 900
 CCTTCTTCCC ATGAAATTTT GCATCTGCTC CAAAACGTCT TTGAGTTACT CAGAACTTCA 960
 5 ACCTCCCAAT GCACTGAAGG CATTCCCTTGT GCAAAGATAC CAGAAATGGGT TACACATTTA 1020
 ACCTGGCAAA CATTGAAGAA CTCTTRATGT TTTCTTTTTA ATAAGAATGA CGCCCCACTT 1080
 10 TGGGGACTAA AATTGTGCTA TTGCCGAGAA GCAGTCTAAA ATTTATTTTT TAAAAAGAGA 1140
 AACTGCCCCA TTATTTTGGG TTTGTTTTAT TTTTATTTTA TATTTTGGG CTTTGGGTCA 1200
 TTGTCAAATG TGGAATGCTC TGGGTTTCTA GTATATAATT TAATTCTAGT TTTTATAATC 1260
 15 TGTTAGCCCA GTTAAATGT ATGCTACAGA TAAAGGAATG TTATAGATAA ATTTGAAAGA 1320
 GTTAGGTCTG TTTAGCTGTA GATTTTTTAA ACGATTGATG CACTAAATTG TTTACTATTG 1380
 20 TGATGTTAAG GGGGGTAGAG TTTGCAAGGG GACTGTTTTA AAAAAGTAGC TTATACAGCA 1440
 TGTGCTTGCA ACTTAAATAT AAGTTGGGTA TGTGTAGTCT TTGCTATACC ACTGACTGTA 1500
 TTGAAACCA AAGTATTAAAG AGGGGAAACG CCCCTGTTTA TATCTGTAGG GGTATTTTAC 1560
 25 ATTCAAAAAT GTATGTTTTT TTTCTTTTC AAAATTAAAG TATTTGGGAC TGAATTGCAC 1620
 TAAGATATAA CCTGCAAGCA TATAATACAA AAAAAAATTG CAAAACGTGTT TAGAACGCTA 1680
 30 ATAAAATTTA TGCAGTTATA AAAATGGCAT TACTGCACAG TTTTAAGATG ATGCAGATTT 1740
 TTTTACAGTT GTATTGTGGT GCAGAACTGG ATTTTCTGTA ACTTAAAAAA AAATCCACAG 1800
 TTTTAAAGGC AATAATCAGT AAATGTTATT TTCAGGGACT GACATCCTGT CTTTAAAAAG 1860
 35 AAATGAAAAG TAAATCTTAC CACAATAAAT ATAAAAAAT CTTGTCAGTT ACTTTTCTTT 1920

TACATATTTT GCTGTGCAAA ATTGTTTTAT ATCTTGAGTT ACTAACTAAC CACGCGTGT 1980
 40 GTTCCTATGT GCTTTTCTTT CATTTTCAAT TCTGTTTATA TCAAGAAAAG AATAATCTAC 2040
 AATAATAAAC GGCATTTTTT TTTGAAAAAA AAAAAA AA 2082

45

(2) INFORMATION FOR SEQ ID NO: 252:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

CAGGCAGGCT GGGCCCGGGG ACTTCTCTCT GGCCCTGCTC CCTCCGAGCG CTCCGCGT 60
 60 GCCCGCCTGG CCCCTACGGA GTCCTTAGCC AGGATGGAGG CTGTTGTGAA CTTGTACCAA 120

GAGGTGATGA AGCACGCAGA TCCCCGGATC CAGGGCTACC CTCTGATGGG GTCCCCCTTG 180
CTAATGACCT CCATTCTCCT GACCTACGTG TACTTCGTTC TCTCACTTGG GCCTCGCATC 240
5 ATGGCTAATC GGAAGCCCTT CCAGCTCCGT GGCTTCATGA TTGTCTACAA CTTCTCACTG 300
GTGGCACTCT CCCTCTACAT TGTCTATGAG TTCTGATGT CGGGCTGGCT GAGCACCTAT 360
10 ACCTGGCGCT GTGACCCTGT GGACTATTC AACAGCCCTG AGGCACTTAG GATGGTTCGG 420
GTGGCCTGGC TCTTCCTCTT CTCCAAGTTC ATTGAGCTGA TGGACACAGT GATCTTTATT 480
CTCCGAAAGA AAGACGGGCA GGTGACCTTC CTACATGTCT TCCATCACTC TGTGCTTCCC 540
15 TGGAGCTGGT GGTGGGGGGT AAAGATTGCC CCGGAGGAA TGGGCTCTTT CCATGCCATG 600
ATAAACTCTT CCGTGCATGT CATAATGTAC CTGTACTACG GATTATCTGC CTTTGGCCCT 660
20 GTGGCACAAC CCTACCTTTG GTGGAAAAAG CACATGACAG CCATTCACTG GATCCAGTTT 720
GTCCTGGTCT CACTGCACAT CTCCCAGTAC TACTTTATGT CCAGCTGTAA CTACCAGTAC 780
CCAGTCATTA TTCACCTCAT CTGGATGTAT GGCACCATCT TCTTCATGCT GTTCTCCAAC 840
25 TTCTGGTATC ACTCTTATAC CAAGGGCAAG CGGCTGCCCC GTGCACTTCA GCAAAATGGA 900
GCTCCAGGTA TGCCAAGGT CAAGGCCAAC TGAGAAGCAT GGCCTAGATA GGCGCCACC 960
30 TAAGTGCTC AGGACTGCAC CTTAGGGCAG TGTCCGTCAG TGCCCTCTCC ACCTACACCT 1020
GTGACCAAGG CTTATGTGGT CAGGACTGAG CAGGGGACTG GCCCTCCCT CCCACAGCT 1080
GCTCTACAGG GACCACGGCT TTGGTTCTC ACCCACTTCC CCCGGGCAGC TCCAGGGATG 1140
35 TGGCCTCATT GCTGTCTGCC ACTCCAGAGC TGGGGGCTAA AAGGGCTGTA CAGTTATTTT 1200

CCCCCTCCCTG CCTTAAAACT TGGGAGAGGA GCACTCAGGG CTGGCCCCAC AAAGGGTCTC ----- 1260
40 GTGGCCTTTT TCCTCACACA GAAGAGGTCA GCAATAATGT CACTGTGGAC CCAGTCTCAC 1320
TCCTCCACCC CACACACTGA AGCAGTAGCT TCTGGGCCAA AGGTCAGGT GGGCGGGGGC 1380
CTGGGAATAC AGCCTGTGGA GGCTGCTTAC TCAACTTGTG TCTTAATTAA AAGTGACAGA 1440
45 GGAAACCAAA AAAAAAAAAA AAAAATCGA GGGGGGCCG TA 1482

50 (2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

60 GGCACGAGCG CCGTTGCCCG CCTGGCCCCT ACGGAGTCCT TAGCCAGGAT GGAGGCTGTT 60

5 GTGAAC TTGT ACCAAGAGGT GATGAAGCAC GCAGATCCCC GGATCCAGGG CTACCCTCTG 120
ATGGGGTCCC CCTTGCTAAT GACCTCCATT CTCCTGACCT ACGTGTACTT CGTTCTCTCA 180
CTTGGGCCTC GCATCATGGC TAATCGGAAG CCCTTCCAGC TCCGTGGCTT CATGATTGTC 240
TACAACTTCT CACTGGTGGC ACTCTCCCTC TACATTGTCT ATGAGTTCCT GATGTCGGGC 300
10 TGGCTGAGCA CCTATACCTG GCGCTGTGAC CCTCAGGACT GCACCTTAGG GCAGTGTCCG 360
TCAGTGCCCT CTCCAMCTAC ACCTGTGACC AAGGCTTATG TGGTCAGGAC TGAGCAGGGG 420
ACTGGCCCTC CCTTCCCCAC AGCTGCTCTA CAGGGACCAC GGCTTTGGTT CCTCACCCAC 480
15 TTCCCCGGG CAGCTCCAGG GATGTGGCCT CATGTCTGTC TGCCACTCCA GAGCTGGGGG 540
CTAAAAGGGC TGTACAGTTA TTTCCCTCCTC CTGCTTAA AACTTGGGAG AGGAGCACTC 600
20 AGGGCTGGCC CCACAAAGGG TCTCGTGGCC TTTTTCCTCA CACAGAAGAG GTCAGCAATA 660
ATGTCAC TGT GGACCCAGTC TCACTCCTCC ACCCCACACA CTGAAGCAGT AGCTTCTGGG 720
CCAAAGGTCA GGGTGGGCGG GGGCCTGGGA ATACAGCCTG TGGAGGCTGC TTACTCAACT 780
25 TGTGTCTTAA TTAAAAGTGA CAGAGGAAAC CACGAAAAAA AAAAAAAAAA AAAA 834

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(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

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TTGAAC TTTT AAAATTTTAG ATCAGCAAAC TCTAAGATCC TAGAATGGAA GCTGTTCCCTC 60
ATTTCTCCAT GCTCACCTC CCAGGTCAGC GAGATGGTGA AGAAGCTGCA CGCGGCAACA 120
CCACCAACGT TCGGAGTGA CCTCATCAAT GAGCTTGTGG AGAACTTTGG CAGATGTCCC 180
AAGTGGTCTG GTCGGCAAGC CTTTGTCTTT GTCTGCCAGA CTGTCATTGA GGATGACTGC 240
CTTCCCATGG ACCAGTTTGC TGTGCATCTC ATGCCGCATC TGCTAACCTT AGCAAATGAC 300
AGGGTTCCTA ACGTGCAGT GCTGCTTGCA AAGACATTAA GACAACTCT ACTAGAAAAA 360
GACTATTTCT TGGCCTCTGC CAGCTGCCAC CAGGAGGCTG TGGAGCAGAC CATCATGGCT 420
CTTCAGATGG ACCGTGACAG CGATGTCAAG TATTTTGCAA GCATCCACCC TGCCAGTACC 480
AAAATCTCCG AAGATGCCAT GAGCACAGCG TCCTCAACCT ACTAGAAGGC TTGAATCTCG 540
GTGTCTTTCC TGCTTCCATG AGAGCCGAGG TTCAGTGGGC ATTCGCCACG CATGTGACCT 600

GGGATAGCTT TCGGGGAGG AGAGACCTTC CTCTCCTGCG GACTTCATTG CAGGTGCAAG 660
 TTGCCTACAC CCAATACCAG GGATTTCAG AGTCAAGAGA AAGTACAGTA AACACTATTA 720
 5 TCTTATCTTG ACTTTAAGGG GAAATAATTT CTCAGAGGAT TATAATTGTC ACCGAAGCCT 780
 TAAATCCTTC TGTCTTCCTG ACTGAATGAA ACTTGAATTG GCAGAGCATT TTCCTTATGG 840
 AAGGGATGAG ATTCCAGAG ACCTGCATTG CTTTCTCCTG GTTTTATTTA ACAATCGACA 900
 10 AATGAAATTC TTACAGCCTG AAGGCAGACG TGTGCCCAGA TGTGAAAGAG ACCTTCAGTA 960
 TCAGCCCTAA CTCTTCTCTC CCAGGAAGGA CTTGCTGGGC TCTGTGGCCA GCTGTCCAGC 1020
 15 CCAGCCCTGT GTGTGAATCG TTTGTGACGT GTGCAAATGG GAAAGGAGGG GTTTTACAT 1080
 CTCCTAAAGG ACCTGATGCC AACACAAGTA GGATTGACTT AACTCTTAA GCGCAGCATA 1140
 TTGCTGTACA CATTTACAGA ATGGTGTCTG AGTGTCTGTG TCTGATTTTT TCATGCTGGT 1200
 20 CATGACCTGA AGGAAATTTA TTAGACGTAT AATGTATGTC TGGTGTTTTT AACTTGATCA 1260
 TGATCAGCTC TGAGGTGCAA CTTCTTCACA TACTGTACAT ACCTGTGACC ACTCTTGGGA 1320
 25 GTGCTGCAGT CTTTAATCAT GCTGTTTAAA CTGTTGTGGC ACAAGTTCTC TTGTCCAAAT 1380
 AAAATTTATT AATAAGATCT ATAGAGAGAG ATATATACAC TTTTGATTGT TTTCTAGATG 1440
 TCTACCAATA AATGCAATTT GTGACCTGTA TTAATAAAAA NTAAAAAAC TCGAGGGGGG 1500
 30 CCCGGTAC 1508

35

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 2514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA 60
 GCACCTACCT GTGTTGGTGA GGTTTGTGTA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
 50 AGGCTTCCTG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTTT AACTATGAT 180
 AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG 240
 TGGATTTTCT TCCAAAATGA AAGTTGTTGC TTCTAGACTT TTAGAGAAAT ATCCCAAGC 300
 55 TATCTACACA CTCTGCTCTT CCTGTGCCTT AAATATGTGG TTGGCAAAAT CAGTACCTGT 360
 TATGGGAGTA TCTGTTGCAT TAGGAACAAT TGAGGAAGTT TGTCTTTTTT TCCATCGATC 420
 60 ACCACAAC TG CTTTGTAGAAC TTGACAACGT AATTTCTGTT CTTTTTCAGA ACAGTAAAGA 480

	AAGGGGTAAA GAACTGAAGG AAATCTGCCA TTCTCAGTGG ACAGGCAGGC ATGATGCTTT	540
5	TGAAATTTTA GTGGAAGTCC TGCAAGCACT TGTTTTATGT TTAGATGGTA TAAATAGTGA	600
	CACAAATATT AGATGGAATA ACTATATAGC TGGCCGAGCA TTTGTACTCT GCAGTGCAGT	660
	GTCAGATTTT GATTTTCATTG TTACTATTGT TGTTCTTAAA AATGTCCTAT CTTTTACAAG	720
10	AGCCTTTGGG AAAAACCTCC AGGGGCAAAC CTCTGATGTC TTCTTTGCGG CCGGTAGCTT	780
	GACTGCAGTA CTGCATTAC TCAACGAAGT GATTGGAAAA TATTGAAGTT TATCATGAAT	840
15	TTTGGTTTGA GGAAGCCACA AATTTGGCAA CCAAACTTGA TATTCAAATG AAACCTCCCTG	900
	GGAAATTCGG CAGAGCTCAC CAGGGTAACT TGAATCTCA GCTAACCTCT GAGAGTTACT	960
	ATAAAGAAAC CCTAAGTGTC CCAACAGTGG AGCACATTAT TCAGGAAGTT AAAGATATAT	1020
20	TCTCAGAACA GCACCTCAAA GCTCTTAAAT GCTTATCTCT GGTACCTCA GTCATGGGAC	1080
	AACTCAAATT CAATACGTCG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA	1140
25	ATCCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA	1200
	AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTTT	1260
	TTCTTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA	1320
30	ATGAGCGGTA TGAAATGGA CGAAAGCGTC TTAAAGCATA TTTGAGGAAC ACTTTGACAG	1380
	ACCAAAGGTC AAGTAACTTG GCTTTGCTTA ACATAAATTT TGATATAAAA CACGACCTGG	1440
35	ATTTAATGGT GGACACATAT ATTAAGTCT ATACAAGTAA GTCAGAGCTT CCTACAGATA	1500
	ATTCCGAAAC TGTGGAAAAT ACCTAAGAGA CTTTTAAAA TAGGCTTTCT TATATTTGAT	1560
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	ATTTGGAAGA AAAAGCCGTA AGTGTATGTA GACCACTTAA TCACTAAATA TCTTTGCCTA	1620
40	TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG CCCCTGTTTG	1680
	AACTCTCAAG CTTTGAAGAC CTACCTGTTT TCCAGAAGA GAACGTTGAA AGTGCCATGT	1740
45	TTCTTTTGC GTGATCTCTG TTGATGGCAC TCTGGAATTG TTTCAAGTTAA GTCATTTTAG	1800
	ACATAGCATT TATTATCACT GTGGATCTCT ACTTGTGGG TGTTATGAAT TCTTTGAAGA	1860
	AATATATTTT GAAGAGGTGT GGGAGGAAGG AATACATTTT ATAAATGTT GTAGTGAAGC	1920
50	CCACAATTGA CCTTTGACTA ATAGGAGTTT TAAGTATGTT AAAAATCTAT ACTGGACAGT	1980
	TACAAGAAAT TACCGGAGAA AAGCTTGTGA GCTCACCAAA CAAGGATTTT AGTGTAGATT	2040
55	TGTCTTTCT TGAACCTAAA GAAACAAATG ACAAAGTTTG AATGGAAAAG CCTGCTGTTG	2100
	TTCCACATCT CGTTGCTGTT TACATTCCTT TGTGGAGCCT ACATCTTCCT AAGCTTTTTTA	2160
	GCAGGTATAT GTTGAACACT TCTGTTTCAT GGTGAGACA GAATCAGAGG CCATGGATAC	2220
60	TGACAACTGA TTTGTCTGTT TTTTTCTCT GTCTTTTCC ATGACTCTTA TATACTGCCT	2280

CATCTTGATT TATAAGCAAA ACCTGGAAAA CCTACAAAAT AAGTGTTGTG GTTTATCTAG 2340
 5 AAAAATATGG AAAATATTGC TGTTATTTT GGTGAAGAAA ATCAATTTTG TATAGTTTAT 2400
 TTCAATCTAA ATAAAATGTG AATTTTGT TT AAAGCTTAGG CACATTATTT TTTGTGGGGT 2460
 CAAAACATTC TTGTGTAAAT TCTCTTAAAC ATTTGATAAA CAGCTTCACA ATTC 2514

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(2) INFORMATION FOR SEQ ID NO: 256:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CTGCCTTATG AAGCCGATGC AGAAATTTTG GCTGTGAAAT TTCACACTAT GATAACTGAG 60
 25 AAGTGGGGAT TAAATATGGA GTATTGTGCT GCCAGGCTT ACATTGTCTC TAGTGGATTT 120
 TCTTCCAAAA TGAAAGTTGT TGCTTCTAGA CTTTATAGAGA AATATCCCA AGCTATCTAC 180
 30 AACTCTGCT CTTCTGTGC CTTAAATATG TGGTTGGCAA AATCAGTACC TGTATGGGA 240
 GTATCTGTTG CATTAGGAAC AATTGAGGAA GTTGTCTT TTTCCATCG ATCACCACAA 300
 CTGCTTTTAG AACTTGACAA CGTAAATYCT GTTCTTTTTC AGAACAGTAA AGAAAGGGGT 360
 35 AAAGAACTGA AGGAAATCTG CCATTCTCAG TGGACAGGCA GGCATGATGC TTTTGAAATT 420
 TTAGTGAAC TCCTGCAAGC ACTTGTTTA TGTATAGATG GTATAAATAG TGACACAAAT 480
 40 ATTAGATGGA ATAACATAT AGCTGGCCGA GCATTTGTAC TCTGCAGTGC AGTGTGAGAT 540
 TTTGATTCA TTGTTACTAT TGTTGTCTT AAAAATGTCC TATCTTTTAC AAGAGCCTTT 600
 GGGAAAAACC TCCAGGGGCA AACCTCTGAT GTCTTCTTTG CGGCCGGTAG CTTGACTGCA 660
 45 GTACTGCATT CACTCAACGA AGTGANTGGA AAATATTGAA GTTATCATG AATTTTGGTT 720
 TGAGGAAGCC ACAAATTTGG CAACCAAACT TGATATTCAA ATGAACTCC CTGGGAAATT 780
 50 CCGCAGAGCT CACCAGGGTA ACTTGGAATC TCAGCTAACC TCTGAGAGTT ACTATAAAGA 840
 AACCTTAAGT GTCCCAACAG TGGAGCACAT TATTCAGGAA CTAAAGATA TATCTCAGA 900
 ACAGCACCTC AAAGCTCTTA AATGCTTATC TCTGGTACCC TCAGTCATGG GACAACTCAA 960
 55 ATTCAATACG TCGGAGGAAC ACCATGCTGA CATGTATAGA AGTGACTTAC CCAATCCTGA 1020
 CACGCTGTCA GCTGAGCTTC ATGTGTGGAG AATCAAATGG AAACACAGGG GGAAAGATAT 1080
 60 AGAGCTTCCG TCCACCATCT ATGAAGCCCT CCACCTGCCT GACATCAAGT TTTTCTCTAA 1140

	TGTGTATGCA TTGCTGAAGG TCCTGTGTAT TCTTCCTGTG ATGAAGGTTG AGAATGAGCG	1200
	GTATGAAAAT GGACGAAAGC GTCTTAAAGC ATATTTGAGG AACACTTTGA CAGACCAAAG	1260
5	GTCAAGTAAC TTGGCTTTGC TTAACATAAA TTTTGATATA AAACACGACC TGGATTTAAT	1320
	GGTGGACACA TATATTAAAC TCTATACAAG TAAGTCAGAG CTCCTACAG ATAATCCGA	1380
10	AACTGTGGAA AATACCTAAG AGACTTTTAA AAATAGGCTT TCTTATATTT GATATTTGGA	1440
	AGAAAAAGCC GTAAGTGTAT GTAGACCACT TAATCACTAA ATATCTTTGC CTATAGGACT	1500
	CCATTGAATA CATTAGCCAT TGATAATCTA CCTGTTTAAA TGGCCCCTGT TTGAACTCTC	1560
15	AAGCTTTGAA GACCTACCTG TTCTTCCAGA AGAGAACGTT GAAAGTGCCA TGTTTCCTTT	1620
	TGCGTGATCT CTGTIGATGG CACTCTGGAA TTGTTTCAGT TAAGTCATTT TAGACATAGC	1680
20	ATTTATTATC ACTGTGGATC TCTACTTGTG GGGTGTATG AATTCTTTGA AGAAATATAT	1740
	TTTGAAGAGG TGTGGGAGGA AGGAATACAT TTTATAAAAT GTTGTAGTGA AGCCCACAAT	1800
	TGACCTTTGA CTAATAGGAG TTTTAAGTAT GTTAAAAATC TATACTGGAC AGTTACAAGA	1860
25	AATTACCGGA GAAAAGCTTG TGAGCTCACC AAACAAGGAT TTCAGTGTAG ATTTTGTCTT	1920
	TCTTGAACCTT AAAGAAACAA ATGACAAAGT TTGAATGGAA AAGCCTGCTG TTGTTCCACA	1980
30	TCTCGTTGCT GTTTACATTC CTTGTGGAG CCTACATCTT CCTAAGCTTT TTAGCAGGTA	2040
	TATGTTGAAC ACTTCTGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC	2100
	TGATTTGTCT GTTTTTTTTC TCTGTCTTTT TCCATGACTC TTATATACTG CCTCATCTTG	2160
35	ATTTATAAGC AAAACCTGGA AAACCTACAA AATAAGTGTT GTGGTTTATC TAGAAAAATA	2220
	TGGAAAAATAT TGCTGTTATT TTTGGTGAAG AAAATCAATT TTGTATAGTT TATTTCAATC	2280
40	TAAATAAAAT GTGAATTTTG TTAAAGCTT AGGCACATTA TTTTGTGG GGTCAAAACA	2340
	TTCTTGTTGA AATTCTC	2357

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(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

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ACTTCTGGT GCAAAAAGAT GTTCAAGCCT TATTTTATAC TTGCCTGCCC CTTTCTCTTT 60

CATTTATTGG AGTGAGCTGC AGCTCTAAGA AGACCTGTTC TTTTGAATGG AGAGTAGCAT 120

60

CAGGAACCAG GATGTGGGTG CGAGGCGTGC TCCTGGCTGT TGCAGATTGC TGCACCCGGG 180

5 AGCTCTTAGT GGACAGAGCT AGAGGATATG TGCACGTACT TCCATCTCTC TCTCTGTCTC 240
 CGATTTTAGC CCAGCACCAC AGGGTACGTT CCAGTTTTTC TCTCTTTCCA TAGCTGTAAG 300
 GCCCTTTCTG GGAATGGTTC TCATTCTCCT TAATCTATTA TTGGGTCAGT TTTCTGTCAT 360
 GTCCCCAGCC TCCCATCACT GCCACCCACT CCCCACAGAG ATGCCCTGCT CATCCGACTG 420
 10 GGGCTTTGAC TCCCACACTG TGTACCCCTC TTGTGTGGAC GCCCTGCTGC CAAAACCTTC 480
 AGCAAACAGC TTTCCAAATG GAAGTTGTCA CTGTCARGGS CTTTACAATC AGCAAACAGCA 540
 AAATCTACAT GCTGCTGAGG GTCCTGCCTC ATTAAGATGC AATAAATATG TAAGTACATA 600
 15 AAAACAGCAA TAGAAGAAAC GTAATGCTTT ATTCTCAAAT ATGNATGTCT ACATAGAAAA 660
 GCCAAAATTA TTAAGAATAG TAAGGAATT 689

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(2) INFORMATION FOR SEQ ID NO: 258:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TCGACCCACG CGTCCGCCGA TGTGATGATT CCTGCGTATT CCAAGAACCG GGCCTATGCC 60
 35 ATCTTCTTCA TAGTCTTCAC TGTGATAGGG GACGCCCCCG GCGCTGTGCT ATCCTGTGCC 120
 -----GGCCACCCCTT GCGTTGGTTT TGCTGCTGTA CTGGTGGCGC CCCTGACCGT GGCTGTCTCC----- 180
 TCTTGAAGGA AGCCTGTTTC TGATGAACCT GCTGACAGCC ATCATCTACA GTCAGTTCGG 240
 40 GGGCTACCTG ATGAAATCTC TCCAGACCTC GCTGTTTCGG AGGCGGGTGG GAACCCGGCT 300
 GCCTTTGAAG TCCTATCCTC CATGGTGGGG GAGGGAGGAG CCTTCCCTCA GGCAGTTGGG 360
 45 GTGAAGCCCC AGAAGTTGCT GCAGGTGCTT CAGAAGGTCC AGCTGGACAG CTCCCACAGA 420
 CAGGCCATGA TGGAGAAGGT GCGTTCTPAT GGCAGTGTTC TGCTCTCAGC TGAGGAGTTT 480
 CAGAAGCTCT TCAACGAGCT TGACAGAAGT GTGGTTAAAG AGCACCCGCC GAGGCCCGAG 540
 50 TACCACTCTC CGTTTCTGCA GAGCGNCCCA GTTCTCTTTC GGCCACTNAC TACTTTGACT 600
 ACCTGGGGAA CCTCATCGCC CTGGCAAACC TGGTGTCCAT TTGCGTGTTC CTGGTGTGG 660
 55 ATGCAGATGT TGCTGCCTGC TGAGCGTGAT GACTTCATCC TGGGGGTCT CAACTGCGTC 720
 TTCATTGTGT ACTACCTGTT GGAGATGCTG GCTCAAGTTC TTTTGCCCTG GGGCCTGCGA 780
 RGGTACYKKT CCTAACCCCA RCAAMGTGTT TTGAACGGGC TCCTCAMCGT TTGTCCTGGC 840

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	TGGWWKKGSM	GATCTCAACT	CTGGCTGTGT	ACCGATTGCC	ACACCCAGGC	TGGAGGCCGG	900
	ANATGGTGGG	CCTGCTGTCG	CTGTGGGACA	TGACCCGCAT	ACTGAACATG	CTCATCGTGT	960
5	TCCGCTTCCT	GCGTATCATC	CCCAGCATGA	AGCCGATGGC	CGTGGTGGCC	AGTACCGTCC	1020
	TGGGCCTGGT	GCAAAACATG	CGTGCCTTTG	GCGGGATCCT	GGTGGTGGTC	TACTACGTAT	1080
10	TTGCCATCAT	TGGGATCAAC	TTGTTTAGAG	GCGTCATTGT	GGCTCTTCCT	GGAAACAGCA	1140
	GCCTGGCCCC	TGCCAATAGG	TCGGCGCCCT	GTGGGAGCTT	CGAGCAGCTG	GAGTACTGGG	1200
	CCAACAACCT	CGATGACTTT	GCGGCTGCCC	TGGTCACTCT	GTGGAACCTG	ATGGTGGTGA	1260
15	ACAACTGGCA	GGTGTTCCTG	GATGCATATC	GGCGCTACTA	AGGCCCGTGG	TCCAAGATCT	1320
	ATTTTGTATT	GTGGTGGCTG	GTGTCGTCTG	TCATCTGGGT	CAACCTGTTT	CTGGCCCTGA	1380
20	TTCTGGAGAA	CTTCCTTCAC	AAGTGGGACC	CCCGCAGCCA	CCTGCAGCCC	CTTGCTGGGA	1440
	CCCCAGAGGC	CACCTACCAG	ATGACTGTGG	AGCTCCTGTT	CAGGGATATT	CTGGAGGAGC	1500
	CCGGGGAGGA	TGAGCTCACA	GAGAGGCTGA	GCCAGCACCC	GCACCTGTGG	CTGTGCAGGT	1560
25	GACGTCCGGG	TCTGCCATCC	CAGCAGGGGC	GGCAGGAGAG	AGAGGCTGGC	ATAACACAGG	1620
	TGCCCATCAT	GGAAGAGGCG	GCCATGCTGT	GGCCAGCCAG	GCAGGAAGAG	ACCTTTCCTC	1680
30	TGACGGACCA	CTAAGCTGGG	GACAGGAACC	AAGTCCTTTG	CGTGTGGCCC	AACAACCATT	1740
	TACAGAACAG	CTGCTGGTGC	TTCAGGGAGG	CGCCGTGCCC	TCCGCTTTCT	TTTATAGCTG	1800
	CTTCAGTGAG	AATTCCCTTG	TCGACTCCAC	AGGGACCTTT	CAGACAAAAA	TGCAAGAAGC	1860
35	AGCGGCCTCC	CCTGTCCCTT	GCAGCTTCCG	TGGTGCCCTT	GCTGCCGGCA	GCCCTTGGGG	1920
	ACCACAGGCC	TGACCAGGCG	CTGCACAGGT	TAACCGTCAG	ACTTCCGGGG	CATTTCAGCTG	1980
40	GGAATGATAC	TAATACCTCC	GATTTTAGCC	CAGCACCACA	GGGTACGTTT	CAGTTTATAT	2040
	TTCTTTCCAT	AGCTGTAAGG	CCCTTTCTGG	GAATGGTTAT	CATTCTCCTT	AATCTATTAT	2100
	TGGGTCAGTT	TTCTTGCAAT	TCCCCAGCCT	CCCATCACTG	CCACCCACTC	CCCACAGAGA	2160
45	TGCCCTGCTC	ATCCGACTGG	GGCTTTGACT	CCCACACTGT	GTACCCCTCT	TGTGTGGACG	2220
	CCCTGCTGCC	AAAACCTTCA	GCAACAGCTT	TTCCAAATGG	AAGTTGTCAC	TGTCAGGGCC	2280
50	TTTACAATCA	GCAACAGCAA	AATCTACATG	CTGCTGAGGG	TCCTGCCTCA	TTAAGATGCA	2340
	ATAAATATGT	AAGTACATAA	AAAAAAAAAA	AAAAAAA			2377

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(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1193 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

5 TCTGNTCGCC GTCGCCCCGC CCTTGGCCTT TGCCCCGTGC GGCGGGACTT CCTGTGTCGT 60
 ATTTCCAAGG ACTCCAAAGC GAGGCCGGGG ACTGAAGGTG TGGGTGTCGA GCCCTCTGGC 120
 10 AGAGGGTTAA CCTGGGTCAA ATGCACGGAT TCTCACCTCG TACAGTTACG CTCTCCCGCG 180
 GCACGTCCGC GAGGMYTTGA AGTCCTGAGC GCTCAAGTTT GTCCGTAGTC GAGAGAAGGC 240
 15 CATGGAGGTG CCGCCACCGG CACCGCGGAG CTTTCTCTGT AGAGCATTGT GCCTATTTCC 300
 CCGAGTCTTT GCTGCCGAAG CTGTGACTGC CGATTCCGAA GTCCTTGAGG AGCGTCAGAA 360
 GCGGCTTCCC TACGTCCCAG AGCCCTATTA CCCGGAATCT GGATGGGACC GCCTCCGGGA 420
 20 GCTGTTTGGC AAAGACACAG TGAACACTAG TCTGAATGTA TACCGAAATA AAGATGCCTT 480
 AAGCCATTTT GTAATTGCAG GAGCTGTCAC GGAAGTCTT TTTAGGATAA ACGTAGGCCT 540
 GCGTGGCTGG TGGCTGGTGG CATAATTGGA GCCTTGCTGG GCACTCCTGT AGGAGGCCTG 600
 25 CTGATGGCAT TTCAGAAGTA CTCTGGTGAG ACTGTTTCAGG AAAGAAAACA GAAGGATCGA 660
 AAGGCACTCC ATGAGCTAAA ACTGGAAGAG TGGAAAGGCA GACTACAAGT TACTGAGCAC 720
 30 CTCCCTGAGA AAATTGAAAG TAGTTTACAG GAAGATGAAC CTGAGAATGA TGCTAAGAAA 780
 ATTGAAGCAC TGCTAAACCT TCCTAGAAAC CCTTCAGTAA TAGATAAACA AGACAAGGAC 840
 TGAAAGTGCT CTGAACTTGA AACTCACTGG AGAGCTGAAG GGAGCTGCCA TGTCCGATGA 900
 35 ATGCCAACAG ACAGGCCACT CTTTGGTCAG CCTGCTGACA AATTTAAGTG CTGGTACCTG 960

TGGTGGCAGT GGCTTGCTCT TGTCTTTTTT TTTTCTTTTT AACTAAGAAT GGGGCTGTTG 1020
 40 TACTCTCACT TTAATTATCC TTAAATTAA ATACATACTT ATGTTTGTAT TAATCTATCA 1080
 ATATATGCAT ACATGAATAT ATCCACCCAC CTAGATTTTA AGCAGTAAAT AAAACATTTT 1140
 45 GCAAAAGATT AAAGTTGAAT TTTACAGTTA AAAAAAAAAA AAAAAAAAAA AAA 1193

(2) INFORMATION FOR SEQ ID NO: 260:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1262 base pairs

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

60

GAAAAACCCA AAGATGCAGA CAATCTCTTT GAACATGAAT TGGGGGCTCT CAATATGGCT 60

	GCATTACTAC GAAAAGAAGA AAGAGCAAGT CTTCTTAGTA ATCTTGGCCC ATGTTGTAAG	120
	GCGTTGTGCT TCAGACGGGA TTCTGCAATT CGAAAGCAGC TTGTTAAAAA TGAGAAGGGC	180
5	ACCATAAAAAC AAGCTTACAC GAGTSCCTCA ATGGTAGACA ATGAATTACT TCGATTGAGT	240
	CTTCGGTTAT TTAAGCGGAA GACTACTTGC CATGCTCCAG GACATGAAAA GACTGAAGAT	300
10	AATAAACTTT CACAGTCCAG TATCCAACAG GAACTGTGTG TGTCTTAAGA CCGAAGTTCA	360
	ATATGGTATT TTTGGTACTG TCTTCCTTCA GCAGTGCATA TTCTTTTGCA AAGTTCTTTG	420
	GTTTGACAAG CATTAGTGAC AAAGGCAGAA AAGATTATC AGCCATGCTA AAAGAGTGAA	480
15	GAATTTTGAT CTTTAGAGAC ACTAGTTTTC GCCAACTTAA GATTTTACGT TAATTTTAC	540
	ATAGTATTTG ACACTCATGC AAAATAATGT GAAAACATCT AGATTTAGTA GTTTATCTG	600
	CGCCTTTTGT TAAAACTGAA GATTTTGGAA AATGGTTGTC ACTGCTCTTC CAGCCTATGA	660
20	ATATTTTGT GAAATGGAAC CATGGATTTA TGTCTGGATC ATCCATACAG AACCAACAAT	720
	TTTATTCAAA AACAAATGTGT TCATCAAAGT AATTGCTCAC ATTGTGCAGT ACTATGTTGT	780
25	ACAGACCACG TGAAAGGGAA TGCTGGTCTA GCTGGCGTGG TATGTTTATA GGCGAATTC	840
	AGCAGAAGGA AGCCAAAATA GTTTTTTCCT TTTGAAAGTT TTTTAAAAAT TATTTTCATGG	900
	GTCTTTTTTT TAATTAATAT GTGTGCATTG TTACAATGTA TGTGGATGT CTTTGGACCC	960
30	TAAATGCTTT TTTTGTATC AGAGATTGTG TACTATTTT ATTTTAAATA AATGTATCTT	1020
	CCCTTTCCTT GTTTTAGATT TACTTTGCTC TTCGTTAATC TTATTCCTGA TGATCTAGAA	1080
35	CATTAGTCAT CAACATTACA TGTTCATGC TTCAGATATT TTACTGCTTG TGTCTTATT	1140
	GTGGACAGC TTTAAACAGA GTTGATGGTA CTTCAAATAT AGCTCATTGA TACTTAAGGG	1200
40	CANCTTCCTT GGGATGTGGG CTTTTTGGAA GGAAAAAAT TNCCCCAAAG GCAAATCCCA	1260
	GT	1262

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(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

55

GGCAAACTTT CCCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60

GGGTGCGNC GCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120

60

CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180

	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
5	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
	ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360
	CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT	420
10	GGATTCCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC	480
	TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTT ACCCCACAAT	540
15	AATCGGGGAG AGCGTCTATG GCGATTTCCT GGAAGCCTTT GATCACCTTT GTAACAAGAT	600
	CATTGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTPAAGT ACTGCAACCT	660
	CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG	720
20	TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA	780
	TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCCTCA	840
25	TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA	900
	CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTC CTAATGTGGC	960
	TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA	1020
30	CTACATTGCA CAGGTTGAGC CAGTATTCAC GTGCCAGCAA CAGACCTACT CCACTTGGCT	1080
	ACCCTGCAAT TAAGAATCAT TTAAAAATGT CCTGTGGGGA AGCCATTTC AACAAGACAG	1140
35	GAGAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAGAGC	1179

40 (2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

50	GGCAAACTTT CCCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT	60
	GGGTTGCGNC GGCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT	120
	CAACGGCTCG GCAGCCAGCC ATGTCTTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC	180
55	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
60	ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360

CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT 420
 GGATTCCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC 480
 5 TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTT ACCCCACAAT 540
 AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT 600
 10 CATTGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT 660
 CTTGGTGAGG GCCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG 720
 TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA 780
 15 TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA 840
 TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA 900
 CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTC CTAATGTGGC 960
 20 TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA 1020
 CTACATGCA CAGGTTACGC CAGTATTCAC GTGCCAGCAA CAGACCTACT CCACTTGGCT 1080
 25 ACCCTGCAAT TAAGAATCAT TTAAAAATGT CCTGTGGGGA AGCCATTTC AACAAGACAG 1140
 GAGAGAAAAA NAANGAAAAG AG 1162

30

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CGGGCTGGGT ATTTGCCTCG CACCATGGCG CCCAAGGGCA AAGTGGGCAC GAGAGGGAAG 60
 AAGCAGATAT TTGAAGAGAA CAGAGAGACT CTGAAGTTCT ACCTGCGGAT CATACTGGGG 120
 45 GCCAATGCCA TTTACTGCCT TGTGACGTTG GTCTTCTTTT ACTCATCTGC CTCATTTTGG 180
 GCCTGGTTGG CCTTGGGCTT TAGTCTGGCA GTGTATGGGG CCAGCTACCA CTCTATGAGC 240
 50 TCGATGGCAC GAGCAGCGTT CTCTGAGGA TGGGGCCCTG ATGGATGGTG GCACGAGCTC 300
 AACATGGAGC AGGGCATGGC AGAGCACCTT AAGGATGTGA TCCTACTGAC AGCCATCGTG 360
 CAGGTGCTCA GCTGCTTCTC TCTCTATGTC TGGTCTTCTT GGCTTCTGGC TCCAGGCCGG 420
 55 GCCCTTTACC TCCTGTGGGT GAATGTGCTG GGCCCCGGT TCACTGCAGA CAGTGGCACC 480
 CCAGCACCAG AGCACAATGA GAAACGGCAG CGCCGACAGG AGCGGCGGCA GATGAAGCGG 540
 60 TTATAGCCAT TGACATGTG GCCACAGGCC ACTGGCCCTG GGTGGCTCTG TCAGGGTGCA 600

5 CAGCCCCTCA TGCCTGGAGC AATGAGGGTC TAGTCCAGGG GCCAAAAGCA GTCTGAGGTA 660
TTGGGTATAC TTATACTCTA TAGGGTCGTT GAATAAATGG CTTAGAATGT GAAAAAAAAA 720
AAAAAAAAAA ATTTT 735

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(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

25

AAGTGCATGA GCTGCCGATG TGGTGCTTAG TGATGCGGT TTCGGTCGCT CTCCCGTGTT 60

TCCCGGGCTG GGTATTTGCC TCGCACCATG GCGCCCAAGG GCAAAGTGGG CACGAGAGGG 120

AAGAAGCAGA TATTTGAAGA GAACAGAGAG ACTCTGAAGT TCTACCTGCG GATCATACTG 180

GGGGCCAATG CCATTTACTG CCTTGTGACG TTGGTCTTCT TTTACTCATC TGCCTCATTT 240

30

TGGGCCTGGT TGGCCTGGGC TTTAGTCTGG CAGTGTATGG GGCCAGCTAC CACTCTATGA 300

GCTCGATGGC ACGAGCAGCG TTCTCTGAGG ATGGGGCCCT GATGGATGGT GGCATGGACC 360

TCAACATGGA GCAGGGCATG GCAGAGTGAG TGTCCCCAC CGCCAGCCCA GGCACCTTAA 420

35

GGATGTGATC CTACTGACAG CCATCGTGCA GGTGCTCAGC TGCTTCTCTC TCTATGTCTG 480

GTCCTTCTGG CTTCTGGCTC CAGGCCGGGC CCTTTACCTC CTGTGGGTGA ATGTGCTGGG 540

40

CCCCTGGTTC ACTGCAGACA GTGGCACCCC AGCACCAGAG CACAATGAGA AACGGCAGCG 600

CCGACAGGAG CGGCGGCAGA TGAAGCGGTT ATAGCCATTG ACGATTTKGC SACNRGCCAC 660

TGGCCCTGGG TGGCTCTGTC AGGGTGCACA GCCCCTCATG CCTGGAGCAA TGAGGGTCTA 720

45

GTCCAGGGGC CAAAAGCAGT CTGAGGTATT GGGTATACTT ATACTCTATA GGGTCGTGTA 780

ATA 783

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(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 1638 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

	GGCACGAGGC GCGGCGAGCG GTGGCGGCGG CGCCCCCGG CGGGAGCCGT NCCCTTTCCC	60
5	GTGCGGGAGC GCGGGGYCGG GGYCCAGGGG ANCCCGGMC ACGGAGAGCG GGAAGAGGAT	120
	GGATTGCCCG GCCCTCCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAGAAGT TCAGAAGCAA	240
10	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGTATCTC AGCAGTTTTG ACTTCAGAAC	300
	TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
15	CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC	420
	AATTTTCAAA CAACCGGTAA CCAAAGTCAC AAATCATCCT AGTAATAAAG TGAAATCAGA	480
	CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT	540
20	TAGTGCATCA GATGTAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGGTCTTCA	600
	AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA	660
25	CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCGCTGCT GTGGAAAAGA ACCCTGCTGT	720
	TTGGCTTAAC ACATCTCAAC CCCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG	780
	GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA	840
30	CATCTTGTCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA	900
	AGCCTAAGAA TATGATCAGG TAACTTTTCA CCGACTTTCC CCAAGAGAAA ATTCTAGAA	960
35	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTTFAGATG TATTTTGTAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA	1140
40	TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAAACATT TGTTCCTCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
45	TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAAACA TATTTTATA	1320
	CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCRTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTAC AGACTGATTG GAATTCCTTC TGTGTAAAAG CACACACAAT AAAGAACCCC	1440
50	TCGTTAGCCT TCCTCTGATT TACATTCAAC TCTGATCCCG GGGCCTTAGG TTTGACATGG	1500
	GAGGTGGGAG GAAGATAGCG CATATATTTG CAGTATGAAC TATTGCCTCT GGGACGTTGT	1560
55	GAGGAATTGT GCTTTCACCA GAATTTCTAA GGATTCTGG CTTAAATATC ACCTAGCCTG	1620
	TGGTAATTTT TTTTCCCT	1638
60		

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

10 CGTGCGTACT GCCATGCAGG TACCGGGTCC GGAATGCCCA GGGTCGACCC ACGCGTCCGC 60
 TCAGTTGGCA AGGTACCTGG GAAATACTGT TGATCTCAGC AGTTTGTACT TCAGAACTGG 120
 15 AAAGATGATG CCTAGTAAAT TACAGAAGAA CAAACAGAGA CTGCGAAACG ATCCTCTCAA 180
 TCAAAATAAG GGTAACCAG ACTTGAATAC AACATTGCCA ATTAGACAAA CAGCATCAAT 240
 20 TTTCAAACAA CCGGTAACCA AAGTCACAAA TCATCTAGT AATAAAGTGA AATCAGACCC 300
 ACAACGAATG AATGAACAGC CACGTCAGCT TTTCTGGGAG AAGAGGCTAC AAGGACTTAG 360
 TGCATCAGAT GTAACAGAAC AAATTATAAA AACCATGGAA CTACCCAAAG GTCTTCAAGG 420
 25 AGTTGGTCCA GGTAGCAATG ATGAGACCCT TTTATCTGCT GTTGCCAGTG CTTTGACAC 480
 AAGCTCTGCG CCAATCACAG GGCAAGTCTC CGCTGCTGTG GAAAAGAACC CTGCTGTTTG 540
 GCTTAACACA TCTCAACCCC TCTGCAAAGC TTTTATGTGC ACAGATGAAG ACATCAGGAA 600
 30 ACAGGAAGAG CGAGTACAGC AAGTACGCAA GAAATTGGAA GAAGCACTGA TGGCAGACAT 660
 CTGTGCGCGA GCTGCTGATA CAGAAGAGAT GGATATTGAA ATGGACAGTG GAGATGAAGC 720
 35 CTAAGAATAT GATCAGGTAA CTTTCGACCG ACTTTCCCA AGAGAAAATT CCTAGAAATT 780
 ----- GAACAAAAAT GTTTCCACTG GCTTTTGCCT GTAAGAAAAA AATGTACCC GAGCACATAG ----- 840
 40 AGCTTTTTTAA TAGCACTAAC CAATGCCTTT TTAGATGTAT TTTTGATGTA TATATCTATT 900
 ATTCAAAAAA TCATGTTTAT TTTGAGTCCT AGGACTTAAA ATTAGTCTTT TGTAATATCA 960
 AGCAGGACCC TAAGATGAAG CTGAGCTTTT GATGCCAGGT GCAATCTACT GGAAATGTAG 1020
 45 CACTTACGTA AAACATTTGT TTCCCCACA GTTTTAATAA GAACAGATCA GGAATTCTAA 1080
 ATAAATTTCC CAGTTAAAGA TTATGTGAC TTCACTGTAT ATAAACATAT TTTTATACTT 1140
 TATTGAAAGG GGACACCTGT ACATTCTTCC ATCRTCCTG TAAAGACAAA TAAATGATTA 1200
 50 TATTCACAGA CTGATTGGAA TTCCTTCTGT TGAAAAGCAC ACACAATAAA GAACCCCTCG 1260
 TTAGCCTTCC TCTGATTTAC ATTCAACTCT GATCCCGGGG CCTTAGGTTT GACATGGGAG 1320
 55 GTGGGAGGAA GATAGCGCAT ATATTGCAG TATGAACTAT TGCCTCTGGG ACGTTGTGAG 1380
 GAATTGTGCT TTCACCAGAA TTTCTAAGGA TTTCTGGCTT AAATATCACC TAGCCTGTGG 1440
 60 TAATTTTTTT TCCCT 1455

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CGCCTGCAGT ACCGGTCCGG AATTCCTGGG TCGACCCACG CGTCGCTGAC CCAGGAGAAG 60
CTGCCTGTCT ACATCAGCCT GGGCTGCAGC GCGCTGCCGC CGCGGGGCCG GCAGCTGAAC 120
TATGTGCTCT TCAGGGCGGG CACCGTGTTC CATTTCATCTT TGTACCCCA GCATCTAGCA 180
GTGTTGGCAT GTAGTAGGCA CTCAAGAAAT GTGTGTTGAA TGAACGATGC CTGTGACAAG 240
CAAGCGGACT TTATTCTTTC CTGACCCCTG CTCCTATGAC ACACCTCCTC CTGACTGCCA 300
CTGTCACTCC TTCAGAGCAG AACTCCTCTA GGAACCTGG ATGGGAAACA GCCATGGCCA 360
AGGACATCCT GGGTGAAGCA GGGCTACACT TTGATGAACT GAACAAGCTG AGGGTGTGG 420
ACCCAGAGGT TACCCAGCAG ACCATAGAGC TGAAGGAAGA GTGCAAAGAC TTTGTGGACA 480
AAATTGGCCA GTTTCAGAAA ATAGTTGGTG GTTTAATTGA GCTTGTGAT CAACTTGCAA 540
AAGAAGCAGA AAATGAAAAG ATGAAGGCCA TCGGTGCTCG GAACTTGCTC AAATCTATAG 600
CAAAGCAGAG AGAAGCTCAA CAGCAGCAAC TTCAAGCCCT AATAGCAGAA AAGAAAATGC 660
AGCTAGAAAG GTATCGGGT GAATATGAAG CTTTGTGTAA AGTAGAAGCA GAACAAAATG 720
AATTTATTGA CCAATTTATT TTTCAGAAAT GAACTGAAAA TTTGCTTTT ATAGTAGGAA 780
GGCAAAACAA AAAAAAGCCT CTCAAAACCA AAAAAACCTC TGTAGCATTC CAGCGGCTTG 840
ACCAATGACC TATGTCACAA GAGGTGGCGT GTAAGGAATG CAGCCCCCTG AAGACAGCAC 900
TACAAGTCTG GGGAGCCAG TTTTAACATC AGTGCACAGC TGCTGCTGGT GGCCCTGCAG 960
TGTACGTTCT CACCTCTTAT GCTTAGTTGG AACTAAGCAG TTGTAAACT TTCATCCTTT 1020
TTTTTGTAAT TCACAAAGC TTTGGAAGGA GARGCAATAA ATTTTGTGTT TCNAAATGGC 1080
TTGATG 1086

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

5 GGCACGGGAG CAGCCGGGCT GGTCTGCTG CGAGCCGGCG GCCCGGAGTG GGGCGGCGGA 60
 GCAAACATGA ACCTTGAGT TGCCACAGT GAAGTGAATC CAAATACCCG TGTCATGAAC 120
 AGCCGGGGTA TGTGGCTGAC ATATGCATTG GGAGTTGGCT TGCTTCATAT TGTCTTACTC 180
 10 AGCATTCCCT TCTTCAGTGT TCCTGTTGCT TGGACTTTAA CAAATATTAT ACATAATCTG 240
 GGGATGTACG TATTTTTCGA TGCAGTGAAA GGAACACCTT TCGAACTCC TGACCAGGGT 300
 15 AAAAGCAAGG CTCCTAACTC ATTGGGAACA ACTGGACTAT GGAGTACAGT TTACATCTTC 360
 ACGGAAGTTT TTCACAATTT CTCCAATAAT TCTATATTTT CTGGCAAGTT TCTATACGAA 420
 GTATGATCCA ACTCACTTCA TCCTAAACAC AGCTTCTCTC CTGAGTGTAC TAATTCCCAA 480
 20 AATGCCACAA CTACATGGTG TTCGGATCTT TGAATTAAT AAGTATTGAA ATGTTTTGAA 540
 ACTGAAAAAA AATTTTACAG CTACTGAATT TCTATAAGG AAGGAGTGGT TAGTAACTG 600
 25 CACTGTTTCT CTGATAATGT GAAATGAGAA GTATTTACAT TGGAGGGCCA ATGGCTGGTC 660
 CTTCAAGTGC TGTTTTGAAG TGCAGATTTT CATTAAATGA TGCCTCTGTT TAATACACCT 720
 GGTACATTTT TGAAGAGGGG CTTTATAAGC AGGCTGGGCA GGCCAGCTT ATAAGTTAAA 780
 30 GGGCATCACA GTGAGGGTGT AGTAGATAAA TTCAAGGAAA TAAGAGATTT GTAAGAACT 840
 AGGACCAGCT TAACTTATAA TGAATGGGCA TTGTGTTAAG AAAAGAACAT TTCCAGTCAT 900
 35 TCAGCTGTGG TTATTTAAAG CAGACTTACA TGTAAACCGG AATCCTCTCT ATACAAGTTT 960
 -----ATFAAGATT-ATTTTATTA-CCGTAAAAAA-AAAAAAAAAA-AAA-----1003-----

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(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ATCAGCATCT ACAAGTAGCA TATTTTGGAT GGTGTTGTG TGCTACTTCA AAGTAACTAG 60
 GAAAAAATAA TCCTCGCAAC ACAGGTACCT TGTCATGTCA GAATTGGGGG TGTTAGGTTG 120
 55 CCAGTTGTAT CAGTGTGAT TCATTTTATT ACTTCCTACA GAGCAAACAT GAACGTGGA 180
 GTTGCCACA GTGAAGTGAA TCCAAATACC CGTGTATGA ACAGCCGGGG TATGTGGCTG 240
 60 ACATATGCAT TGGGAGTTGG CTGTCTCAT ATTGTCTTAC TCAGCATTC CTTCTTCAGT 300

	GTTCTCTGTG CTTGGACTTT AACAAATATT ATACATAATC TGGGGATGTA CGTATTTTGTG	360
5	CATGCAGTGA AAGGAACACC TTTCGAAACT CCTGACCAGG GTAAAGCAAG GCTCCTAACT	420
	CATTGGGAAC AACTGGACTA TGGAGTACAG TTTACATCTT CACGGAAGTT TTTCACAATT	480
	TCTCCAATAA TTCTATATTT TCTGGCAAGT TTCTATACGA AGTATGATCC AACTCACTTC	540
10	ATCCTAAACA CAGCTTCTCT CCTGAGTGTA CTAATTCCTA AAATGCCACA ACTACATGGT	600
	GTTCCGATCT TTGGAATTAA TAAGTATTGA AATGTTTGA AACTGAAAAA AAATTTTACA	660
15	GCTACTGAAT TTCTTATAAG GAAGGAGTGG TTAGTAAACT GCACTGTTTC TSTGATAATG	720
	TGAAATGAGA AGTATTTACA TTGGAGGGCC AATGGCTGGT CCTTCAAGTG CTGTTTGTAA	780
	GTGCAGATTT CCATTAAATG ATGCCTCTGT TTAATACACC TGGTACATTT CTGAAGAGGG	840
20	GCTTTATAAG CARGCTGGGC AGGCCAGCT TATAAGTTAA AGGGCATCAC AGTGAGGGTG	900
	TAGTAGATAA ATTCAAGGAA ATAAGAGATT TGTAAGAAAC TAGGACCAGC TTAACCTATA	960
25	ATGAATGGGC ATTGTGTAA GAAAAGAACA TTTCCAGTCA TTCAGCTGTG GTTATTTTAA	1020
	GCAGACTTAC ATGTAAACCG GAATCCTCTC TATACAAGTT TATTAAAGAT TATTTTATT	1080
	ACCRTACATA TTTCKCTTGT TTTATGTAAG YGGATGTATA TCCTCTTGTT TTATACAAGC	1140
30	CAGTTCCAC TTATGAGGGT ACTTTTTTGG TTTTGCTGGG CTTAATATTG TGTATTGGTC	1200
	AATGAGGCCA TTTTACANT TATTAACGTT ACAG	1234
35		

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

	NGAGGTGCGT TCTGAGCCGT CTGTCTGCG CCAAGATGCT TCAAAGTATT ATTAAAAACA	60
50	TATGGATCCC CATGAAGCCC TACTACACCA AAGTTTACCA GGAGATTGG ATAGGAATGG	120
	GGCTGATGGG CTTTCATCGTT TATAAAATCC GGGCTGCTGA TAAAAGAAGT AAGGCTTTGA	180
	AAGCTTCAGC GCCTGCTCCT GGTCACTACT AACCAGATTT ACTTGGAGTA CATGTGAAAG	240
55	AAAACGTCAG TCTGCCTGTA AATTTTCAGCA AGCCGTGTTA GATGGGGAGC GTGGAACGTC	300
	ACTGTACACT TGTATAAGTA CCGTTTACTT CATGGCATGA ATAAATGGAT CTGTGAGATG	360
60	CACTGCTACC TGGTACTGCT TTCAGTGTGT TCCCCCTCAG CCCTCCGGCG TGTCAGGCAT	420

ACTCTGAGTA GATAATTTGT CATGCAGCGC ATGCAATCAG AATCTCACTG AGCCACCCAT 480
 CATTGTGAAA TAATTACCTC AGTTGTACAG GACTTGGTGA TCAGGATCCA GGCACCTACT 540
 5 TGTATTCTAC TGCTCAATAA ACGTTTATTA AACT 574

10 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1731 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

20 GCTGCAAGGT GCGCCTCGTG CCGCTGCAGA TCCAGCTCAC TACCCTGGGA AATCTTACAC 60
 CTTCAAGCAC TGTGTTTTTC TGCTGTGATA TGCAGGAAAG GTTCAGACCA GCCATCAAGT 120
 ATTTTGGGGA TATTATTAGC GTGGACAGA GATTGTTGCA AGGGGCCCGG ATTTTAGGAA 180
 25 TTCCTGTTAT TGTAACAGAA CAATACCCTA AAGGTCTTGG GAGCACGGTT CAAGAAATTG 240
 ATTTAACAGG TGTAAAACTG GTACTTCCAA AGACCAAGTT TTCAATGGTA TTACCAGAAG 300
 30 TAGAAGCGGC ATTAGCAGAG ATTCCCGGAG TCAGGAGTGT TGTATTATTT GGAGTAGAAA 360
 CTCATGTGTG CATCCAACAA ACTGCCCTGG AGCTAGTTGG CCGAGGAGTC GAGGTTTACA 420
 TTGTTGCTGA TGCCACCTCA TCAAGAAGCA TGATGGACAG GATGTTTGCC CTCGAGCGTC 480
 35 TOGCTCRARC CNGGGATCAT AGTGACCACG AGTGNAGGCT GTTCTGCTTC AGCTGGTAGC 540

TGATAAGGAC CATCCAAAAT TCAAGGAAAT TCAGAATCTA ATTAAGGCGA GTGCTCCAGA 600
 40 GTCGGGTCTG CTTTCCAAAG TATAGGACAT TTGAAGAACT GGTATGCTAC TCACTGGTGA 660
 AGGACAGTCA GGTGAAGGAC TGTAAGCCCA CACAAGCTCT TCTTATCTCT ACTAGAATTA 720
 AAATGTTAAG TCAAAAACGG CTCCTTTTTT GCGCCTCCTA GTGAACCTAA CCAGCTAGAC 780
 45 CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT CCGGTGCTGC TTACCTTCCT 840
 TTTTGTGTTA TGTGCTTTTA TTTATTAAAA AAAATTACAA TGAAGATGCC TGTTTTGTCT 900
 50 CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT CTTGTGAAGT TTTCTTAAAT 960
 TGTTCACCTT AAAGAAAATG ACGTACCAAC AATGATTTGG CTTTTATATT ACTGTAAGAT 1020
 GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG ATTGATTGGA ATAAGATTAT 1080
 55 TGCATATGAA TTTACCCACA GGA CTCTGAA TCATGTTACC CACTCCCCTC ACAATGTTGT 1140
 CCACCTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT GTTGAATAAT TACATATCTT 1200
 60 TCTKGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA AATCTCTGTT AATATTCTCT 1260

CTTTAACTG AAAAGGGATG GGATAGAAGG GTTGTCAATG CCATATTATT GGTGGAGGGC 1320
 TGTTTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT ACCAACATCT TGAATATATA 1380
 - 5 TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG GTGGAATATC ATTTTAAAT 1440
 GTTCATGTC TGTCTATAT TTTCTCACC TACTCTCAA ATATTGTAAT GCAAAAAGTC 1500
 10 TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATGTT TCTCTCGAT AAATTTATTT 1560
 TCATTAAATA CTTRTTAGAG GGTMTTGAAA TGTMTTCAA ATATGTGAAA TGTGAACTG 1620
 CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG ATTGAAATTA TTTTGNCCTC 1680
 15 CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT ATTTATTTAA G 1731

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(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1320 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

30 CTGCTTAGGA AGAGAAGGTC AGAGTTCGCG GGGCAGAGG CATCTTGCC GCTGGCCCG 60
 TCACTATGTA GTGGAGGGGC AGACACCCTC CCGCAAATTC TGGAAGGTTT TTAGTCTCGA 120
 35 CTAGGGCAGT AGCCCAGGAC TCCTAGTCGC CGGCTTCAGG TCACTGCCCG CTGAACGGAG 180
 CTGCCGTGCG CATGTTTGGC TGCTTGGTGG CGGGAGGCT GGTGCAAACA GCTGCACAGC 240
 AAGTGGCAGA GGATAAATTT GTTTTGAAGT TACCTGATTA TGAAAGTATC AACCATGTTG 300
 40 TGGTTTTTAT GCTGGGAACA ATCCCATTTT CTGAGGGAAT GGGAGGATCT GTCTACTTTT 360
 CTTATCCTGA TTCAAATGGA ATGCCAGTAT GGMAACTCCT AGGATTTGTC ACGAATGGGA 420
 45 AGCCAAGTGC CATCTTCAAA ATTTCAAGTC TTAAATCTGG AGAAGGAAGC CAACATCCTT 480
 TTGAGCCAT GAATATTGTC CGAACTCCAT CTGTTGCTCA GATTGGAATT TCAGTGAAT 540
 TATTAGACAG TATGGCTCAG CAGACTCCTG TAGGTAATGC TGCTGTATCC TCAGTTGACT 600
 50 CATCACTCA GTTCACACAA AAGATGTTGG ACAATTTCTA CAATTTTGCT TCATCATTTG 660
 CTGTCTCTCA GGCCAGATG ACACCAAGCC CATCTGAAAT GTTCATTCCG GCAAATGTGG 720
 55 TTCTGCAAAT GGTATGAGGC ATNTTCTGTC TCCAATATTA AGGCTTTTTA TAACTGAATA 780
 TCTATTTTGT CTATGAATAT ATTCTTTT TTGACATTTAA ACATATTCTT TTATTGTGAA 840
 CATCAGCACT GCATGCCATT AAAGTATGTA CTATAGAGAT CTGATGAGAA ACAGTTCTTA 900
 60

CCCTAAATAT TTTGTTATAT TGTCGCCATT ATGAATTTAT AAAGACAGGA AAATATAGTT 960
GCCTATGTTT TAGGGACCAC TATTAAAGCT TATAAATATT TGTGTATTTT CATTTAGAAG 1020
- 5 TACCATCTAT GAGAGTAGTT TATACTGCAC TGTGTACATG AATGGCTAAT GAATCTATTT 1080
TCCAACTTTC CCGTGTTTTA TAGATATTTT TTTTCACTTT GAGTATCCTA GAGATGGGAG 1140
GATGCCTAGG AAGAGTTTGT TGAGAAGTGG TACCATGGTG TAGCATGGGA GAGCATTGGG 1200
10 AATGCACTAG GTTTGAATTT GGCATAATGG TAGCTATGTG ACCCTGAGCA AATTTCTCTC 1260
ATCTGCTCAT CTGANGAATG AGGAAATAGG AGTGAATTTG ATNTTTCCTA GGTCCTCTA 1320

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(2) INFORMATION FOR SEQ ID NO: 273:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG GGAGGGTCTG GGATGGGGCT GCCCCTGATG 60
30 GCCCCTGATGT GGAGTACCTT GCCAGCATCT GCTGGGGTGA ACTTTATTTT AGCCCTTCCC 120
TTGTTGYTCT TATGAAGAAC AGAGGAGGGG TGGCAGGTC AGTGATGTCA GCAGTGAGTA 180
TTCCCAGCAC AGCGCTCTG GAAGAGGCAT GAGGCATTTT TTTTCAGGAAA TGRTCATTAT 240
35 TCAGCCAGAA GGCATTCAIT AAGTAAGTCC TGACTTTGTG CCCAGCTCTG TGTATAGGC 300

CCTTGGCGAG ACTCAGGAGG GGCARAGGAC GCTAGKTTKT AGWTAACACG GAACCTCARA 360
40 GGWTATATGG TCCAAGAAGA CCCGGGGGCG GTGAAAACCC TGTGGACTAA TGCTCACGGG 420
AGCCCAGAGT CACACTTTGA CTTTGCTACC ATGGGCTGTG TCTANGNACG TATATATGCT 480
CGGTAATTAT TACAGAGGCA GTCCATGTGC ATTGT 515

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(2) INFORMATION FOR SEQ ID NO: 274:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

TGACACCCAT AAGGAATTCA TGAAGAAAGT AGAAGAAAAG CGAGTGGACG TTAACCTCAGC 60

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	AGTAGCCATG GGAGAAGTCA TCCTGGCTGT CTGCCACCCC GATTGCATCA CAACCATCAA	120
	ACACTGGATC ACCATCATCC GAGCTCGCTT CGAGGAGGTC CTGACATGGG CTAAGCAGCA	180
5	CCAGCAGCGT CTTGAAACGG CCTTGTGAGA ACTGGTGGCT AATGCTGAGC TCCTGGAAGA	240
	ACTTCTGGCA TGGATCCAGT GGGCTGAGAC CACCCTCATT CAGCGGGATC AGGAGCCAAT	300
10	CCCCAGAAC ATTGACCGAG TTAAAGCCCT TATCGCTGAG CATCAGACAT TTATGGAGGA	360
	GATGACTCGC AAACAGCCTG ACGTGGACCG GGTACCAAG ACATACAAA GGAAAAACAT	420
	AGAGCCTACT CACGCGCCTT TCATAGAGAA ATCCCGCAGC GGAGGCAGGA AATCCCTAAG	480
15	TCAGCCAACC CCTCCTCCCA TGCCAATCCT TTCACAGTCT GAAGCAAAA ACCCACGGAT	540
	CAACCAGCTT TCTGCCCCGT GGCAGCAGGT GTGGCTGTTA GCACTGGAGC GGCAAAGGAA	600
20	ACTGAATGAT GCCTTGGATC GGCTGGAGGA GTTGAAAGAA TTTGCCAACT TTGACTTTGA	660
	TGTCTGGAGG AAAAAGTATA TGCCTTGGAT GAATCACAAA AAGTCTCGAG TGATGGATTT	720
	CTTCCGGCGC ATTGATAAGG ACCAGGATGG GAAGATAACA CGTCAGGAGT TTATCGATGG	780
25	CATTTTAGCA TCCAAGTCC CCACCACCAA GTTAGAGATG ACTGCTGTGG CTGACATTTT	840
	CGACCGAGAT GGGGATGGTT ACATTGATTA TTATGAATTT GTGGCTGCTC TTCATCCCAA	900
30	CAAGGATGCG TATCGACCAA CAACCGATGC AGATAAAATC GAAGATGAGG TTACAAGACA	960
	AGTGGCTCAG TGCAAATGTG CAAAAGGTT TCAGGTGGAG CAGATCGGAG AGAATAAATA	1020
	CCGGTTCTTC CTCGGCAATC AGTTTGGGGA TTCTCAGCAG TTGCGGCTGG TCCGTATTCT	1080
35	GCGCAACCGT GATGGTTCCG GTTGGTGGAG GATGGATGGC CTTGGATGAA TTTTATGTA	1140
	AAAATGATCC CTGCCGAGCA CGAGGTAGAA CTAACATTGA ACTTAGAGAG AAATTCATCC	1200
40	TACCAGAGGG AGCATCCCAG GGAATGACCC CCTTCCGCTC ACGGGTCTGA AGGTCCAAAC	1260
	CATCTTCCCG GGCAGCTTCC CCTACTCGTT CCAGTCCAG TGCTAGTCAG AGTAACCACA	1320
	GCTGTACATC CATGCCATCT TCTCCAGCCA CCCCAGCCAG TGGAAACCAAG GTTATCCCAT	1380
45	CATCAGGTAG CAAGTTGAAA CGACCAACAC CAACTTTTCA TTCTAGTCGG ACATCCCTTG	1440
	CTGGTGATAC CAGCAATTAG TTCTTCCCCG GCCTCCACAG GTGCCAAAAC TAATCGGGCA	1500
50	GACCTTAAA AGTCTGCCAG TCGCCCTGGG AGTCGGGCTG GGAGTCGAGC CGGGAGTCGA	1560
	GCCAGCAGCC GGCAGGAAG TGACGCTTCT GACTTTGACC TCTTAGAGAC GCATTGCTTG	1620
	TTCCGACACT TCAGAAAGCA GCGCTGCAGG GGGCCAAGGC AACTCCAGGA GAGGGCTAAA	1680
55	CAAACCTTCC AAAATCCCAA CCATGTCTAA GAAGACCACC ACTGCCTCCC CCAGGACTCC	1740
	AGGTCCCAAG CGATAACACT GTCTAAGCAC CCCCAGCCA CTATCCACTT TGAATCCTGC	1800
60	TCCATACATT GGGTGTATAT TTATTCTGAA CGGGAGAAGT TATATTGTTA AAAGTGTAAG	1860

AGAATAATTG TGTTATGAAG CTGCCTTATT TTTTTCCTTT TTGTAAGTTA CTATTTTCAT 1920
 GTGAATATTT ATGTAGATAA AATTGCCTC CTGGTAACCC TGTAATGGAT GGGGCCCAGA 1980
 5 AATGAAATAT TTGAGAAAA CAAGTGAAAA GGTCAAGATA CAAATGTGTA TTAAAAAAA 2040
 AAAAGCCTAT TAATAGGGTT TCTGCGCGGT GCAGGGTTGT AAACCTGCTT TATCTTTTAG 2100
 10 GATTATTCCT AAATGCATCT TCTTTATAAA CTGACTTGC TATCTCAGCA AGATAAATTA 2160
 TATTAAAAAA ATAAGAATCC TGCAGTGTTC AAGGAACTCT TTTTGTGTA ATCACGGACA 2220
 CCTCAATTAG CAAGAACTGA GGGGAGGGCT TTTCCATTG TTTAATGTTT TGTGATTTT 2280
 15 AGCTAAAGAG AGGGAACCTC ATCTAAGTAA CATTTGCACA TGGATACAGC AAAAGGAGTT 2340
 CATTGCAATA CTGTCTTTGG ATATGTGTTT AGTACTGGGT GTTTAAAGGA CAAATAGCTG 2400
 CTAGAATTCA GGGGTAAATG TAAGTGTTCA GAAAACGTCA GAACATTTGG GGTTTAAAC 2460
 20 TGATTTGTTG CTCCCTATCC AGCCTAGACA CCAGTAACTC TTGTGTCAC CAGGACCCAG 2520
 ACCCTTGGCA AGGGATAGGC TCGTTGGTGA CATTTGTGAAT TTCAGATTTG TTTTATCCAC 2580
 25 TTTTPTTGCT ATTTATTTAA ATGGTCGATC AACTTCCCAC AAAC TGAGGA ATGAATTCCA 2640
 CGAGCCTGTT CTGAAAATGT GGACGTAAGA CAAACACGTG CTCGTCCTTT AATGGAGTTC 2700
 ACCAGCACAC TTGTTAACCA GTCTGTGTTG CTTCGTCTT TTTTGTGCG TAATAAAGTC 2760
 30 AACTGACCAA GTGACCATGA AAAGGGGCTG TCTGGGGCTC CTGTTTMTTA GCTGCTGTTT 2820
 TTCAGCTCCG ACCATGTTGC TGTGTGATTA TCTCAATTGG TTTTAATTGA GGCAGAACT 2880
 35 GAAGCTCTAC CAATGAAC TGTTAGAAACA AGACACACTT TTGTATTAAA ATTGCTTGCA 2940
 -----GTAACAAAAA-AAAAAAAAA-AAAAAAAAA-AAAAAACTCG-AGGGGGGCEC-GGTAC-----2995-----

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(2) INFORMATION FOR SEQ ID NO: 275:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

GGGACCCGCG CGSCTCCCGG GGATGGTGAG CAAGGCGCTG CTGCNWCCTG TCTGCCGTCA 60
 ACCGCAGAGG ATGAAGCTGC TGCTGGGCAT CGCCTTGCTG GCCTACGTCG CCTCTGTTTG 120
 55 GGGCAACTTC GTTAATATGA GGTCTATCCA GGAAAATGGT GAACTAAAAA TTGAAAGCAA 180
 GATTGAAGAG ATGGTTGAAC CACTAAGAGA GAAAATCAGA GATTTAGAAA AAAGCTTTAC 240
 60 CCAGAAATAC CCACCAGTAA AGTTTTTTATC AGAAAAGGAT CGGAAAAGAA TTTTGAWTAA 300

	CAGGAGGCGC AGKGTTCGTG GGCTCCCATC TKAAC TGACA AACTCATGAT GGACGGCCAC	360
	GAGGTGACCG TGGTGGACAA TTTCTTCACG GGCAGGAAGA GAAACGTGGA GCACTGGATC	420
5	GGACATGAGA ACTTCGAGTT GATTAACCAC GACGTGTGGG AGCCCCCTCTA CATCGAGGTT	480
	GACCAGATAT ACCATCTGGC ATCTCCAGCC TCCCCTCCAA ACTACATGTA TAATCCTATC	540
10	AAGACATTAA AGACCAATAC GATTGGGACA TTAAACATGT TGGGGCTGGC AAAACGAGTC	600
	GGTGCCCGTC TGCTCCTGGC CTCCACATCG GAGGTGTATG GAGATCCTGA AGTCCACCCT	660
	CAAAGTGAGG ATTACTGGGG CCACGTGAAT CCAATAGGAC CTCGGGCCTG CTACGATGAA	720
15	GGCAAACGTG TTGCAGAGAC CATGTGCTAT GCCTACATGA AGCAGGAAGG CGTGGAAGTG	780
	CGAGTGCCA GAATCTTCAA CACCTTTGGG CCACGCATGC ACATGAACGA TGGGCGAGTA	840
20	GTCAGCAACT TCATCCTGCA GGCCTCCAG GGGGAGCCAC TCACGGTATA CGGATCCGGG	900
	TCTCAGACAA GGGCGTTCCA GTACGTCAGC GATCTAGTGA ATGGCCTCGT GGCTCTCATG	960
	AACAGCAACG TCAGCAGCCC GGTCAACCTG GGAACCCAG AAGAACACAC AATCCTAGAA	1020
25	TTTGCTCAGT TAATTAAAAA CCTGTGTTGGT AGCGGAAGTG AAATTCAGTT TCTCTCGAA	1080
	GCCCAGGATG ACCCACAGAA AAGAAAACCA GACATCAAAA AAGCAAAGCT GATGCTGGGG	1140
30	TGGGAGCCCG TGGTCCCCTG GGAGGAAGGT TTAAACAAAG CAATTCACTA CTTCCGTAAA	1200
	GAACTCGAGT ACCAGGCAAA TAATCAGTAC ATCCCCAAAC CAAAGCCTGC CAGAATAAAG	1260
	AAAGGACGGA CTCGCCACAG CTGAACTCCT CACTTTTAGG ACACAAGACT ACCATTGTAC	1320
35	ACTTGATGGG ATGTATTTT GGCTTTTTTT TGTGTGCGTT TAAAGAAAGA CTTTAACAGG	1380
	TGTCATGAAG AACAACTGG AATTTTCATTC TGAAGCTTGC TTAAATGAAA TGGATGTGCC	1440
40	TAAAAGCTCC CCTCAAAAAA CTGCAGATTT TGCCTTGAC TTTTGAATC TCTCTTTTAA	1500
	TGTAAATAG CGTAGATGCA TCTCTGCGTA TTTTCAAGTT TTTTATCTT GCTGTGAGAG	1560
45	CATATGTTGT GACTGTGCTT GACAGTTTAA TTTACTGGTT TCTTTGTGAA GCTGAAAAGG	1620
	AACATTAAGC GGGACAAAAA ATGCCGATTT TATTTATAAA AGTGGGTACT TAATAAATGA	1680
	GTCGTTATAC TATGCATAAA GAAAAAYCCT AGCAGTATTG TCAGGTGGTG GTGCGCCGGC	1740
50	ATTGATTTTA GGCAGATAA AAGAATCTG TGTGAGAGCT TTATGTTTCT CTTTAAATTC	1800
	AGAGTTTTTC CAAGGTCTAC TTTTGAGTTG CAACTTGAC TTGAAATAT TCCTGTTGGT	1860
55	CATGATCAAG GATATTTGAA ATCACTACTG TGTMTGCTG CGTATCTGGG GCGGGGCGAG	1920
	GTTGGGGGGC ACAAAGTTAA CATATTCTTG GTTAACCATG GTTAAATATG CTATTTTAAAT	1980
	AAAATATTGA	1990
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(2) INFORMATION FOR SEQ ID NO: 276:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

	AAC TTCGCTT AGCTCTCCAG GGTNAAACGG GTGAGNCCTT AAAACAGAA GAGAACAAGA	60
15	TTTAAAGTCC GTTGCATTGA AAATAACAAA CAATATCAAT GTTTTAATCA AGGATCTCTT	120
	CCACATTCCT CTTCTTATA AGAGCACAGT AACACTATCC TGGAAACCTG TACAAAAGGT	180
20	TGAGATTGGG CAAAAGAGAG CCAGTGAAGA TACAACTTCA GGTTCACCAC CCAAGAAATC	240
	TTCAGCAGGA CAAAAAGAG ATGCCAGGCA GATTTATAAC CCTCCCAGTG GGAAATATAG	300
	CAGCAATTG GGCAACTTTA ATTATGAGCA GAGAGGAGCC TTCAGGGGAA GTAGAGGTGG	360
25	CCGAGGTGG GGCACACGAG GAAATCGTAG TCGGGGAAGA CTCTACTGAA TAAGACATCA	420
	GCATTCTTCA GCATTGTCAT GAGCTTAATA TACTTAAATT CTACTACTCA TTGGATTGCC	480
30	GGGGATGTCC CTTTAAACAG ACTGCTGCCT TCAGCTAAAA ACTTAATGTT CTTTATACCT	540
	TTGTATGTAT GACCTACTTT TGTAACAGAC CATGGTTGTG TCCAAGGTAA AACCACAGTG	600
	ATATTTTGG ATGCTTTGTC TGCAATCTTG ACTTGTTTTT GCAGTATCAT TATTCAGACT	660
35	TCAAATGTG AATCTTTTAA ACATCTTGAT AATTTGTTGT TGAGAGCTGT TCATTCTAAA	720
	ATGTAATGAA ATTCACTCTA GTTCTGCTGA TAAAGATCAT CAGTTTTGAA AGGTTACTGA	780
40	TTTTCTCTT CCTCTTAGT TTTTACCCA ATATATGGAG AAGAGTAATG GTCAATCTTA	840
	ACATTTTGTT TTAATTGTTT AATAAAGCTG CTGGGCAGTG GTGCAGCATT CCTACCTAGT	900
	GTCATAAAG CAAAATACTT ACATAGCTTT CTTAAAATAT AGGAATGACA TTACATTTT	960
45	AGGAGAAAGT AAGTTGCTTT GCACCGCCTA CTTAATTCCT TTCCATATAT TGTGATACAA	1020
	ACTTTTGAAT ATGGAATCTT ACTATTTGAA TAGAAATGTG TATGTATAAT ATACATACAT	1080
50	ACATAAGCAT ATATGTGTGT GTGTGTGTGT ATATATATAT ATATGCATGC TGTGAACTT	1140
	GACTACACAA CATAAATCAC TTTTAAATT CCAGGAACGG GTAGTCTGAC ACGGTGATTA	1200
	TCCTTTTGAG GCTGAATCCG TTATTAACTT GTTATTTAGG TTTTACTCC CAGTAGCAAG	1260
55	GGATTCTAAG TTAGTTGCAC TTACATGATT ATTGTTATTT AAAACTAAGA ATAAAGGCTG	1320
	CATTTTCAAA GATAAATTGG AATTGCTGTT GGTGAAATAA CAACCAAAAT ACTGAATCTG	1380
60	ATGTACATAC AGGTTTCTAC AGGAAGAGAT GGTATAATTT ACAATTGGA GATTTAATAA	1440

	CCAGGGCTAC CCAGAAAAAG TGACTTGATA ACATGGTACC AATAAGTAAG GGATGCTCTC	1500
	TCGGTTTGCT TTTGCCACTT TCAAGATTTT AACTTCTCAG GTTATTAATC AAAATTATTG	1560
- 5	TATAAGTTAG CCAATAGAAT TTTTAGGTTA AAACAACAGA TGGGGGGTTT GTGGAGTGTT	1620
	TAATGTCATG GGCATTTTTA GTAGCATAGA CCCTTTGTTC TGCATTTGAA TGTTTCGTAT	1680
10	ATTTTGTGTT CACAGTTAAT CTTCCCTCCC CAAGTTTGCT ATTCAAATCA ACTGCCTGAA	1740
	TGACATTTCT AGTAGTCTGA TGTATTTTTC TGAGGAATAG TTTGTGATTC CAATGCAGGT	1800
	GTCTTCATTA CCATTACCTC TACACTGCAG AAGAAGCAAA ACTCCTTTAT TAGAATTACT	1860
15	GCACATGTGT ATGGGGAAAA TAGTTCTGAA AGGCTAGAAT GATACAAGTG AGCAAAAGTT	1920
	GGTCAGCTTG GCTATGGAGT GGTGGCAATA ATCTCTAAAC ATTCCAAAAG ACCATGAGCT	1980
20	GAACCTAAAC TCCCTTGGA TCTGAACAAA GGAATATAAA ATTGCCATTT GAAAACTGAC	2040
	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	2100
	AATTATAGAG ACTACAGCTA AATAAATTG AACATTAAAT ATAATTTTAC CACTTTTGT	2160
25	CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	2220
	GATACTGAGT TGACTGTTCC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	2280
30	GTGCACAACT TAGGTTATTT TTGCTTCCGA ATTTGAATGA AAACTTAAT GCCATGGATT	2340
	TTTTTCTTTT GCAAGACACC TGTTTATCAT CTTGTTTAAA TGTAAATGTC CCCTTATGCT	2400
	TTTGAAATAA ATTTCTTTT GTAATTTTAA AAAAAA	2436
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(2) INFORMATION FOR SEQ ID NO: 277:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

	GCCACTGACT TCTCCACCC TTCTGTCTCC CCCATAATAG TTTATTTGGT TGGTCTGGAC	60
50	TCACTTGTGG CCTTTRATTA AATTCTAAG GGGCCTGAAG AAGACATTC TACTGCAGAG	120
	GGTTAGAGGC ACTTGAGCAA GGCCCCACA TCCCAACTCT GGGAGTTGTG GTGGGAGGAG	180
55	GCACTTCTGG GGGATAGGAC CAGACAAGAT AACAGGAGCT CACATGNNAA GCAGAAGCTG	240
	TGACAAGTTT AGTAGTCCCA AAATGGGTTA TATCCCTTCC CCCTTTACAT CAGAATCTTG	300
	TGAAATGGGA AAACAACAGA AGGAGGGGAT CAAAGATAGC TGATCTCACA TGCTTCCAG	360
60	GCAGGCARA GGTGGGAGTC AAACCGGGT GACAGGTGGG TGGAGAGCCC TGTTTGAGGT	420

TGTGGCTGAT CCCTCTCTGG TATTAGTTTT TCCCCTGGGA GCAGGAAGCC CTAGGAAGAG 480
 GGGACTGCAG GGTCCCCRGG GGATCTTTCC TCCCTCCCCT GCATGAGGCA GAGGCAAGCT 540
 5 GCCTGCCAAC CCCCTCCCTC AAGGAATGGC CTTGCCCAGG AATGCCACC ACACATACCC 600
 TCTTCTTTTT TTCTAGTCAA ACTCTTGTTC ATTCTTGGC TTGCCTCCCT CCTTCCTCCC 660
 10 CTCTCAACCT TTA CTCTCTGA TTTCTATTC ATGGAATTTG GGATTGAAGT TAAACTACAA 720
 CAGTGCCGCC AACACCAAGT CTGTCAGGAA AAAAATACAA AGAAATTTAA CAAAAAAAAA 780
 AA 782

20 (2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 961 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

30 GAGTTCGGC TGGAGACCCG TGCTCTGGGC CGCGCCTTC ACCATGGCCT CGGCAGAGCT 60
 GGACTACACC ATCGAGATCC CGGATCAGCC CTGCTGGAGC CAGAAGAACA GCCCCAGCCC 120
 AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC TGTGGTGATT CTYTTGGGCT GGGGTGGCTG 180
 35 CAAGGACAAG AACCTTGCCA AGTACAGTGC CATCTACCAC AAAAGGGGCT GCATCGTAAT 240
 -----CCGATACACA GCCCCGTGGC ACATGGTCTT CTCTCCGAG TCACTGGGTA TCECTTCACT----- 300-----
 40 TCGTGTTTTG GCCCAGAAGC TGCTCGAGCT GCTCTTTGAT TATGAGATTG AGAAGGAGCC 360
 CCTGCTCTTC CATGTCTTCA GCAACGGTGG CGTCATGCTG TACCGCTACG TGCTGGAGCT 420
 CCTGCAGACC CGTCGCTTCT GCCGCTGCG TGTGGTGGGC ACCATCTTTG ACAGCGCTCC 480
 45 TGGTGACAGC AACCTGGTAG GGGCTCTGCG GGCCCTGGCA GCCATCCTGG AGCGCCGGGC 540
 CGCCATGCTG CGCTGTGTC TGCTGGTGGC CTTTGCCCTG GTGGTCGTCC TGTCCACGT 600
 CCTGCTTGCT CCCATCACAG CCCTCTTCCA CACCCACTTC TATGACAGGC TACAGGACGC 660
 50 GGGCTCTGCG TGGCCCGAGC TCTACCTCTA YTCGAGGGCT GACGAAGTAG TCCTGGCCAG 720
 AGACATAGAA CGCATGGTGG AGGCACGCCT GGCACGCCG GTCTGGCGC GTTCTGTGGA 780
 55 TTTCGTGTCA TCTGCACACG TCAGCCACCT CCGTGACTAC CCTACTTACT ACACAAGCCT 840
 CTGTGTCGAC TTCATGCGCA ACTGCGTCCG CTGCTGAGGC CATTGCTCCA TCTCAMCTCT 900
 GCTCCAGAAA TAAATGCCTG ACAMCTCCCC AAAAAAAAAA AAAAAAAAAA ACTCGAGGGG 960
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961

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(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

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CGCGCTTTGC AGTTCGGTCT CCTGGTGTC GGCCAACGCC AAGTAGGGGA TTGCGTTCCT 60

TCCAGTCGCA GCCCTATCAG ATTTGGATAT GTCCTTCATA TTTGATTGGA TTTACAGTGG 120

TTTCAGCAGT GTGCTACAGT TTTTAGGATT ATATAAGAAA ACTGGTAAAC TGGTATTTCT 180

TGGATTGGAT AATGCAGGAA AAACAACATT GCTACACATG CTAAAAGATG ACAGACTTGG 240

25

ACAACATGTC CCAACATTAC ATCCCACTTC CGAAGAACTG ACCATTGCTG GCATGACGTT 300

TACAACTTTT GATCTGGGTG GACATGTTCA AGCTCGAAGA GTGTGGAAAA ACTACCTTCC 360

TGCTATCAAT GGCATTGTAT TTCTGGTGGA TTGTGCAGAC CACGAAAGGC TGTTAGAGTC 420

30

AAAAGAAGAA CTTGATTAC TAATGACAGA TGAAACCATT GCTAATGTGC CTATACTGAT 480

TCTTGGGAAT AAGATCGACA GACCTGAAGC CATCAGTGAA GAGAGGTTGC GAGAGATGTT 540

35

TGGTTTATAT GGTGAGACAA CAGGAAAGGG GAGTATATCT CTGAAAGAAC TGAATGCCCG 600

ACCCCTTAGAA GTTTTCATGT GTAGTGTGCT CAAAAGACAA GGTACGGAG AAGGCTTCCG 660

40

CTGGATGGCA CAGTACATTG ATTAACACAA ACTCACATTG GTTCCAGGTC TCAACGTTCA 720

GGCTTACTCA GAGATTTGAT TGCTCAACAT GCATAACTTG AATTCAATAG ACTTTTGCTG 780

GTTATAAAAC AGATGTTTTT TAGATTATTA ATATTAAATC AACTTAATTT GAATGAGAAT 840

45

TGAAACTGA TTCAAGTAAG TTTGAGTATC ACAATGTTAG CTTTCTAATT CCATAAAAGT 900

ACTTGGTTTT TACAGTTTAT AATCTGACAT CACCCAGCG CCATTGTGTA AGAGCAACTT 960

TCCAGCAGTA CATTTGAAGC ACTTTTAAAC AACATGAAAC TATAAACCAT ATTTAAAGC 1020

50

TCATCATGTT AAATTTTTTA TGTACTTTTC TGGAAGTAGT TTTTAAATTT TAGATTATAT 1080

GTCCACCTAT CKTAAGTGTA CAGTTAATAA TTAGCTTATT CAATGATTGC ATGATGCCTT 1140

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ACAGTTTCA ATAACTTTTT TTCTTATGCA AACGTCATGC AATAAAACAA ACTCTAATGT 1200

TTGGCAAAAA AAAAAAAAAA AAANTCGA 1228

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(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

10 TCTCGGGTCT CGGGACAGGT GAGCACCTG ATGAAGGCCA CGGTCCTGAT GCGGCACCTG 60
GGCGGGTGCA GGAGATCGTG GGCGCCCTCC GCAAGGGCGS CGGAGACCGG TTACAGGTGA 120
15 TTTCTGATTT TRACATGACC TTGAGCAGGT TTGCATATAA TGGAAAGCGA TGCCCTTCTT 180
CTTACAATAT TCTGGATAAT AGCAAGATCA TCAGTGAGGA GTGTGGAAA GAGCTCACAG 240
CGCTCCTTCA CCACTATTAC CCAATTGAGA TCGACCCACA CCGGACCGTC AAGGAGAAGC 300
20 TACCTCATAT GGTGGAATGG TGGACCAAAG CGCACAATCT CCTATGTCAG CAGAAGATTC 360
AGAAGTTTCA GATAGCCAG GTGGTTAGAG AGTCCAATGC AATGCTCAGG GAGGGATATA 420
25 AGACCTTCTT CAACACACTC TACCATAACA ACATTCCCTT TTTCATCTTT TCTGCGGGCA 480
TTGGTGATAT CCTGGAAGAA ATTATCCGAC AGATGAAAGT GTTCCACCCC AACATCCACA 540
TCGTGTCTAA CTACATGGAT TTTAATGAAG ATGGTTTTCT CCAGGGATTT AAGGGCCAGC 600
30 TGATACACAC ATACAACAAG AACAGCTCTG TGTGTGAGAA CTGTGGTTAC TTCCAGCAAC 660
TTGAGGGCAA AACCAATGTC ATCCTGCTGG GAGACTCTAT CGGGGACCTC ACCATGGCCG 720
35 ATGGGGTTCC TGGTGTGCAG AACATTCTCA AAATTGGCTT CCTGAATGAC AAGGTGGAGG 780
----- AGCGCGGGA NCGCTAACAT GGACTCCTAT GACATCGTGC TGGAGAAGGA CGAGACTCTG ----- 840
GATGTGGTCA ACGGGCTACT GCAGCACATC CTGTGCCNAG GGGGTCCAGC TGGAGATGCA 900
40 AGGCCCCTGA AGGCGCAGGC TCCNAAGKCC SCTGCAGGCC GTGGTGAGGA GGGGCGCCTC 960
CCCAGAGTCT GCTCCCCCGT GAACACAGAG CAGAGCCAGG GTGGCCAGCA GTGGCTGGGT 1020
45 CCTTCCGCGC CCTCCGTCC TCCTTTCCCT GAGCACCTTC ATCACCAGAG GCTTGAAGGA 1080
ACCCCGCCAT GTGGCAGGGC ACAGGCACTG TTCCTGGTGA ACCTTGACC ACAGCATGTC 1140
AGTGCTCTAG GGATGTCTA CTCCAGGGAT TTTCTTCAAA ATTTTAAAC ATGGGAAGTT 1200
50 CAAACAAATA TAATGTGTGA AACAGATCAA AATTTTAAA ATGAAAAAA AGCTGCTCTG 1260
ATTCAGGGGA TGTGGGTCGG GGTAGAACCT GGACCTCTTG GCCTGGGGGC ACATGGGATG 1320
55 CTTCTAG 1327

60 (2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

10 TCACCCTGCC TACAGCGTGG AGCTCAGATG ACTGCGCCCT CCACGGTCAC TGTGAGCAGG 60
TGGTATTACAG AGCCTGCATG ACCCTCACGG CCAGCCCTGG GGTGTTCCCC GTCAGTGTGT 120
GGCTTTGGCT GAAGCCTAAT TCCACAGCTC CTTGTTTTTT GAGAGAGACT GAGAGAACCA 180
15 TAATCCTTGC CTGCTGAACC CAGCCTGGGC CTGGATGCTC TGTGAATACA TTATCTTGCG 240
ATGTTGGGTT ATTCCAGCCA AAGACATTTT AAGTGCCTGT AACTGATTTG TACATATTTA 300
20 TAAAAATCTA TTCAGAAATT GGTCCAATAA TGCACGTGCT TTGCCCTGGG TACAGCCAGA 360
GCCCTTCAAC CCCACCTTGG ACTTGAGGAC CTACCTGATG GGACGTTTCC ACGTGTCTCT 420
AGAGAAGGAT TCCTGGATCT AGCTGGTCAC GACGATGTTT TCACCAAGGT CACAGGAGCA 480
25 TTGCGTCGCT GATGGGGTTG AAGTTTGGTT TGGTTCTTGT TTCAGCCCAA TATGTAGAGA 540
ACATTGAAA CAGTCTGCAC CTTTGATACG GTATTGCATT TCCAAAGCCA CCAATCCATT 600
30 TTGTGGATTT TATGTGTCTG TGGCTTAATA ATCATAGTAA CAACAATAAT ACCTTTTCTT 660
CCATTTGCT TGCAGGAAAC ATACCTTAAG TTTTCTTGT TTTGTTTGT TTTTCTTGT 720
TTTGTCTTC CTTTATGAAG AAAAAATAAA ATAGTCACAT TTTAATACY AAAAAATGGA 780
35 CAAAAAAGT CGAGGGGGG 799

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(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

50 AAAGACTCTA ACATCCATGA GCTTGAACAT GAGCAAGAGC CTACTTGTGC CKSCCAGATG 60
GCTGAGCCCT TCCGTACCTT CCGAGATGGA TGGGTCTCCT ACTACAACCA GCCTGTGTTT 120
55 CTGGCTGGCA TGGGTCTTGC TTTCTTTAT ATGACTGTCC TGGGCTTTGA CTGCATCACC 180
ACAGGGTACG CCTACACTCA GGGACTGAGT GGTTCATCC TCAGTATTTT GATGGGAGCA 240
TCAGCTATAA CTGGAATAAT GGGAACTGTA GCTTTTACTT GGCTACGTCG AAAATGTGGT 300
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	TTGGTTCCGA CAGGTCTGAT CTCAGGATTG GCACAGCTTT CCTGTTTGAT CTTGTGTGTG	360
	ATCTCTGTAT TCATGCCTGG AAGCCCCCTG GACTTGTCGG TTTCTCCTTT TGAAGATATC	420
5	CGATCAAGGT TCATTCAAGG AGAGTCAATT ACACCTACCA AGATACCTGA AATTACAAC	480
	GAAATATACA TGTCTAATGG GTCTAATTCT GCTAATATTG TCCCGGAGAC AAGTCCTGAA	540
10	TCTGTGCCCC TAATCTCTGT CAGTCTGCTG TTTGCAGGCG TCATTGCTGC TAGAATCGGT	600
	CTTTGGTCCT TTGATTTAAC TGTGACACAG TTGCTGCAAG AAAATGTAAT TGAATCTGAA	660
	AGAGGCATTA TAAATGGTGT ACAGAACTCC ATGAACATC TTCTTGATCT TCTGCATTTC	720
15	ATCATGGTCA TCCTGGCTCC AAATCCTGAA GCTTTTGGCT TGCTCGTATT GATTTTCAGTC	780
	TCCTTTGTGG CAATGGGCCA CATTATGTAT TTCCGATTG CCCAAAATAC TCTGGGAAAC	840
20	AAGCTCTTTG CTTGCGGTCC TGATGCAAAA GAAGTTAGGA AGGAAAATCA AGCAAATACA	900
	TCTGTTGTTT GAGACAGTTT AACTGTTGCT ATCCTGTTAC TAGATTATAT AGAGCACATG	960
	TGCTTATTTT GTACTGCAGA ATTCCAATAA ATGGCTGGGT GTTTTGCTCT GTTTTTACCA	1020
25	CAGCTGTGCC TTGAGAACTA AAAGCTGTTT AGGAAACCTA AGTCAGCAGA AATTAAC	1080
	TTAATTTCCC TTATGTTGAG GCATGGAAAA AAAATTGGAA AAGAAAACT CAGTTTAAAT	1140
30	ACGGAGACTA TAATGATAAC ACTGAATTCC CCTATTTCTC ATGAGTAGAT ACAATCTTAC	1200
	GTAAAAGAGT GGTAGTCAC GTGAATTCAG TTATCATTTG ACAGATTCTT ATCTGTACTA	1260
	GAATTCAGAT ATGTCAGTTT TCTGCAAAAC TCACTCTTGT TCAAGACTAG CTAATTTATT	1320
35	TTTTTGCATC TTAGTTATTT TTAAAAACAA ATTCTTCAAG TATGAAGACT AAATTTTGAT	1380
	AACTAATATT ATCCTTATTG ATCCTATTGA TCTTAAGGTA TTTACATGTA TGTGGAAAAA	1440
40	CAAAACACTT AACTAGAATT CTCTAATAAG GTTTATGGTT TAGCTTAAAG AGCACCTTTG	1500
	TATTTTTATT ATCAGATGGG GCAACATATT GTATGAAGCA TATGTAGCAC TTCACAGCAT	1560
	GGTTATCATG TAAGCTGCAG GTAGAAGCAA AGCTGTAAAG TAGATTTATC ACACAATGAC	1620
45	TGCATACAGA CTTCAAATAT GTCAATAGTT TGGTCATAGA ACCTAGAAGC CAAAAGCCAC	1680
	ACAGAAGGGC AAGAATCCCA ATTTAACTCA TGTTATCATC ATTAGTGATC TGTGTTGTAG	1740
50	AACATGAGGG TGTAAGCCTT CAGCCTGGCA AGTTACATGT AGAAAGCCCA CACTGTGAA	1800
	GGTTTGTGTT TACAAATCAC TTGATTTAAC AACTCAGGT AGAATATTTT TATTTTTACT	1860
	GTTTTATACC CAGAAGTTAT TTCTACATTG TTCTACAGCA AGAATATTCA TAAAAGTATC	1920
55	CCTTTCAAAT GCCTTTGAGA AGAATAGAAG AAAAAAGTT TGTATATATT TAAAAAATT	1980
	GTTTTAAAAG TCAGTTTGCA ACATGTCTGT ACCAAGATGG TACTTTGCCT TAACCGTTTA	2040
60	TATGCACTTT CATGGAGACT GCAATACGTT GCTATGAGCA CTTTCTTTAT CCTTGGAGTT	2100

TAATCCTTTG CTTTCATCTTT CTACAGTATG ACATAATGAT TTGCTATGTT GTAAAATCTT 2160
 TGTAAAAAAT TTCTATATAA AATATTTGAA ACTTAA 2196

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(2) INFORMATION FOR SEQ ID NO: 283:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCAGTTAAGG CTTCTGATAA GGAAAGAGAG TCTGAACAGA GCACACACAT CTGGAGCTCC 60
 20 AGGAGTGGGG GATGCAGCAT CAGATTCCAT CTTGAATTTC TGCTAAAATA CTTTGTACTC 120
 ATAATGGATC TCAACAAAGA TCTGTATTTC ATCTGTGGCT CCATCTTCCC TCTGGGTCAA 180
 25 GTAGATGTTA AGCTGGACCT TGGCAGCCT CTTAACATGA AGAGATCTAG CTAGACAGAC 240
 AGACTCCCCC ATTTATGGGA ACAAGAATTC AATTTATTCT CTATTTATAA AACATTTTTT 300
 TAAAGTGCCT TGGGTATAAA AATCTAAATG TCTGCGGTGT GATCAGTCAG GAGCACGTAA 360
 30 CTATCACTCT TCGCATCCTT TGGTCACTGG GAGATCCTTT GGGGGCTGGG AGGTCCTTCT 420
 GTCCCAGGCT AAAGGAAAAG CTTCAACAAG GTAAGAGCCA CAGAACCCTC GGCAAGAAAG 480
 35 GCCGGTCAGG GAGAATGAAT GGTACAGAGA GGAAAGGAAG GAAAGGGGGT GGAACAGAGG 540
 TAGAAGGCAA GGAAGGGATG CCGCACTGGA GACCGATGGG GACACTCTAA TTGTGCAAGA 600
 GGGAGGATCT TCCTTCTTGA ATGCTGAACA CAGCTAGTCT GAACCTTCCT TGGAAAGTCC 660
 40 AGCTGTTTGC CCATGCATAG GGCCAACTCT CCCTGCAAAG CAGCAAATGT GGCTTCTATC 720
 AGGAAGGAAA AGTATCCATC AGTGTGACAA GAGGTCACCT TCGAACTTGC ATGAACTCCT 780
 45 TGCGCAGCCA CAAAGAGTCC TGGTAGAAGT GAGGATCGCC TAGTCTTACG GCTGTCCGTT 840
 TATAGAAGTA GCAGTACAAC ACTGCTGCTA GTCTCTGGAA TACAAACAGC ATTTGAAGTC 900
 CATCTGTCCA TATGAAGCTG TTGGAGTTTT TCCAGCGTAA GTTCATGACC CAGACATGAA 960
 50 GGGAGATGCT GAGGGCAAAG TACACAGCTG TCAGGATGAT GGTCCCTTTG AACTTATGGA 1020
 ATAGGAGGTT GACCAGGCCA GCCTGGAAGA CGAAGGTGTT GAAGAACATG AGGAAAATGA 1080
 55 TGATGATGTT GAAGAGGACT GCAATATCCT GGATGCACTG AGGGAGAGGY TTCTAGTTCC 1140
 TTTGAATGAG AGCTGTTTCC CTTGCTCTAA GGCAAGCACC TCCAA 1185

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(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1634 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

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AGGGAAAGGG GAGGGTAGCG GGAGGGTAGC AGGTGAGTTC CTAGGGCTGG AAGGTTTAGC 60
 AGCAGCCTGG TGCAGTGGCC TGTCATCAAG ACAAACCCAC GGTCTMCTG GGTGCCTACC 120
 AAGCTTGTT TGTACAAAAG CAAGGTGGGA GTCTATTTTT GTACATGAGA TACATCACAC 180
 TTACCTGTGG GCCAGTATTG TGAAGTGAGT CTGAGTTGTT TACACTGATG CCTTCCCTGC 240
 CCACCACAAA TTGTGTACAT AGTCTTCAGA TGATACCACC CCTTCCCCA GCTCCCAACC 300
 AAGAGCTGGT TCTAGGCCTG TGTATATATG CATATTTAGC STTTTTATAT ATGACCTTTG 360
 ATTTCTGTG TTTGTATTTT AGCACAGTGT ATGCACCTTC ATTTAAATAC ATCTGTGTGC 420
 ATACAGATAC GCATATATGT GTGTGCGTAT GCATATATCT CTCATCTGTA GTTTCCAAGA 480
 GTTCAGCTGA AGCAGATGGA GTCCTGCAGC CCAGGAGACA CCCTGCATCC CTGCTAATAG 540
 TGTTTGCCAC AAGTATTAGT GAGTCTTCCT TATTAATATT TTCATTTTCA AAGACTGAAG 600
 CAAAGCTGAT AGTGTGCTT GTTTCTTTGG CAGCTAAGTG AGGGTCTTGG GATGACTTGC 660
 TGTGTTCTC AAGCTGCACT TTGGGGCCAT CTCCTGCAGTA TTAGCCCCCT TTTTGCTTGG 720
 TGGTACTCTG TCTGTGCCTG TGTGTGTGTG TGATAGTCAC TCTTGCATGG CTTCCATGTC 780
 TGGTTTGTGG CATTTGGGGA TAAGGTGCTG AAGCCAGAGC ATTTGCAGTT TGTFTGAGGC 840
 CTCGTTGCCA ATGATAGATC ACTCCTGTTG ACCTGGTATG TCTGCTTGCT TGCTGCTTTT 900
 CCTTGCTTTC TCTTGAAGA GGAAAGGACT CTGGTCAGGC CCAGGCTGAG TGAGATGAGC 960
 TGCAGCTGGC TCATGGCCTT CTTAGAGCAG AGAGAGGAGT ATGTCATTTT ACTAAGTTCC 1020
 TAAACAAACA TTTATGCAGG CAACACTCCT TGCAGATCCA GAAACTGAGG CACAATAGGG 1080
 TTATGACTTG CTCAAGAATA TGTAGCTGCT AGGGGGTAAA TCAAGGCATC ACAATTTCTG 1140
 TTCAGCGGGC AGGAATAGGC TGTGAATTGC TAGCACTTTT TTTTTTAAAG CAATTACTTT 1200
 TTGACTTGTT CCTCTGAAAG TGCAAGAGGC GTACACCTTT CCCAAATGTA GACTAGAATC 1260
 TGCAGGATGC CACCCACTGT ATAGTTCTGC TTTCCCAGAG AGGAAGAACT TTTAGAAACC 1320
 AAATGATCTT AATTGTTATT GCCACCCCTT GGCTTTTCCG GGTAGAAAAT TCACAGTAGG 1380
 AATGATTGTT AAGAGAGAGT GCTTGAACC ATGGGTAAAC AGGAAAGGCT ACCTAACTTC 1440
 ACATATCTGC AACCAGAGCA GCCACCAAGC ATTACTTAGC AGCAGGAAAA TGATTGTATT 1500

TGAGTTCCTG TGTGTCCAAA ACTGAGGCAC CATGTTCTTT GAAAACATGC CACCTCAAGG 1560
 CTGGGCGCGG TGGCTCACAC CTGTAATCCC AGCAYTTTGG GGAGGCCSAG GCGGGGCGG 1620
 5 KTTACCCGGG GGTC 1634

10 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

20 TTCCCCCAG GTTGGCTTCC TTCGATTCTT TTTCTTGGTA TCAACGTTTG ATTGGAAGAA 60
 CAACCCCTC TTTGTCAACC TCAATAATGA GCTCACTGTG GAGGAGCAGC TCGGGCACAG 120
 CTCMCCGTYA TGGTCATTGT TACCCCCCAA GACCGCAAAA ACTCTGTGTG GACACAGGAT 180
 25 GGACCCTCAG CCCAGATCCT GCAGCAGCTT GTGGTCCTGG CAGCTGAAGC CCTGCCCATG 240
 TTAGAGAAGC AGCTCATGGA TCCCCGGGA CCTGGGGACA TCAGGACAGT GTTCCGGCCG 300
 30 CCCTTGGACA TTTACGACGT GCTGATTGCG CTGTYTCCTC GCCATATCCC GCGGCACCGC 360
 AGGCTTGTGG ACTCGCCAGY TGCCTCCTTC TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC 420
 TCATCCCTGA TGCCCGTGCT GGGTNATGAT CCTNCTCAGC TCTATCTGAC GCAGCTCAGG 480
 35 GAGGCCTTTG GGGATCTGGC CCTTTTCTTC TATGACCAGC ATGGTGGAGA GGTGATTGGT 540
 GTCTCTGGA AGCCACACAG CTTCCAGCCG CAGCCCTTCA AGGCCTCCAG CACAAAGGGG 600
 40 CGCATGGTGA TGTCTCGAGG TGGGGAGCTA GTAATGGTGC CCAATGTTGA AGCAATCCTG 660
 GAGGACTTTG CTGTGCTGGG TGAAGGCTG GTGCAGACTG TGGAGGCCCG AAGTGAGAGG 720
 TGGACTGTGT GATCCCAGCT CTGGAGCAAG CTGTAGACGG ACAGCAGGAC ATTGGACCTC 780
 45 TAGAGCAAGA TGTCAGTAGG ATGACCTCCA CCCTCCTTGG ACATGAATCC TCCATGGAGG 840
 GCCTGCTGGC TGAACATGCT GAATCATCTC CAACAAAACC CAGCCCCAAC TTTCTCTCTG 900
 50 ATGCTCCAGC ATTGGGGCAG GGGCATGGTG GCCCATGTAG TCTCCTGGGC CTCACCATCC 960
 CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA GGAAGTGAAC CCAGGAGATC CATCCACCTA 1020
 TTAGCCCTGG GCCTGGACCT CCCTGCGATT TCCCACTCCT TTCTTAGTCT TCTTCCAGAA 1080
 55 ACAGAGAAGG GGATGTGTGC CTGGGAGAGG CTCTGTCTCC TTCTGCTGC CAGGACCTGT 1140
 GCCTAGACTT AGCATGCCCT TCACTGCAGT GTCAGGCCTT TAGATGGGAC CCAGCGAAAA 1200
 60 TGTGGCCCTT CTGAGTCACA TCACCGACAC TGAGCAGTGG AAAGGGGCTA TATGTGTATG 1260

5 AATAGACCAC ATTGAAGGAG CACAATGCCC TCCTGTGTTG ATGCCACTTC CCAGGGTGA 1320
 GACAGTGGAA AAGAACCGAG GACAGGAAAG GATTGGGTAG GTGAAGGGGT CAGGGGACTG 1380
 GTAGTCACCC AATCTTGGAG AGGTGCAAAA AGCACTGGGG GCTACCCGTT AGCTGCATCT 1440
 GCCCTGGCTG TTTGCCCGTT CATGTCACAA ACTGCCACTA CTATGTACCT GCAGTGGGGT 1500
 10 TGCAGAGATG GGGGAGACTC AAGTCTTACT CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG 1560
 AATGCTGCCT CCTTTCAGTC TGGTCTACAC CCACTTTCCTG GTAGCCTCTC TGCTTCCTGT 1620
 AATTCTGGCT GTTTTCCAG ACTCAGCTCA AATAGTGCCC CTCCTTAAGC CCATCCCTCG 1680
 15 CCCCAGCCT GAGGTGATCT TTCCCTCCTC TGAACTATTA GAGCAGTTAC TGTCTGTTC 1740
 GTTCGTTTGG CAGGCACACA CAGTGGCATA AATTCTATTG TTTTGAAC TCATT 1795

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(2) INFORMATION FOR SEQ ID NO: 286:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCTGCTTTCG GTGCTGCGTG TACTGCTGGG CGGCTTCTTC GCGCTCGTGG GGTGGCCAA 60
 35 GCTCTCGGAG GAGATCTCGG CTCCAGTTTC GGAGCGGATG AATGCCCTGT TCGTGCAGTT 120
 TGCTGAGGTG TTCEGGCTGA AGGTATTTGG CTACCAGCCA GATCCCTGA ACTACCAAAT 180
 AGCTGTGGGC TTTCTGGAAC TGCTGGCTGG GTTGCTGCTG GTCATGGGCC CACCGATGCT 240
 40 GCAAGAGATC AGTAACTTGT TCTTGATTCT GCTCATGATG GGGCTATCT TCACCTGGC 300
 AGCTCTGAAA GAGTACTAA GCACCTGTAT CCCAGCCATT GTCTGCCTGG GGTTCCTGCT 360
 45 GCTGCTGAAT GTCGGCCAGC TCTTAGCCCA GACTAAGAAG GTGGTCAGAC CCACTAGGAA 420
 GAAGACTCTA AGTACATTCA AGGAATCCTG GAAGTAGAGC ATCTCTGTCT CTTTATGCCA 480
 TGCAGCTGTC ACAGCAGGAA CATGGTAGAA CACAGAGTCT ATCATCTTGT TACCAGTATA 540
 50 ATATCCAGGG TCAGCCAGTG TTGAAAGAGA CATTTTGTCT ACCTGGCACT GCTTTCTCTT 600
 TTTAGCTTTA CTACTCTTTT GTGAGGAGTA CATGTTATGC ATATTAACAT TCCTCATGTC 660
 55 ATATGAAAAT ACAAATAAG CAGAAAAGAA ATTTAAATCA ACCAAAATTC TGATGCCCCA 720
 AATAACCACT TTTAATGCCT TGGTGTAAGT ATACCTCTGA ACTTTTTTCT GTGCCTTTAA 780
 60 ACAGATATAT ATTTTTTTTT AATGAAAATA AAACCATATA TCCTATTTTA TTTCTCCTT 840

TTAAAACCTT ATAAACTA

858

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(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

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GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC	60
GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG	120
GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC	180
TACCAGCCAG ATCCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAAGT GCTGGCTGGG	240
TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAAC TTGTT CTTGATTCTG	300
CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC	360
CCAGCCATTG TCTGCCTGGG GTTCCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG	420
ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG	480
AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC	540
ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC	600
ATTTTGICTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC	660
ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA	720
TTTAAATCAA CCAAAATTCT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA	780
TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA	840
AACCATATAT CCTATTTTAT TTCCTCCTTT TAAAACCTTA TAAACTATAA MAAAAAAAAA	900
AAAAAAAAAA CTCGA	915

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(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

	CCTTGTGGCA	ACTAGTGGGT	CCCCCGGGCT	GCAGNAATTC	GGGCAGTGGT	TCTGNGTCTG	60
	AAGATACTCT	GAGTTCCTCT	GAGAGATCCA	AAGGCTCCGG	GAGCAGACCC	CCAACCCCCA	120
5	AAAGCAGCCC	TCAGAAGACC	AGGAAGAGCC	CTCAGGTGAC	CAGGGGTAGC	CCTCAGAAGA	180
	CCAGCTGTAG	CCCTCAGAAG	ACCAGGCAGA	GCCCTCAGAC	GCTGAAGCGG	AGCCGAGTGA	240
10	CCACCTCACT	TGAAGCTTTG	CCCACAGGAC	AGTGCTGACA	GACAAGAGTG	GGCGACAGTG	300
	GAAGCTGAAG	TCCTTCCAGA	CCAGGGACAA	CCAGGGCATT	CTCTATGAAG	CTGCACCCAC	360
	CTCCACCCCTC	ACCTGTGACT	CAGGACCACA	GAAGCAAAAG	TTCTCACTCA	AACTGGATGC	420
15	CAAGGATGGG	CGCTTGTTC	ATGAGCAGAA	CTTCTTCCAG	CGGGCCGCCA	AGCCTCTGCA	480
	AGTCAACAAG	TGGAAGAAGC	TGTACTCGAC	CCCACTGCTG	GCCATCCCTA	CCTGCATGGG	540
20	TTTCGGTGT	CACCAGGACA	AATACAGGTT	CTTGGTGTTA	CCCAGCCTGG	GGAGGAGCCT	600
	TCAGTCGGCC	CTGGATGTCA	GCCCAAAGCA	TGTGCTGTGC	AGAGAGGTCT	GTGCTGCAGG	660
	TGGCTGCCG	GCTGCTGGAT	GCCCTGGAGT	TCCTCCATGA	GAATGAGTAT	GTTTCATGGAA	720
25	ATGTGACAGC	TGAAAATATC	TTTGTGGATC	CAGAGGACCA	GAGTCAGGTG	ACTTTGGCAG	780
	GCTATGGCTT	CGCNTTCCGC	TATTGCCCAA	GTGGCAAACA	CGTGGCCTAC	GTGGAAGGCA	840
30	GCAGGAGCCY	TCACGAGGGG	GACCTTGAGT	TTCATTAGCA	TGGACCTGCA	CAAGGGATGC	900
	GGGCCCTCCC	GCCGCRGYGA	CCTCCAGAGC	CTGGGYTAMT	GCATGCTGAA	GTGGYTCTAM	960
	GGGTTCCTGC	CATGGACAAA	TTGCCCTCCA	AMAMTGAGGA	CATCATGAAG	CAAAAACAGA	1020
35	AGTTGCCTTG	GGATTCAATT	TAATGTAAGC	TKGACTTTGT	CATGCCAGAA	ACAAGGCTCG	1080
	GTCACCGTCA	GCAGTTTGCA	GTTTTCACAC	TCGWCACAGT	TCCTECGTGT	GGTTGACECA	1140
40	GATATCTCCG	TTATGCAGCC	GCCTCCGGGG	GACCACCTCC	CTCCCTTTGA	GTCAGCCACA	1200
	GACAGCCTAC	TTGACGGCCC	CGCTGGCCCC	CACATTCAC	TGAACTGTGC	GGATGCCACA	1260
	GTGACCCCT	CTCAGGCACA	GCATGACCTC	CTGAAGTCGA	GCCTGCTTGC	TTTGAACCTA	1320
45	CCAGTTAAAA	TCTCTCAAA	ATGTTTGGAT	ACCGCCCAT	GGCCCTCAC	AGCCACGAGC	1380
	TCCCTGACCA	GTGTGCGTGT	GTGTGTGTGT	GTGTGTCTGT	GTGTGTGCTT	GGGACGGGTG	1440
50	GGGAGGTCAC	CTTTGGGTGT	GCGGTGTGCC	CCCAGGACCT	GTAAGTAATA	AAATCTTTAT	1500
	TTCCAAAAAA	AAAAAAA					1517

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(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 3865 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5	TGGAGGGGGG GAGCTTCCTT GAGCAGTGGG CCCAGGCCTG GCCCTCCACA CTTCAATCTC	60
	TGACCTTTCT CTCTCCTCAT TTCGGTGCAT GTCCTTTCTG CAGCTGCCTT TCAGCACAGG	120
10	TGGTCCACT GGGGGCAGCT AACGCTGAGT GACAAGGATG GGAAGCCACA GGTGCATTTT	180
	ACTCAAGTCT TCTCTAGTCA ATGAGGGGCA CCCAGTGCTT CTAGGGCAGG CTGGGTGGTG	240
	GTCCCTAGG TATCAGCCTC TCTTACTGTA CTCTCCGGGA ATGTTAACCT TTCTATTTTC	300
15	AGCCTGTGCC ACCTGTCTAG GCAAGCTGGC TTCCCCATTG GCCCCTGTGG GTCCACAGCA	360
	GCGTGGCTSC CCCCCAGGGC CACCGCTTCT TTCTTGATCC TCTTTCCTTA ACAGTGACTT	420
20	GGGCTTGAGT CTGGCAAGGA ACCTTGCTTT TAGCTTCACC ACCAAGGAGA GAGGTTGACA	480
	TGACCTCCCC GCCCCCTCAC CAAGGCTGGG AACAGAGGGG ATGTGGTGAG AGCCAGGTC	540
	CTCTGGCCCT CTCCAGGGTG TTTTCCACTA GTCACTACTG TCTTCTCCTT GTAGCTAATC	600
25	AATCAATATT CTTCCTTGC CTGTGGGCAG TNGGAGAGTG CTGCTGGGTG TACGCTGCAC	660
	CTGCCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTCTGCTC AGAGCTCTG	720
30	ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT GCATGAAACC AGGCCCTGGC	780
	AGCAACCCCTG GGAATGGCTG GAGGTGGGAG AGAACCTGAC TTCTCTTTCC CTCTCCCTCC	840
	TCCAACATTA CTGGAACCTCT ATCCTGTTAG GATCTTCTGA GCTTGTTTCC CTGCTGGGTG	900
35	GGACAGAGGA CAAAGGAGAA GGGAGGGTCT AGAAGAGGCA GCCCTTCTTT GTCCTCTGGG	960
	GTAAATGAGC TTGACCTAGA GTAAATGGAG AGACCAAAG CCTCTGATTT TTAATTTCCA	1020
40	TAAATGTTA GAAGTATATA TATACATATA TATATTCTT TAAATTTTG AGTCTTTGAT	1080
	ATGTCTAAAA ATCCATTCCC TCTGCCCTGA AGCCTGAGTG AGACACATGA AGAAAACTGT	1140
	GTTTCATTTA AAGATGTTAA TTAAATGATT GAAACTTGGC TGTGGCTACT GCTTCTTAAT	1200
45	GTTGGGGGGA CAGGGCAGTG GTCTGGGCCC ACATTTAGAA GGGAAAATGT TTGCCTGCT	1260
	GCACACATFG GACCCAAGTA TGGGCCTCTT CTGCCTAGTA CTGCCAAAGG GACTGTTAAG	1320
50	GTGTCTTGTG CATCTTCTAC CCCCCACCCC CCATTACGGG TAAAGGRAAC CCCAGACTAG	1380
	GTGAGGGGCC AGCAGCTGCC TCACATTGTG TTCTCTCTG AGATGGTCCA GCTCACATCC	1440
	AGACACCTTG TTCAGACATT TTATTTGAAT TTATGACAGT GATGGGGATT TGACTGAGAT	1500
55	GCCTTATGGA GAAGTACCCC ACCCTCTATG AAGACAGAAT CACTCTCTGC CATTCATTCT	1560
	GCCTGATGCT AACAAACAGC AGCTGATTTA GGGAGTGTCC CAGCCTAGCT GGATCAAGGG	1620
60	AAATTCAGG AGCCCTGGGG CAGGCCCTGG NCCCCAGTGC CAAGCCTCAG AGTAAGCAGA	1680

	CATTGGGAAA GTTGCCAACC ACTTGGTAGA CCACTAGGTT CTCTGTTTTT CCTTCCCTTT	1740
5	CCTTTTCAAA TCCCACAGTT TCCTGTTGGG GAGAAGCTGT AATTAGCCTA GTCCAGGTAC	1800
	CAGATCCCAG CTAGGGGCGC AGCTGNCTTG GATAACTCCA AGAAAACCTG GGCACCAGTA	1860
	TTTTTCCAAT TATAAGGACT GTGGCATAAA TTTTAAATG AGTTATATTG AAACCAGATT	1920
10	TCTCCAGCTG CCAAGGGAAG AAGGTAGGGC TGGACTCCCT GCTGTGGCCC AGCCCTTGTT	1980
	AGGGGTTGGT CTCTCACTGC AGCCAGACAG GATGATCCTG GGTCTGGGG AGGGTAAGCT	2040
15	GCCCCTTGCC GAGTTCTGCA CCGAATAAAG AGTCCAAACC CGCTGCTTCC GTGTCTGAG	2100
	AGATGGGTAA ATGGGTGATG GATGGAGCAG ACTGAAGAGA CAGCAGATGA CTCAGTGGTG	2160
	GAAGAAGGGG GGAAGATGCT GGGCTGGCTA GCTAATGTTT CCCCCTTTCA GCGATTTACA	2220
20	GGAAATGGAG CCCAGCTTGG TCATGAAGTT GGTTCGCTT CACTGTGCGA TGCACTCCTC	2280
	AGAAATTTTG AAGTCAGCCT GCAACTTCTC GAAGACTTTC TTCTTGGGCT TGAGCTCCTC	2340
25	ATCTGGTTGG CCCTTTTCAT AGCCCTTCAC AAACACGTGC TCACCAGGAG CAGAGCCTGC	2400
	CGGAGGGTCC AGAGGTTCAA CTGGCGGTTT ATCCCTTCTA TAGAAGCACA CAGAAGCATG	2460
	CCTTGGGACT CGACTCCTCT CATCTTCTGG GGTTCAGGT TGCACAGCAC CACTACCAGC	2520
30	CTGTCTGCA GTTCTCCTT GGGCACGAAC TGTACCAGGC CGCTCACCAC AGTCCGTGGT	2580
	TCAGCTTCCC CCACGTCAAT CTTCTCTACA TACAGGCTGT CTGCATCTGG GTGCTTCTCC	2640
35	ACAGTGATGA TTTTCCCCAC ACGGATATCC AGCCGGGATG GGATGACCTC CTCTGGTTCT	2700
	GAATTCTTGG CAGGCCTTTG GCCATTGGCT TCTGCTTTGA GGGATCTGGG TAGGCAGCGC	2760
	TGGCCAGTTT TTTCAGGGCA GGGGTATTAA ACTTTTCCCG GATTGGATCC AGCAACTTGT	2820
40	TCAGTGGGAC TTCAACAGAA TTCTTCAGGT CTCCAGGATG TACAACCTCA GCAGCAAAGT	2880
	CCTTTTCCAG GTCCACGTAA GCTGTGTAGG TTTTGTTC ACCCCATTTC TCATCTCGTA	2940
45	GGATCACAAA CTCGGACTTA AGGGGAAAAA GGACATGCTT GATGAAGGAC AGAACCCCAT	3000
	TGTTCTCCAC ATTTCTCTGGC TCACAGAAGG CCTTCTTCAG TTTTTCCTTC ACATCCTCCT	3060
	TCCGATCAAG GAGATCAATC TTGGACTCCT CTTCTGAAGA GCTCATTTTG CTGCCTGTTA	3120
50	ATCCTGGAAC CATAGGATTC ATCAGATGGA CCCGTTTTGA ATAGCCAAGT GCAGGGAGGT	3180
	ACTTCTCTGC AAAGGTGAAA ATCTTTCTCT GATCAATGCC TCCAAATTGG GCATCTACTT	3240
55	TTAAATACTC TTCATCCAAA GCCTGCAGTC CGGGGTATAA GAGGCCACTC AGCAAAGGGT	3300
	GCTCCACCTG CTTTACCACC TCAGCTCCAG CCTTCTTGA ATCGTGCTGT GTGACCACGG	3360
	AGGAGAGTCT GTACACATCT AGTGTGTACT CTTTGCTGAG CTGGTAATCA GTGCCTTTGA	3420
60	TGAACCTGAG CTTCTCCAAG GGCACACCAA TGCTCTCCAG CATTGCTTTG ATCACATTCT	3480

CATAGTAACT GACTCGGAGT TCTAGAAGTT CCCATGGGGC TTTCATGTTA TCCAGGTATG 3540
 CGTGGAGGTC CGCAAACAGA ATTGTTACCT CACACCCTGC CTTTAAGAAG TCTGCAATCT 3600
 5 TTGACATGGG CACAAAGTAA GCCACATGTG GTTTGCCCGT GGTGCGCGTT CCCCAGTAAA 3660
 TTTTAAGTTC CCGTCCTTC AGTATCTCCT TCAGCTTCTC TTCCCCCAGA ACCTCCTGCA 3720
 10 GGTTCGGGGT GATAAGGTGC AGTTTCTCTT CAGGGCTGGG AGCGTCCCCC ATGGTCCGCT 3780
 ACCCCTGCTT CCCCCGCTCA GCGCGGCACC AGAGCCCTT CCTGGGTCAC CGTCGCCGCC 3840
 15 GCGTCCGGG AACTGTCACG CGAGT 3865

20 (2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1910 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

30 AGGGAGAGGA GGAGAGGGGG TCTGCGCGCG GCCGCTACCC AGAAGCCAGC GGACGGCAGC 60
 ACGGAGTGGG CTGTCCCCGA GCCCAGCCCC GAGCGAGCCC CCCCCCGCC CCCGMAGGAC 120
 GCGCCTYCCA GCCAGCCCGA CTCCTAGGAG GAGGGGAGGC GGGAAAGCAG CTCAAGCCTC 180
 35 ACCCACCGCC CTGCCCCCAG CCCCGCCACT CCCAGGCTCC TCGGGACTCG GCGGGTCTCT 240
 CTGGGAGTCT CGGAGGGGAC CGNCTGTGCA GACGCCATGG AGTTGGTGCT GGTCTTCTCT 300
 TGCAGCCTGC TGGCCCCCAT GGTCTTGGCC AGTGCAGCTG AAAAGGAGAA GGAAATGGAC 360
 40 CCTTTTCATT ATGATTACCA GACCCTGAGG ATTGGGGGAC TGGTGTTCGC TGTGGTCTCT 420
 TTCTCGGTTG GGATCTCTCT TATCCTAAGT CGCAGGTGCA AGTGCAGTTT CAATCAGAAG 480
 45 CCCCAGGGCC CAGGAGATGA GGAAGCCCAG GTGAGAACC TCATCACCGC CAATGCAACA 540
 GAGCCCCAGA AAGCAGAGAA CTGAAGTGCA GCCATCAGGT GGAAGCCTCT GGAACCTGAG 600
 GCGGCTGCTT GAACCTTTGG ATGCAAATGT CGATGCTTAA GAAAACCGGC CACTTCAGCA 660
 50 ACAGCCCTTT CCCCAGGAGA AGCCAAGAAC TTGTGTGTCC CCCACCCTAT CCCCTCTAAC 720
 ACCATTCTCT CACCTGATGA TGCAACTAAC ACTTGCCTCC CCACTGCAGC CTGCGGTCTT 780
 55 GCCCACCTCC CGTGATGTGT GTGTGTGTGT GTGTGTGTGT GACTGTGTGT GTTTGCTAAC 840
 TGTGGTCTTT GTGGCTACTT GTTGTGGGAT GGTATTGTGT TTGTTAGTGA ACTGTGGACT 900
 60 CGCTTTCCCA GGCAGGGGCT GAGCCACATG GCCATCTGCT CCTCCCTGCC CCCGTGGCCC 960

	TCCATCACCT TCTGCTCCTA GGAGGCTGCT TGTGCCCCGA GACCAGCCCC CTCCCCTGAT	1020
	TTAGGGATGC GTAGGGTAAG AGCACGGGCA GTGGTCTTCA GTCGTCTTGG GACCTGGGAA	1080
5	GGTTTGCAGC ACTTTGTCAT CATTCTTCAT GGACTCCTTT CACTCCTTTA ACAAAAACCT	1140
	TGCTTCCTTA TCCCACCTGA TCCCAGTCTG AAGGTCTCTT AGCAACTGGA GATACAAAGC	1200
10	AAGGAGCTGG TGAGCCCAGC GTTGACGTCA GGCAGGCTAT GCCCTTCCGT GGTTAATTTT	1260
	TTCCCAGGGG CTTCACGAG GAGTCCCCAT CTGCCCCGCC CCTTCACAGA GCGCCCGGGG	1320
	ATTCCAGGCC CAGGGCTTCT ACTCTGCCCC TGGGAATGT GTCCCCTGCA TATCTTCTCA	1380
15	GCAATAACTC CATGGGCTCT GGGACCCTAC CCCTTCCAAC CTTCCCTGCT TCTGAGACTT	1440
	CAATCTACAG CCCAGCTCAT CCAGATGCAG ACTACAGTCC CTGCAATTGG GTCTCTGGCA	1500
20	GGCAATAGTT GAAGGACTCC TGTTCGGTTG GGGCCAGCAC ACCGGGATGG ATGGAGGGAG	1560
	AGCAGAGGCC TTTGCTTCTC TGCCTACGTC CCCTTAGATG GGCAGCAGAG GCAACTCCCG	1620
	CATCCTTTGC TCTGCCTGTC GGTGGTCAGA GCGGTGAGCG AGGTGGGTTG GAGACTCAGC	1680
25	AGGCTCCGTG CAGCCCTTGG GAACAGTGAG AGGTTGAAGG TCATAACGAG AGTGGGAAT	1740
	CAACCCAGAT CCCGCCCTC CTGTCTCTG TGTTCGCGG GAAACCAACC AAACCGTGCG	1800
30	CTGTGACCCA TTGCTGTTCT CTGTATCGTG ATCTATCCTC AACAACAACA GAAAAAAGGA	1860
	ATAAAATATC CTTTGTTCM TAAAAAATA AAAAAAATA AGGGGGGGGG	1910

35

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 3276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

45

	GCGACCGTCG TTTGAGTCGT CGCTGCCGCT GCCGCTGCCA CTGCCACTGC CACCTGCGCG	60
	ATCAGGAGCC AGCGTTGTTC GCCCGACGCC TCGCTGCCGG TGGGAGGAAG CGAGAGGGAA	120
50	GCCGCTTGCG GGTTTGTGCG CGCTGCTCGC CCACCGCCTG GAAGAGCCGA GCCCCGCCCC	180
	AGTCGGTCGC TTGCCACCGC TCGTAGCCGT TACCCGCGGG CCGCCACAGC CGCCGGCCGG	240
55	GAGAGGCGCG CGCCATGGCT TCTGAGCCG ATTCAAAAGG TGATGACCTA TCAACAGCCA	300
	TTCTCAAACA GAAGAACCGT CCAATCGGT TAATTGTTGA TGAAGCCATC AATGAGGACA	360
	ACAGTGTGGT GTCCTTGTC CAGCCCAAGA TGGATGAATT GCAGTTGTTC CGAGGTGACA	420
60	CAGTGTGCT GAAAGGAAAG AAGAGACGAG AAGCTGTTG CATCGTCCTT TCTGATGATA	480

	CTTGTTCTGA TGAGAAGATT CGGATGAATA GAGTTGTTTCG GAATAACCTT CGTGACGCC	540
	TAGGGGATGT CATCAGCATC CAGCCATGCC CTGATGTGAA GTACGGCAA CGTATCCATG	600
- 5	TGCTGCCCCAT TGATGACACA GTGGAAGGCA TTAAGTTGTA TCTCTTCGAG GTATACCTTA	660
	AGCCGTACTT CCTGGAAGCG TATCGACCCA TCCGAAAGG AGACATTTTT CTTGTCCGTG	720
10	GTGGGATGCG TGCTGTGGAG TTCAAAGTGG TGGAAACAGA TCCTAGCCCT TATTCATTG	780
	TTGCTCCAGA CACAGTGATC CACTGCGAAG GGGAGCCTAT CAAACGAGAG GATGAGGAAG	840
	AGTCCTTGAA TGAAGTAGGG TATGATGACA TTGGTGGCTG CAGGAAGCAG CTAGCTCAGA	900
15	TAAAGGAGAT GGTGGAAC TG CCCCTGAGAC ATCCTGCCCT CTTTAAGGCA ATTGGTGTGA	960
	AGCCTCCTAG AGGAATCCTG CTTTACGGAC CTCCTGGAAC AGGAAAGACC CTGATTGCTC	1020
20	GAGCTGTAGC AAATGAGACT GGAGCCTTCT TCTTCTTGAT CAATGGTCCT GAGATCATGA	1080
	GCAAATTGGC TGGTGAGTCT GAGAGCAACC TTCGTAAAGC CTTTGAGGAG GCTGAGAAGA	1140
	ATGCTCCTGC CATCATCTTC ATTGATGAGC TAGATGCCAT CGCTCCCAA AGAGAGAAAA	1200
25	CTCATGGCGA GGTGGAGCGG CGCATTTGTAT CACAGTTGTT GACCCTCATG GATGGCCTAA	1260
	AGCAGAGGGC ACATGTGATT GTTATGGCAG CAACCAACAG ACCCAACAGC ATTGACCCAG	1320
30	CTCTACGGCG ATTTGGTTCG TTTGACAGG AGGTAGATAT TGAATTCCT GATGCTACAG	1380
	GACGCTTAGA GATTCTTCAG ATCCATACCA AGAATCATG GCTGGCAGAT GATGTGGACC	1440
	TGGAACAGTA GCCAATGAGA CTCACGGGCA TGTGGGTGCT GACTTAGCAG CCCTGTGCTC	1500
35	AGAGGCTGCT CTGCAAGCCA TCCGCAAGAA GATGGATCTC ATTGACCTAG AGGATGAGAC	1560
	CATTGATGCC GAGGTCATGA ACTCTCTAGC AGTTACTATG GATGACTTCC GGTGGGCCTT	1620
40	GAGCCAGAGT AACCCATCAG CACTGCGGGA AACCGTGGTA GAGGTGCCAC AGGTAACCTG	1680
	GGAAGACATC GGGGGCCTAG AGGATGTCAA ACGTGAGCTA CAGGAGCTGG TCCAGTATCC	1740
	TGTGGAGCAC CCAGACAAAT TCCTGAAGTT TGGCATGACA CCTTCCAAGG GAGTTCTGTT	1800
45	CTATGGACCT CCTGGCTGTG GGAAAACCTT GTTGGCCAAA GCCATTGCTA ATGAATGCCA	1860
	GGCCAACTTC ATCTCCATCA AGGGTCCTGA GCTGCTCACC ATGTGGTTTG GGGAGTCTGA	1920
50	GGCCAATGTC AGAGAAATCT TTGACAAGGC CCGCCAAGCT GCGCCCTGTG TGCTATTCTT	1980
	TGATGAGCTG GATTTCGATT CCAAGGCTCG TGGAGGTAAC ATTGGAGATG GTGGTGGGGC	2040
	TGCTGACCGA GTCATCAACC AGATCCTGAC AGAAATGGAT GGCATGTCCA CAAAAAAAAA	2100
55	TGTGTTTCATC ATTGGCGCTA CCAACCGGCC TGACATCATT GATCCTGCCA TCCTCAGACC	2160
	TGGCCGTCTT GATCAGCTCA TCTACATCCC ACTTCTGAT GAGAAGTCCC GTGTTGCCAT	2220
60	CCTCAAGGCT AACCTGCGCA AGTCCCCAGT TGCCAAGGAT GTGGACTTGG AGTTCCTGGC	2280

	TAAATGACT AATGGCTTCT CTGGAGCTGA CCTGACAGAG ATTTGCCAGC GTGCTTGCAA	2340
5	GCTGGCCATC CGTGAATCCA TCGAGAGTGA GATTAGGCGA GAACGAGAGA GGCAGACAAA	2400
	CCCATCAGCC ATGGAGGTAG AAGAGGATGA TCCAGTGCCT GAGATCCGTC GAGATCACTT	2460
	TGAAGAAGCC ATGCGCTTTG CGCGCCGTTT TGTCAGTGAC AATGACATTC GGAAGTATGA	2520
10	GATGTTTGCC CAGACCCTTC AGCAGAGTCG GGGCTTTGGC AGCTTCAGAT TCCCTTCAGG	2580
	GAACCAGGGT GGAGCTGGCC CCAGTCAGGG CAGTGGAGGC GGCACAGGTG GCAGTGTATA	2640
15	CACAGAAGAC AATGATGATG ACCTGTATGG CTAAGTGGTG GTGGCCAGCG TGCAGTGAGC	2700
	TGGCCTGCCT GGACCTTGTT CCCTGGGGGT GGGGGCGCTT GCCCAGGAGA GGGACCAGGG	2760
	GTGCGCCAC AGCCTGCTCC ATTCTCCAGT CTGAACAGTT CAGCTACAGT CTGACTCTGG	2820
20	ACAGGGGGTT TCTGTTGCAA AAATACAAAA CAAAAGCGAT AAAATAAAAG CGATTTTCAT	2880
	TTGGTAGGCG GAGAGTGAAT TACCAACAGG GAATTGGGCC TTGGGCTATG CCATTCTGT	2940
25	TGTAGTTTGG GGCAGTGCAG GGGACCTGTG TGGGGTGTGA ACCAAGGCAC TACTGCCACC	3000
	TGCCACAGTA AAGCATCTGC ACTTGACTCA ATGCTGCCCG AGCCCTCCCT TCCCCCTATC	3060
	CAACCTGGGT AGGTGGGTAG GGGCCACAGT TGCTGGATGT TTATATAGAG AGTAGGTTGA	3120
30	TTTATTTTAC ATGCTTTTGA GTTAATGTTG GAAACTAAT CACAAGCAGT TTCTAAACCA	3180
	AAAAATGACA TGTGTAAAA GGACAATAAA CGTTGGGTCN AAATGGGWRA AAAAAAAAAA	3240
35	AAAAAAGGGG GGCCCTCTA AAGNNCCANN CTTCGT	3276

- (2) INFORMATION FOR SEQ ID NO: 292:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

50	TTGCAATGGT TGAATTCCTT TCCTCACGCC AGCCTAGGAG AAGAAGTTCG TAGTCCCAGA	60
	GGTGAGGCAG GAGGCGGCAG TTTCTGGCGG GTGAGGGCGG AGCTGAAGTG ACAGCGGAGG	120
	CGGAAGCAAC GGTCCGTGGG GCGGAGAAGG GGGCTGGCCC CAGGAGGAGG AGGAAACCTT	180
55	TCCGAGAAAA CAGCAACAAG CTGAGCTGCT GTGACAGAGG GGAACAAGAT GGCGGCGCCG	240
	AAGGGAGCCT CTGGGTGAGG ACCCAACTGG GGCTCCCGCC GCTGCTGCTG CTGACCATGG	300
60	CCTTGGCCGG AGGTTGGGG ACCGCTTCGG CTGAAGCATT TGAATCGGTC TTGGGTGATA	360

	CGGCGTCTTG CCACCGGGCC TGTCAGTTGA CCTACCCCTT GCACACCTAC CCTAAGGAAG	420
	AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTT AATTTGTCAG TTTGTGGATG	480
- 5	ATGGAATTGA CTTAAATCGA ACTAAATTGG AATGTGAATC TGCATGTACA GAAGCATATT	540
	CCCAATCTGA TGAGCAATAT GCTTGCCATC TTGGTTGCCA GAATCAGCTG CCATTGCGTG	600
10	AACTGAGACA AGAACAACCTT ATGTCCCTGA TGCCAAAAAT GCACCTACTC TTTCTCTTAA	660
	CTCTGGTGAG GTCATTCTGG AGTGACATGA TGGACTCCGC ACAGAGCTTC ATAACCTCTT	720
	CATGGACTTT TTATCTTCAA GCCGATGACG GAAAAATAGT TATATTCCAG TCTAAGCCAG	780
15	AAATCCAGTA CGCACCACAT TTGGAGCAGG AGCCTACAAA TTTGAGAGAA TCATCTCTAA	840
	GCAAAATGTC CTATCTGCAA ATGAGAAATT CACAAGCGCA CAGGAATTTT CTTGAAGATG	900
20	GAGAAAGTGA TGGCTTTTTA AGATGCCTCT CTCTTAACCT TGGGTGGATT TTAACACAA	960
	CTCTTGTCCT CTCGGTGATG GTATTGCTTT GGATTTGTTG TGCAACTGTT GCTACAGCTG	1020
	TGGAGCAGTA TGTTCCTCT GAGAAGCTGA GTATCTATGG TGACTTGGAG TTTATGAATG	1080
25	AACAAAAGCT AACAGATAT CCAGCTTCTT CTCTTGTTGGT TGTTAGATCT AAAACTGAAG	1140
	ATCATGAAGA AGCAGGGCCT CTACCTACAA AAGTGAATCT TGCTCATTCT GAAATTTAAG	1200
30	CATTTTTCTT TTAAAAGACA AGTGTAATAG ACATCTAAAA TTCCACTCCT CATAGAGCTT	1260
	TTAAAATGGT TTCATTGGAT ATAGGCCTTA AGAAATCACT ATAAAATGCA AATAAAGTTA	1320
	CTCAAATCTG TGAAGACTGT ATTTGCTATA ACTTTATTGG TATTGTTTTT GTAGTAATTT	1380
35	AAGAGGTGGA TGTTTGGGAT TGTATTATTA TTTTACTAAT ATCTGTAGCT ATTTTGTTTT	1440
	TTGCTTTGGT TATTGTTTTT TTCCCTTTTC TTAGCTATGA GCTGATCATT GCTCCTTCTC	1500
40	ACCTCTGCC ATGATACTGT CAGTTACCTT AGTTAACAAG CTGAATATTT AGTAGAAATG	1560
	ATGCTTCTGC TCAGGAATGG CCCACAAATC TGTAAATTGA AATTTAGCAG GAAATGACCT	1620
	TTAATGACAC TACATTTTCA GGAACGAAA TCATTAAAAT TTTATTGAA TAATTAAAAA	1680
45	AAAAAAAAA AANCT	1695

50 (2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1501 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

60 CACTTTCAGC AGTCCTTTC TCTCTTTGCT TCTACCTCAA ATAGCCCCAG GAGTGGGCTT 60

	TAGTCTCCAA TATGGAGCAT CTCAAGCTTC TCCTGGGGGA TGGGGATTGG GATGGGCAGA	120
5	ATCTGTTTTG GWTCTCCGGG TTATTTCCAG TGGGTGTAAA AGCAGAGCTG GGCCTTTCCC	180
	TCTCTTATCC CTGAGGGTGG GTAAGAAGGA CTGTATCTAC ACCTGTTCTT CCCTACCTTC	240
	TCTTTTGTGA GGGAGGCCTC ATTCTAAGTT CCTCAAGAGA GTCCTTGGCT TAAAGCTGTA	300
10	GCAAGGGTGT GCTAGGTGGG GGATTTGGAG CAAAACCGTC GAGTAGGCAT GATACTGGTA	360
	TGGAGTGGGC CTGCAAAATC AGACAGAAAT GGCTTGAGAA GCCGCAGGGG AGCATGCCTG	420
15	TCTCTCAGTG ATAGAGTATG GGAGGGACCT CCCTAGCTTG GAAAATGAGA ATTGAAGGGG	480
	TTATGAACAA ATAGGATGCC TAGTTGAGGA TGTTCCTCAA GTTTTGTCCA ATCTTATCAT	540
	TAGTAGATTT TATAAGCCAC AGAGACAAAC CAGAAACGGA ATAATGTTAC TTTGGATGCT	600
20	TTATTTTTTT GTTCTAGGTG TGGCTTTGTA CATGCAGAAG AATGCTATAT GCTGCACATT	660
	TTGCCTTTAA AGTCTTACGA CTTTCCCAT TTTAGTCTAA TGGGAAGATA CAGATGTGCA	720
25	AGTCTGCTTT TTTGTTTTTT GTTATTATTT TTTTTTTTTT GCTCTGTGTT ATGGACATTT	780
	TCAGACATGC ACAGAAGTGG AGAGGATGGT CCTTGGACCC MATGTGTCCA TCACCTAGCT	840
	GCATCACTTA TCAGCTATGG TCAACCTGGT TTCATCTGTA TCTCTCTCTT TTCACCTGTA	900
30	TTGTTTATTG AAAATCCAAG ACACTATGCC AATGCAACCG TGACTIONTT GGGAGATTGG	960
	TAGTCTCTTT TGATGGTGAT AGTGATGGGG TGCATATCA TAATCACATC AGGTCTGCTT	1020
35	TTTGCTTTTA ATGTTAACTA ATGAAGTTCC AGAGATGGGC CTTAGAAATG TGTTTTAAGA	1080
	ATTAACAAGG AGTCTCAAAA AGAAATGAGA GGGATGCTTC CTTTNCCTT GCATCTACAA	1140
	AACMAGAGAG AGACTGTTCT GTTGTAACAC TCTTTCAAAA ATTCTGATAT GGTAAGGTAC	1200
40	TTGAGACCCT TCACCAGAAT GTCAATCTTT TTTTCTGTGT AACATGGAAA CTGTGTGAC	1260
	CATTAGCATT GTTATCAGCT TGTACTGGTC TCATAACTCT GGTTTTGGAA GAATAATTG	1320
45	GAAATTGTTG CTGTGTTCTG TGAAAATAAC CTCCCCAAA TAATTAGTAA CTGGTTGTTT	1380
	TACTTGGTAA TTTGACACCC TGTAAATAAC GCAATTATTT CTGTGTTCTT AAACAGTATA	1440
	AATAGTTGTA AGTTTGCATG CATGATGGAA AAATAAAAAC CTGTATCTCT GTTAAAAAAA	1500
50	A	1501

55 (2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

5	TGANTGTGGT CCCGGGTGCN GATTGGCAGN GCCTCCGCCG CGGCTCGTGG TTGTCCCGCC	60
	ATGGCACTGT CGCGGGGGCT GCCCGGGAG CTGGCTGAGG CGGTGGCCGG GGGCCGGGTR	120
10	CTGGTGGTGG GGGCGGGCGG CATCGGCTGC GAGCTCCTCA AGAATCTCGT GCTCACCAGT	180
	TTCTCCACACA TCGACCTGAT TGATCTGGAT ACTATTGATG TAAGCAACCT CAACAGACAG	240
	TTTTTGTTC AAAAGAAACA TGTGGAAGA TCAAAGGCAC AGGTTGCCAA GGAAAGTGTA	300
15	CTGCAGTTTT ACCCGAAAGC TAATATCGTT GCCTACCATG ACAGCATCAT GAACCTGAC	360
	TATAATGTGG AATTTTTCCG ACAGTTTATA CTGGTTATGA ATGCTTTAGA TAACAGAGCT	420
	GCCCGAAACC ATGTTAATAG AATGTGCCTG GCAGCTGATG TTCCTCTTAT TGAAAGTGGA	480
20	ACAGCTGGGT ATCTTGACA AGTAACACT ATCAAAAAGG GTGTGACCGA GTGTTATGAG	540
	TGTCATCCTA AGCCGACCCA GAGAACCCTT CCTGGCTGTA CAATTCGTAA CACACCTTCA	600
25	GAACCTATAC ATTCATCGT TTGGGCAAAG TACTTGTTCA ACCAGTTGTT TGGGGAAGAA	660
	GATGCTGATC AAGAAGTATC TCCTGACAGA GCTGACCCTG AAGCTGCCTG GGAACCAACG	720
	GAAGCCGAAG CCAGAGCTAG AGCATCTAAT GAAGATGGTG ACATTAAACG TATTTCTACT	780
30	AAGGAATGGG CTAAATCAAC TGGATATGAT CCAGTTNAA CTTTTTACCA AGCTTTTTTAA	840
	AGATGACATC AGGTATCTGT TGACAATGGA CAACTATGG CGGAAAAGGA AACCTCCAAT	900
35	TCCGTTGGAC TGGGCTGAAG TACAAAGTCA AGGAGAAGAA ACGAATGCAT CAGATCAACA	960
	GAATGAACCC CAGTTAGGCC TGAAAGACCA GCAGGTTCTA GATGTAAAGA GCTATGCACG	1020
	TCTTTTTTCA AAGAGCATCG AGACTTTGAG AGTTCATTTA GCAGAAAAGG GGGATGGAGC	1080
40	TGAGCTCATA TGGGATAAGG ATGACCCATC TGCAATGGAT TTTGTCACCT CTGCTGCAAA	1140
	CCTCAGGATG CATATTTTCA GTATGAATAT GAAGAGTAGA TTTGATATCA AATCAATGGC	1200
45	AGGGAACATT ATTCCTGCTA TTGCTACTAC TAATGCAGTA ATTGCTGGGT TGATAGTATT	1260
	GGAAGGATG AAGATTTTAT CAGGAAAAAT AGACCACTGC AGAACAATTT TTTTGAATAA	1320
	ACAACCAAAC CCAAGAAAGA AGCTTCTTGT GCCTTGTCGA CTGGATCCTC CCAACCCCAA	1380
50	TTGTTATGTA TGTGCCAGCA AGCCAGAGGT GACTGTGCGG CTGAATGTCC ATAAAGTGAC	1440
	TGTTCTCACC TTACAAGACA AGATAGTGAA AGAAAAATTT GCTATGGTAG CACCAGATGT	1500
55	CCAAATTGAA GATGGGAAAG GAACAATCCT AATATCTTCC GAAGAGGGAG AGACGGAAGC	1560
	TAATAATCAC AAGAAGTTGT CAGAATTTGG AATTAGAAAT GGCAGCCGGC TTCAAGCAGA	1620
60	TGACTTCCTC CAGGACTATA CTTTATTGAT CAACATCCTT CATAGTGAAG ACCTAGGAAA	1680

	GGACGTTGAA TTTGAAGTTG TTGGTGATGC CCCGAAAAA GTGGGSCCA AACAAGCTGA	1740
	AGATGCTGCC AAAAGCATAA CCAATGGGCA GTGATGATGG AGCTCAGCCC TCCACCTCCA	1800
5	CAGCTCAAGA GCAAGATGAC GTTCTCATAG TTGATTCGGA TGAAGAAGAT TCTTCAAATA	1860
	ATGCCGACGT CATGAAGAAG AGAGAAGCCG CAAGAGGAAA TTAGATGAGA AAGAGAATCT	1920
10	CAGTGCAAAG AGGTCACGTA TAGAACAGAA GGAAGAGCTT GATGATGTCA TAGCATTAGA	1980
	TTGAACAGAA ATGCCTCTAA ACAGAACCCCT CTTACTATTT AGTTTATCTG GGCAGAACCA	2040
	GATTGTTATG TCCTTTGTTT CAAAGGGAAA AAATTGACAG CAGTGACTTG AAAATGATTC	2100
15	TGCTCCCTTT GAAAGCATTC ATTTTGCTAG AACTGTTAGA CACATTGCAG TATGCTGTAT	2160
	TGAAAGTAGG AATATAGTTT TAAAAACCCT TTGAACAAAG TGTGTGCATA ACCAGTCATG	2220
20	AGATAAACA ACACAATGCA TGTTCCTTTT TTAATGTAAA TACCCTTAGG TATCATTAAT	2280
	AGTTTCAAAA TATTGTGGTT TAGTAAAGTT GATACCTGGT TATAAATATT ATGCCTTTAT	2340
	TTTTGGCTAG AAGAAGAATT ATTTTGTAGC TAGATCTAAC CATTTTCATA CTCTTAACTG	2400
25	ATTGAAACAG ATTCAAAGAA GTATCGAGTG CTATGCATTG AAAGTTGTTT TTAAATGTTA	2460
	GATGGCACTA TGTATATTAA TGTAACAA TGTTAATTTA CTCAAGTTTT CAGTTTGTAC	2520
30	CGCCTGGTAT GTCTGTGTAA GAAGCCAATT TTTGTGTATT GTTACAGTTT CAGGTTATTT	2580
	ATATTCGATG TTTTGTAAAA CTCAAATAAC GACTATACTT ATGGACCAA TAAATGGCAY	2640
35	TGCATTCTKG TKAAAAAAN NACAGAAAAA AAAAAAACA AGA	2683

(2) INFORMATION FOR SEQ ID NO: 295:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

	GGACTCGGGG TGGCTCTAAG GGCAGGGAT AGGGCTGGG AGCGCCGGCC TGTGGCCCTG	60
50	ACCAGCCCCCT TCTCGTGAG GTTCCACCCC GATGCAGGTG GTCACGTGCT TGACGCGGGA	120
	CAGCTACCTG ACGCACTGCT TCCTCCAGCA CCTCATGGTC GTGCTGTCCT CTCTGGAACG	180
55	CACGCCCTCG CCGGAGCCTG TTGACAAGGA CTTCTACTCC GAGTTTGGGA ACAAGACCAC	240
	AGGGAAGATG GAGAACTACG AGCTGATCCA CTCTAGTCGC GTCAAGTTTA CCTACCCAG	300
	TGAGGAGGAG ATTGGGGACC TGACGTTTAC TGTGGCCCAA AAGATGGCTG AGCCAGAGAA	360
60	GGCCCCAGCC CTCAGCATCC TGCTGTACGT GCAGGCCTTC CAGGTGGGCA TGCCACCCCC	420

TGGGTGCTGC AGGGGCCCCC TCGCCCCAA GACACTCCTG CTCACCAGCT CCGAGATCTT 480
 CCTCCTGGAT GAGGACTGTG TCCACTACCC ACTGCCCGAG TTGCCAAAG AGCCGCCGCA 540
 - 5 GAGAGACAGG TACCGGCTGG ACGATGGCCG CCGCGTCCGG GACCTGGACC GAGTGCTCAT 600
 GGGCTACCAG ACCTACCCGC AGCCCTCACC CTCGTATTTCG ATGACGTGCA AGGTCATGAC 660
 10 CTCATGGGCA GTGTACCCCT GGACCACTTT GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC 720
 AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG TTTGTCCCA GTGCTGAGAG CAGAGAGAAG 780
 CTCATCTCGC TGTGGGCTCG CCAAGTGGGAG GCCCTGTGTG GCCTGAGCTG CCTGTGAGC 840
 15 TCACCGGCTA GCCCAGGCCA CAGCCAGCCT GTCGTGTCCA GCCTGACGCC TACTGGGGCA 900
 GGGCAGCAGG CTTTGTGTGT CTCTAAAAAT GTTTTATCCT CCCTTTGGTA CCTTAATTG 960
 20 ACTGTCTCG CAGAAATGTG AACATGTGTG TGTGTGTGT TAATTCTTTC TCATGTTGGG 1020
 AGTGAGAATG CCGGGCCCCT CAGGGCTGTT CCGTGTGCTG TCAGCCTCCC ACAGGTGGTA 1080
 CAGCCGTGCA CACCAAGTGT GTGTCTGCTG TTGTGGGACC GTTGTAAACA CGTGACACTG 1140
 25 TGGGTCTGAC TTTTCTTCT ACACGTCCCT TCCTGAAGTG TCGAGTCCAG TCCTTTGTG 1200
 CTGTGTGCTG TGCTGTGCT GTTGTGTGTT GCATCTTGCT GCTAATCCTG AGGCTGGTAG 1260
 30 CAGAATGCAC ATTGGAAGCT CCCACCCCAT ATTGTTCTTC AAAGTGGAGG TCTCCCCTGA 1320
 TCCAGACAAG TGGGAGAGCC CGTGGGGGCA GGGGACCTGG AGCTGCCAGC ACCAAGCGTG 1380
 ATTCTGTCTG CCTGTATTCT CTATTCCAAT AAAGCAGAGT TTGACACCGW MAAAAAAAAA 1440
 35 AAAAAAAAAA AACN 1454

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(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

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ACCCTGGCAT GCCCCACAAA CAGATCACCA GCCAGCTTAC ACAGGCATTA ACTCTCTCA 60
 ATGAGGAAGA ATCATTCACA ACTGAGCAAG ACATTCATAT GATCATTTAA GGAAGTGTTT 120
 CCCTTATGTG TTAGCAAGTA TAATCGGCTA ACTCCTAAAT CCCAATGAAT AGTCCTAGGC 180
 TGGACAGCAA TGGGCTGCAA TTAGGCAGAT AAAGACATCA GTCCCAGTAA ATGAATCCAT 240
 AGACTCATCT AGCACCAACT ACCATTAGCA CTATGTTAGG AGCTGCAAGG CCCCAGTA 300

GAAGATGTGC ATAATGTCTG CTCTTGTTGA GCTCAGGAGA CAATTCCAGC ACAGACACTA 360
 CAGTTAACGC TGAAGTGCAG CTGCAAGTAA TAGCAWGAAC AGTCAGAAAA ATACCTTATG 420
 - 5 AGGGGGCAGG GCTGAAGCTG GGCCTTGAAG GATGGATGAA ATTTGGATAG AGAATGAGGA 480
 AGACAGAGGG NCTCCAAGTG AGAGAAGCAT GAAAAATGAG CARGGGCCTG GATCAGTGGG 540
 10 GTGTATTTCAG AGCACCTTTC CAGATGCACC ATGCATGCTC ACAGTCCCTT GCCTATGTGT 600
 GGCAGAGTGT CCCAGCCAGA TGTGTGCCCC CACCCCATGT CCATTTACAT GTCCTTCAAT 660
 GCCCACCTCA AAAGGYACYT CTTCTGTAAA GCTTTCCTK GGTATCAGGA ATCAAAATTA 720
 15 ATCAGGGATC TTTTCACACT GCTGTTTTTT CCTCTTTGGT CCTTCTATCA CTAAACTCA 780
 TCTCATTCAG CTTACAGCA TAACTAATTA TTGTTTTCC TCACTACA 828

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(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 2416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

TCAATTTCCA TTAAGTCTGA TCAGCCATTG TGATTCACCA TTTGTCAGGC TCTCAGGTTT 60
 AACAAAACCT ACTATCACCA TCATCCTTCA ACAGCCACAG TCTGAATTGA GCCAACATTT 120
 35 TTTTTTCTTT GAGAAAGAAG TGGACTGGGG CACAACCTTT AGTCTGAGGG GAGCTAGTGG 180
 AAATCTAGAC AATAGAAGTC ATCGATAGCA GCTTTTCCTC AAATGTGTGA CTCTCAGGG 240
 40 GCTAAACTGC TCTTAGCTTA GAATTATGCT TTAGTAGAGA TCTAGCAGAT AAGTGGGTTA 300
 ATCACTACCA TCCTGTAACT AGTTATATAG CTTCCAGACA TGAGGGAGAC ATCAAACAGG 360
 GATGGAAGCA ACCCAAGGA TATGCAAGAA GGGCATGATG AACCCCTTC CCTCTGGCAG 420
 45 GAGAACAAGG CCAACCAAGG GACAGACTGG AAAGCACTTA GATGTTTAAG GAGGAGAAAG 480
 GGAAGCTTT GACCAGTCCT TGCCTTTTGC CAAGTTCAGC CAGTTCTCCG CTGCTTGCAA 540
 50 CCTCTAGCGC AGTAACATTT GCAGAATTGC AGATTTTCCC CCAGATACTA GGAGGAAAGG 600
 GACTTTGGGG GGTGGGAAG GGGTCGTGGT GTTTTAAAAG CATAAGTTAC CTGTTTGCAC 660
 TGTTTTAAGA TAGGAAAAAA AAATAGTGGG CAAGGTGAAC ATCAGACGTA AATTTGTGTG 720
 55 TTTTATTTT GTCATGCTCT TGAAAATGTT TGACCATTTG TAGTATACAC AGTGAAACTT 780
 GATTCTCTGT TGCATAAAAC ACTATATTTT TTTGGAAATG TTAGTGCCA AAAGCCTCTT 840
 60 CCTCCCTTT CCTTTTCTA TGTACTTCCT TCATACTGTC TTTACTGATC AGCCAGGCAA 900

	TAGCCATCCA AGAGCTAGAG CATGAAACAG GGCCCTTTCC AAGTAGGCTC TGGGTGTCCT	960
- 5	AAGCCAGCGT GTGCCCTCTG GTTTAGTGAG TGTAATAGAG TCCCTGGCAC CTTTCTTTGC	1020
	AAATGAGGCT AACAGACCAG ACTGCAGCAA GTTATCAGAT TCCTCAATCA GATGCACTAG	1080
	GAGTGAGGAG CCCAGGGATG GAGGGGGTTC CTGAAGTATT GCAGTTGGCT GTAGTAGCTG	1140
10	AGTTCTTTTC CATGTTACCG AAAGTGTAGC CAGTTACAGT TTAATCAGGA AAACGGTAGA	1200
	TCAATTCAGC CATGGTAGTG CTGGTTGGCA GGGATTGGTA ACGGAGAGAA CTGCTCATCA	1260
15	GCCAAACTC AAGCCTTGCC TTTTAGGAGG CCACCAGCAG AGGGACTTGG TCCTCCTTGT	1320
	CTGGTACTTG TGTACATGCC GGTGACCTGA GGAATCCACT CACACTGGCG AGCAAAAAGG	1380
	GAGCAGTGAT TCTCTTTTCT CTCCCCACCC CCTGCCCTTT GTTACCAACA CCAGTTTCCC	1440
20	AGGGGGTACA TGAGTTTCTG AATTTTAA AAATGTTTTT GGTTTGGTTT TTCTGGGGAC	1500
	TGATAAGTGC TTAAAGCAAT GTCCATACCC CGTCAAGACT CCCAGCTTAG TCATTTTCTT	1560
25	GTATTTTCT GTTCACAGTA TTTGTGTGTG TGCTTGTTT GGCAGCTCAT TTTGGCTGTA	1620
	TTATATATTG AGTGATGAAT TGATCCTCTT TTTTCCCTAA GGGATATGAA TTGTTTTTCT	1680
	TGTGTTATAT TCTGCTTGTG AATAGCTGGA GCAAACCTGG GGCTGACACG CGTAAGSTAG	1740
30	GGCTGCAAAAR CGAGAAGAGA GCCGGTGGAG TGTACTTGTC CCTGACAGGC TGACCTACCT	1800
	GAGTCTCTGA GCTTTTCAGT CCAAATCTTT GCAAGGCTCA AAATGCCACA GAACCTCTCC	1860
35	TCTTCTCCCC ACTCCCCATG GCAGGGACCG GACCATCCCT ACATGCAACA TGCTGTTTCT	1920
	CCAGCCCCCTC CCATTGCCAT GGCAAAACAG GTACCTTTGG GGCATGGGGG CATTACATGG	1980
	GATGCTTGTG TAATCGACCA CCTAGCCTTC TCTCTCCCT CCCGTCTCTC CCCAGAATCA	2040
40	CTTCCTAGGA CACCCGAGCT GCTTGCCCAG GGTCTCTGTT CCCTGCTAAC TCCAGAGAAG	2100
	CATCCCAGGG CTTTGTGACA GTCTCTAATT CCCTTCCCTT CTCGTTAAGA ATCATATTGT	2160
45	ATAGTAGCTT TCAGACCATA CAGTATTCAT TGGGTTACTC CTATTATTAT CAAGTAGCTG	2220
	GAATTGTGAA GGTCGGAGTA GTTAGATCTT TAGCTTTTAT TCCTTATTTT TTTGTATTAC	2280
	TCTCCATGTG TATAAATTAT TGATCATGTT GCTGGCTTTT ATAAACTCTA AGCGAAGGAG	2340
50	GAGCACTGCC TCAGCCTTTG CACATGGTAA TGAAGCACTG TTTTAAATA AAAGRGRGAA	2400
	MCMCCAAAAA AAAAAA	2416

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(2) INFORMATION FOR SEQ ID NO: 298:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

	GAATTCGGCA CGAGCCATGC YTGGCCTCTC CTTGATTCTT ACAGTCACTT TGTTGGCTGT	60
10	TTCTGACTCA GCAGCTACCT GCATTGTGGC CAAAGGATGA CCTATTCTTT CTCAGGAGGG	120
	CAAAAATGTG GAATAGTGTG TGTCCATGCC TCTCCTCATG GGCTACCACC TCTGCCACCG	180
	TGGTTAATCA GTAACAACCA GGAGAGAAGC TGCTGGAAC TACCTCTGGG AACTCCCTGG	240
15	ATGGTTTGGT GCAGGAATGT AGTAGGCATA CACGTGGTTG CGTGGATCTG GGCCCTCTCTG	300
	ATGTGAGTAG AGAGGTAAAA GGSCACCATC TCCTTGACCT YTGGGGAAC TATCCACAAA	360
20	GAAGATGTTT CCAAGATGCT TCTGAAGATT GSCTAAAAAT AGCCGGTTTC CACCCCGTG	420
	AATGCATCCA TTCTAGAATG CTCCTTCACC AGGACCAGAG AACTGATTTA CAGAAGTGAC	480
	ATGAAAACAT TCCATCCCAG AATTTGCANT ACCTCAAATT NAATTTCTAC CTATTAAAAA	540
25	NAAAA	545

30 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

40	GGCTCTGCTG GGCATCATAC TTGTCACTGG GTAAACAGTT TGCCCACTTA CCGCAGATGA	60
	AGCTGCTTGC CAGGGCTCTC CGGCTCTGTG AGTTTGGGAG GCAGGCATCT TCCAGGAGGC	120
45	TGGTGGCTGG CCAGGGATGT GTGGGGCCCC GCGGAGGGTG CTGCGCTCCC GTCCAGGTGG	180
	TTGGGCCCAG GGCTGATCTC CCACCCTGTG GAGCCTGCAT TACTGGAAGG ATCATGCGGC	240
	CAGATGATGC CAACGTGGCC GGCAATGTCC ACGGGGGGAC CATCTGAAG ATGATCGAGG	300
50	AGGCAGGCGC CATCATCAGC ACCCGGCATT GCAACAGCCA GAACGGGGAG CGCTGTGTGG	360
	CCGCCCTGGC TCGTGTGAG CGCACCGACT TCCTGTCTCC CATGTGCATC GGTGAGGTGG	420
55	CGCATGTTCG CGCGGAGATC ACCTACACCT CCAAGCACTC TGTGGAGGTG CAGGTCAACG	480
	TGATGTCCGA AAACATCCTC ACAGGTGCCA AAAAGCTGAC CAATAAGGCC ACCCTGTGGT	540
	ATGTGCCCCCT GTCGCTGAAG AATGTGGACA AGGTCTCGA GGTGCCTCCT GTTGTGTATT	600
60	CCCGGCANGA GCAGGAGGAG GAGGGCCGGA AGCGGTATGA AGCCGAGAAG CTGGAGCGCA	660

	TGGAGACCAA GTGGAGGAAC GGGGACATCG TCCAGCCAGT CCTCAACCCA GAGCCGAACA	720
	CTGTCAGCTA CAGCCAGTCC AGCTTGATCC ACCTGGTGGG GCCTTCAGAC TGCACCCTGC	780
5	ACGCGCTTTGT GCACGGAGGT GTGACCATGA AGCTCATGGA TGAGGTCGCC GGGATCGTGG	840
	CTGCACGCCA CTGCAAGACC AACATCGTCA CAGCTTCCGT GGACGCCATT AATTTTCATG	900
10	ACAAGATCAG AAAAGGCTGC GTCATCACCA TCTCGGGACG CATGACCTTC ACGAGCAATA	960
	AGTCCATGGA GATCGAGGTG TTGGTGGACG CCGACCCTGT TGTGGACAGC TCTCAGAAGC	1020
	GCTACCGGGC CGCCAGTGCC TTCTTCACCT ACGTGTGCT GAGCCAGGAA GGCAGGTGCG	1080
15	TGCCTGTGCC CCAGCTGGTG CCCGAGACCG AGGACGAGAA GAAGCGCTTT GAGGAAGGCA	1140
	AAGGCGGTA CCTGCAGATG AAGGCGAAGC GACAGGGCCA CGCGGAGCCT CAGCCCTAGA	1200
20	CTCCCTCCTC CTGCCACTGG TGCCTCGAGT AGCCATGGCA ACGGGCCCAG TGTCCAGTCA	1260
	CTTAGAAGTT CCCCCCTTGG CCAAAAACCC AATTCACATT GAGAGCTGGT GTTGTCTGAA	1320
	GTTTTCGTAT CACAGTGTTA ACCTGTACTC TCTCTGCAA ACCTACACAC CAAAGCTTTA	1380
25	TTTATATCAT TCCAGTATCA ATGCTACACA GTGTGTCCC GAGCGCCGGG AGGCGTTGGG	1440
	CAGAAACCCCT CGGGAATGCT TCCGAGCAGC CTGTAGGGTA TGGGAAGAAC CCAGCACCAC	1500
30	TMATAAAGCT GNTGCTTGGC TGGGGAAGNA	1530

35 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 997 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

45	AGGTAGTGAG AGACACATTA CACCTAACCA ACAAGAAGAA GGATCCTCCC CCTTATAATT	60
	TAACTATGTT TACAGGGAAT GCGTACATTG TGGCTTCCCG AGNATTTTCGT CCAACATGTT	120
	TTGAAGAACC CTAAATCCCA ACAACTGATT GAATGGGTAA AAGACACTTA TAGCCCAGAT	180
50	GAACACCTCT GGGCCACCTC TCAGCGTGCA CGGTGGATGC CTGGCTCTGT TCCCAACCAC	240
	CCCAAGTACG ACATCTTCAG ACATGACTTC TATTGCCAGG CTGGTCAAGT GGCAGGGTCA	300
55	TGAGGGAGAC ATCGATAAGG GTGCTCCTTA TGCTCCCTGC TCTGGAATCC ACCAGCGGGC	360
	TATCTGCGTT TATGGGGCTG GGGACTTGAA TTGGATGCTT CAAAACCATC ACCTGTTGGC	420
60	CAACAAGTTT GACCCAAAGG TAGATGATAA TGCTCTTCAG TGCTTAGAAG AATACCTACG	480

TTATAAGGCC ATCTATGGGA CTGAACTTTG AGACACACTA TGAGAGCGTT GCTACCTGTG 540
 GGGCAAGAGC ATGTACAAAC ATGCTCAGAA CTTGCTGGGA CAGTGTGGGT GGGAGACCAG 600
 5 GGCTTTGCAA TTCGTGGCAT CCTTTAGGAT AAGAGGGCTG MTATTAGATT GTGGGTAAGT 660
 AGATCTTTTG CCTTGCAAAT TGCTGCCTGG GTGRATGCTG CTTGTTCTCT CACCCCTAAC 720
 10 CCTAGTAGTT CCTCCACTAA CTTTCTCACT AAGTGAGAAT GAGAACTGCT GTGATAGGGA 780
 GAGTGAAGGA GGGATATGTG GTAGAGCACT TGATTTTCAGT TGAATGCCTG CTGGTAGCTT 840
 TTCCATTCTG TGGAGCTGCC GTTCCTAATA ATTCCAGGTT TGGTAGCGTG GAGGAGAACT 900
 15 TTGATGGAAA GAGAACCCTC CCTTCTGTAC TGTTAACCTA AAAATAAATA GCTCCTGATT 960
 CAAAGTAAGG AAAAAA AAAAGAAAAA AACTCGA 997

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(2) INFORMATION FOR SEQ ID NO: 301:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TTGAGGCCGA CGCTAGGGGC CCGGAAGRAA ACTGCGAGGC GAAGGTGACC GGGGACCGAG 60
 CATTTTCAGAT CTGCTCGGTA GACCTGGTGC ACCACCACCA TGTGCGCTGC AAGGCTGGTG 120
 35 TGTCTCCGGA CACTACCTTC TAGGGTTTTTC CACCCAGCTT TCACCAAGGC CTCCCCTGTT 180
 GTGAAGAATT CCATCACGAA GAATCAATGG CTGTTAACAC CTAGCAGGGA ATATGCCACC 240
 40 AAAACAAGAA TTGGGATCCG GCGTGGGAGA ACTGGCCAAG AACTCAAAGA GGCAGCATTG 300
 GAACCATCGA TGGAAAAAAT ATTTAAATTT GATCAGATGG GAAGATGGTT TGTGCTGGA 360
 45 GGGGCTGCTG TTGGTCTTGG AGCATTGTGC TACTATGGCT TGGGACTGTC TAATGAGATT 420
 GGAGCTATTG AAAAGGCTGT AATTTGGCCT CAGTATGTCA AGGATAGAAT TCATTCCACC 480
 TATATGTACT TAGCAGGGAG TATTGGTTTA ACAGCTTTGT CTGCCATAGC AATCAGCAGA 540
 50 ACGCCTGTTT TCATGAACTT CATGATGAGA GGCTCTTGGG TGACAATTGG TGTGACCTTT 600
 GCAGCCATGG TTGGAGCTGG AATGCTGGTA CGATCAATAC CATATGACCA GAGCCCAGGC 660
 55 CCAAAGCATC TTGCTTGGTT GCTACATTCT GGTGTGATGG GTGCAGTGGT GGCTCCTCTG 720
 ACAATATTAG GGGGTCCTCT TCTCATCAGA GCTGCATGGT ACACAGCTGG CATGTGGGA 780
 GGCCTCTCCA CTGTGGCCAT GTGTGCGCCC AGTGAAAAGT TTCTGAACAT GGGTGCACCC 840
 60 CTGGGAGTGG GCCTGGGTCT CGTCTTTGTG TCCTCATTGG GATCTATGTT TCTTCCACCT 900

ACCACCGTGG CTGGTGCCAC TCTTACTCA GTGGCAATGT ACGGTGGATT AGTTCTTTTC 960
AGCATGTTCC TTCTGTATGA TACCCAGAAA GTAATCAAGC GTGCAGAAGT ATCACCAATG 1020
5 TATGGAGTTC AAAAATATGA TCCCATTAACT TCGATGCTGA GTATCTACAT GGATACATTA 1080
AATATATTTA TGCGAGTTGC AACTATGCTG GCAACTGGAG GCAACAGAAA GAAATGAAGT 1140
10 GACTCAGCTT CTGGCTTCTC TGCTACATCA AATATCTTGT TTAATGGGGC AGATATGCAT 1200
TAAATAGTTT GTACAAGCAG CTTTCGTTGA AGTTTAGAAG ATAAGAAACA TGTCATCATA 1260
TTTAAATGTT CCGGTAATGT GATGCCTCAG GTCTGCCTTT TTTTCTGGAG AATAAATGCA 1320
15 GTAATCCTCT CCCAAATAAG CACACACATT TTCAATTCTC ATGTTTGAGT GATTTTAAAA 1380
TGTTTGGTG AATGTGAAAA CTAAAGTTTG TGTCATGAGA ATGTAAGTCT TTTTCTACT 1440
20 TTAAATTTA GTAGGTTTAC TGAGTAACTA AAATTTAGCA AACCTGTGTT TGCATATTTT 1500
TTTGGAGTGC AGAATATTGT AATTAATGTC ATAAGTGATT TGGAGCTTTG GTAAAGGGAC 1560
CAGAGAGAAG GAGTCACCTG CAGTCTTTTG TTTTMTTAA TACTTAGAAC TTAGCACTTG 1620
25 TGTTATIGAT TAGTGAGGAG CCAGTAAGAA ACATCTGGGT ATTTGGAAAC AAGTGGTCAT 1680
TGTTACATTC ATCTGCTGAA CTTAACAAA CTGTCATCC TGAAACAGGC ACAGGTGATG 1740
30 CATTCTCCTG CTGTTGCTTC TCAGTGCTCT CTTTCCAATA TAGATGTGGT CATGTTTGAC 1800
TTGTACAGAA TGTTAATCAT ACAGAGAATC CTTGATGGAA TTATATATGT GTGTTTACT 1860
TTTGAATGTT ACAAAGGAA ATAACTTTAA AACTATTCTC AAGAGAAAAT ATTCAAAGCA 1920
35 TGAAATATGT TGCTTTTCC AGAATACAAA CAGTATACTC ATGATTGCTA AGTGTTTTTT 1980
TATTTTGA TATTTATTGA ACTGTCTAAT TGAATACAGC TTGCTCTTGT CACCTCTTCA 2040
40 AGCTTTCAAG CCTTTATAGA AAAGCTTCTT TGTGGCTTAC ACTGGAAATT ATGAAAGCAG 2100
TTTTTCTCCT AAGACTTTTG GTTCTCGCA TTGCCTCTCA GACTAAGCAC TAAAAAGCAA 2160
AGCAAAACAG AACTAGTNCT GTCTTAATGA AATATATCAA CCCAAAAGTG TAATGAGGAA 2220
45 AATGCTTCAT TAGTTTCCCC TAGCAGACTT TTAATTCTCT TACACTGCTA CACCATTACT 2280
TTCTTGAGAC ATTTGTAAGT CCTTGATAC AGAAGAGTTA TATTTAGGAG GNCPTTAATG 2340
50 AAGGG 2345

55 (2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

5	TTTTTTTTTT TTTTTTTTTT TTTTINCAAG ATCATGTGTT ATTTATTACT TCAGATAAAA	60
	AGATAGTATA CATATTAGGG AATCCCTTAA AATTCAACTC TAGAGTTATA CACCATCTAG	120
10	TACTTTTGCA ATGAATGTTA ACAACAACAA AAAAAATCTC TAAACACCTG AAAGCCCCAC	180
	TATTAACATG GACTATGGTA ATAAAAAATT TTGACATTTA ATTTGTTCAA CATATAGTAT	240
	TTACATTATG AAACCAATGG TGATGATACA ATAAAGTGAT AAAGAAATAG TAAAAATAAA	300
15	CTTTAAAAAG CAAAGGTTTA TAGTCTGACA ATGCTAATTA TCCTAATTGT ATATAAAAAA	360
	TTAAACATA GAGCTTTCTG TTACAAAATT CTTAATCCTC TGGGTTGTAA TCATTACTTG	420
20	CTACCAATTT ACATGCAACA TCTGCTAGGA CTGACATTTG ATTTTTTTTCC CCAAGAATGT	480
	GTGAGTAGAT AAATGACATT TCAGAGCAGA TATTAAATTTA CTTGTGGACA GAAAAAGAAA	540
	CTCAAGATTG GTACTGGTCA CAAGCCTCTT CCCAATAGAA ATTATAAAAA CAGTAAGATA	600
25	AAATTTAAAA AAAATCTAAA AAGGGGATGC ATAGGCAAAG AGTACCATAA ATGGCACAGC	660
	TCAAAAATC CCAGGACCAA TCAGACACAC ATCTTTTCTC TCTCCTTCAG CGACAAGAGG	720
30	TCGATTTTGC CATCAAATAA CCATGATTGA AGCAAGCGAG GGGCACCAGG TGTACAACTG	780
	ATTAGATCTT GCAAAATACT AAGATGGGAG CAGGGGTGGC CAGAAGAAGG GGTAATTTAT	840
	ATATAATTCA AACTATATAC AGCATAAATG GAATGCAGCC CATCCCAAAC TGGCTCTGIG	900
35	AAACAATTGG ACCTTTATAG TTAAATTTAT AACAAGTGTA ATAATACAAT AGATTTACAT	960
	GGGAAGCAAA ATCCAAGGGA CATTTTATAT TAAGTATTTA CTGTGCTGTT TCAATTTAAA	1020
40	AATAATTTTG CTAAGTATAC ATCTCAACTG AAGTCTATGT AAAAAATGTC CTAATAGATA	1080
	CAGATATTTA CCTTTGGTGA GTTGAAGGCC TTTTGTGAC TTCTGTCTGA ACTGTAGGCA	1140
	GAATGCTAGA TGTACATGCA CATATGGAGA AACTCAAGCT GAGGTCATCC AAAAGCTGTG	1200
45	CGTATGAGGA GGCTGGAGGT ACTTTGAAAG TCAAAGTAGA CCAGAAACCC AAAACAGGTA	1260
	ACAGTGAGGA TGGCAACAGG GAATGGAATG CCAATATGGC AGTAAACTT TTTTTAAAAA	1320
50	CAGAAAGAGG AAGGCCTCTC GTACCAGCAG AATCCTGTAC ACGTACAAA AAGAAAAAGC	1380
	CACCCACCAT TTTGTAAAAC AGAAGCCAAT TATAGTGTGG GAAAGTACAA ATTACAGAAA	1440
	ACCAGAAGTC AACAGAAGAA AACTACTGG TTTACTTGAG AGAAAGGAGA ATGGTTTACC	1500
55	CCGAGCAGAG TTACTTGGTG AACGCCGCCA CCACGCCCA CAGAACCTCA TTGGTGTGTG	1560
	CCTTCAGACA TTCCACTTCA GGGTCTAAGT CGAGAARNIG CCGCACTCTC TTGGTAGCCA	1620
60	AATCATACTG CTCGTCCAGA AGAGGAGCAA AAGCATTTCT CAGGACGTCC GAGGCATGAG	1680

	CCAGGTAAAT GAGGGCCAGC AAGCGCCTGT CCATGCGGTG AGGGTCATTG ACCCATTTGT	1740
	CAAGAACGGC TTCCTGFACT TTCTTGATGA GCGCTGCTT AATGTTGTTA TTGGTGAGGG	1800
- 5	GATGTGTTGT CATGTCAAAA AGTAGGAAGT TCTGTTTCTC TGTGTCAAT ACACCCTTTT	1860
	CCACCAGGTT TTTAGCTAAT CGTCCCGTA CATTTCTTAA CTGATAATGC AATTTTAATG	1920
10	GATTCCATGT CTCACCACTA AGTAATTCAA TCCAGTTCTG GACCGTTTCT GGAGGCTGAG	1980
	TTTCCTTAAC ATGCTTCAGA GCTTCATCAA GAAGAACATC CCCTGTTGGA GCATCTGACT	2040
	TACAGATTAC CTTTCTTGTT AATAGACTTT TACGTCTCAT TCCACAAGCC TCTAGTTGTA	2100
15	ACCTTCCTCT CAATGCTAAT TCAATTAACA TACAGCCAAG TAATCCAGAT GATATACAGT	2160
	CATTCCAAAA TGATGTGTAA ACCTTCGCGG TCCTTGAGGC CCAGCAGGAG CACTTCCTCC	2220
	ATCAGGGTCA GCCGCGTTTC CTGGAGTCG CCCTTGTCGT CGTCGTCCTG CTCGTCGCGG	2280
20	CGGCTCTGCG CGTCGTCTC GCTGCTAGCC GCGCCGCCG CCGCCGCCG CTCCTGTGCG	2340
	GCGGCGTTGC GGGAGGCCTC GGTGCGCCG	2369
25		

(2) INFORMATION FOR SEQ ID NO: 303:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

	GGGACGTGTG GTTTCAGCTC GTGCGCCTCC CCGTGGGTTT GCGACGTTTA GCGACTATTG	60
40	CGCCTGCGCC ACGCCGGCTG CGAGACTGGG GCCGTGGYTG CTGGTCCCGG GTGATGCTAG	120
	GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG GTGTAGGTGG GAGTCACGGA CGGTTCCGGG	180
45	CCCAGGTGT CCGCGAAGGT GCGGCACATG GGCGGCAGG GAGAGCATGG CTCAGCGGAT	240
	GGTCTGGGTG GACCTGGAGA TGACAGGATT GGACATTGAG AAGGACCAGA TTATTGAGAT	300
	GGCCTGTCTG ATAACTGACT CTGATCTCAA CATTTTGGCT GAAGGTCCTA ACCTGATTAT	360
50	AAAACAACCA GATGAGTTGC TGGACAGCAT GTCAGATTGG TGTAAAGAGC ATCACGGGAA	420
	GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG TACAATTACA TTGCAGCAGG CAGAGTATGA	480
55	ATTCTGTCC TTTGTACGAC AGCAGACTCC TCCAGGGCTC TGTCCACTTG CAGGAAATTC	540
	AGTTCATGAA GATAAGAAGT TTCTTGACAA ATACATGCCC CAGTTCATGA AACATCTTCA	600
	TTATAGAATA ATTGATGTGA GCACTGTAA AGAACTGTGC AGACGCTGGT ATCCAGAAGA	660
60	ATATGAATTT GCACCAAAGA AGGCTGCTTC TCATAGGGCA CTTGATGACA TTAGTGAAAG	720

CATCAAAGAG CTCAGTTTT ACCGAAATAA CATCTTCAAG AAAAAAATAG ATGAAAAGAA 780
 5 GAGGAAAATT ATAGAAAATG GGGAAAATGA GAAGACCGTG AGTTGATGCC AGTTATCATG 840
 CTGCCACTAC ATCGTTATCT GGAGGCAACT TCTGGTGGTT TTTTTCCTC ACGCTGATGG 900
 CTGGCAGAG CMCTTCGGTT AACTTGCATC TCCAGATTGA TTAACAAGC AGACAGCACA 960
 10 CGAAATACTA TTTTCTCCT AATATGCTGT TTCCATTATG ACACAGCAGC TCCTTTGTAA 1020
 GTACCAGGTC ATGTCCATCC CTTGGTACAT ATATGCATTG GCTTTTAAAC CATTTCTTTT 1080
 GTTTAAATAA ATAAATAAGT AAATAAAGCT AGTCTATTG AAATGCAAAA AAAAAAAAAA 1140
 15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA N 1181

20

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 1537 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

35

CTTTTGTGT TCGGCCGAT CCCACCTCTC CTCGACCTG GACGTCTACC TTCCGGAGGC 60

CCACATCTTG CCCACTCCGC GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA 120

GGGACATGGC AACTACAGCG GCGCCGGCGG GCGGCGCCG AANATGGAGC TGGCCCGGAA 180

TGGGGAGGGT TCGAAGAAAA CATCCAGGGC GGAGGCTCAG CTGTGATTGA CATGGAGAAC 240

40

ATGGATGATA CCTCAGGCTC TAGCTTCGAG GATATGGGTG AGCTGCATCA GCGCCTGCGC 300

GAGGAAGAAG TAGACGCTGA TGCAGCTGAT GCAGCTGCTG CTGAAGAGGA GGATGGAGAG 360

TTCTGGGCA TGAAGGGCTT TAAGGGACAG CTGAGCCGGC AGGTGGCAGA TCAGATGTGG 420

45

CAGGCTGGGA AAAGACAAGC CTCCAGGGCC TTCAGCTTGT ACGCCAACAT CGACATCCTC 480

AGACCCTACT TTGATGTGGA GCCTGCTCAG GTGCGAACAG GGCTCCTGGA GTCCATGATC 540

50

CCTATCAAGA TGGTCAACTT CCCCAGAAA ATTGCAGGTG AACTCTATGG ACCTCTCATG 600

CTGGTCTTCA CTCTGGTTGC TATCCTACTC CATGGGATGA AGACGTCTGA CACTATTATC 660

CGGGAGGGCA CCTGATGGG CACAGCCATT GGCACCTGCT TCGGCTACTG GCTGGGAGTC 720

55

TCATCCTTCA TTTACTTCTT TGCCTACCTG TGCAACGCCC AGATCACCAT GCTGCAGATG 780

TTGGCACTGC TGGGCTATGG CCTCTTTGGG CATTCATTG TCCTGTTTAT CACCTATAAT 840

60

ATCCACCTCC ACGCCCTCTT CTACCTCTTC TGGCTGTTGG TGGGTGGACT GTCCACACTG 900

CGCATGGTAG CAGTGTGGT GTCTCGGACC GTGGGCCCCA CACAGCGGCT GCTCCTCTGT 960
 GGCACCCTGG CTGCCCTACA CATGCTCTTC CTGCTCTATC TGCATTTTGC CTACCACAAA 1020
 - 5 GTGNTAGAGG GGATCCTGGA CACACTGGAG GGCCCCAACA TCCCGCCCAT CCAGAGGGTC 1080
 CCCAGAGACA TCCCTGCCAT GCTCCCTGCT GCTCGGCTTC CCACCACCGT CCTCAACGCC 1140
 10 ACAGCCAAAG CTGTTGCGGT GACCCCTGCAG TCACACTGAC CCCACCTGAA ATTCTTGGCC 1200
 AGTCCTCTTT CCCGCAGCTG CAGAGAGGAG GAAGACTATT AAAGGACAGT CCTGATGACA 1260
 TGTTTCGTAG ATGGGGTTTG CAGCTGCCAC TGAGCTGTAG CTGCGTAAGT ACCTCCTTGN 1320
 15 AGCTGTGCGC ACTTCTGAAA GCACAAGGCC AAGAACTCCT GGCCAGGACT GCAAGGCTCT 1380
 GCAGCCAATG CAGAAAATGG GTCAGCTCCT TTGAGAACCC CTCCCCACCT ACCCCTTCCT 1440
 20 TCCTCTTTAT CTCTCCACA TTGTCTTGCT AAATATAGAC TTGGTAATTA AAAAAAAAAA 1500
 AAAAAAAAAA AAAAAAAAAA AAAAAAGGGG GGNCCCC 1537

25

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 1493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

35

TGCATGCCAA AACCAATGCC TGCCAAACAA AATCTTAGAC ATCCCAATAT AATATGTTAG 60
 TTATATTTCT ATTACATCA TTATTGAAAA TACCCAGCTC AGTGCCTGGC TTAATAAATG 120
 40 TTTAATTCCC TTACCTACTC TTGCTCTATT TTTTATTTG AAATGGAGAT GAGCAAAATA 180
 ACACATTCAT GGCTGAAGCA ATTTTPTGGA CATTTCTTGT TACCAAAAGA TCTATAATCA 240
 45 GGATGATCCT GAGCTGTTCA AACAAGCTGT ATATAACAG ACAATGAAAC TCTTTGCAGA 300
 GCTGGAAATT AAAAGGAAAG AGAGAGAAGC CAAAGAGATG CATGAAAGGA AACGACAAAG 360
 GGAAGAAGAG ATTGAAGCTC AAGAAAAAGC CAAACGGGAA AGAGAGTGGC AGAAAACTT 420
 50 TGAGGAAAGT CGAGATGGTC GTGTGGACAG CTGGCGAAAC TTCCAAGCCA ATACGAAGGG 480
 GAAGAAAGAG AAGAAAAATC GGACCTTCCT GAGACCACCG AAAGTAAAAA TGGAGCAACG 540
 55 TGAGTGACCG CCCAAGGTCA CAGGCACAGA ACCTTTCCCC TGCTATCTCC CTTCTGCTT 600
 CGAAGGACTC ATTCTTTCCT CCCACTTCCA CCCCACATA GAGTAGTATT TGCTTTTITAG 660
 TCCATTTTGT TTTCAATACG ATTTAATATC GATCAGAGTA ATTCTTTTGT ACATTGAAAT 720
 60 GAGGGGCTTG GTTTAAAAA AGACCTTTCC CTCTCCCTGC CCCTAGAACA ACCAGTATTA 780

GAAGGTGCCA CCATTGGTGC TGCCTTCTCT TCCCACAGCC TGTAATCAG TGTITTGTAC 840
 TTCCTGAAT TGTGATGGTT AGAACTTCG TGGATAGTTT GTGGAAATCA TCCAATTAAA 900
 CATACTGCTT AAAACAGTGT TGCTGTGACT TCAGAGACAA GCCTGGAAGG GGCACCTTAG 960
 GAAGCCCCCTT CGCTTCAGTT GCTCGCTTCT GGGTGTGCTC CCTTCGAAGG CCCAGATAAG 1020
 10 ACAGGGAACA CTTGTGAGCA CACAGAGCAG CATCTGATGC CCTGTGGTGT TTGGCATGTG 1080
 CCCCCTGTCT ACTGACCAAT CAGTGTGGCA TGAGGCCAC GCCACCCAAA CCTTTCACTT 1140
 TCCAAAGAGC TAGCCGTCCT CCACCCAGTA CCATGTCCTA GCCTGTCTGC ATTGTAGT 1200
 15 GGTAATATTC TTTATGTATA ATAAATTTTT ATACCCAAGC CATTGATGTA CTTTTCCTTG 1260
 TACTCTCCCT TGTGGGTCCC TTGTCTGGCT TGGCTGAACC CCAAAATGCT TTGGGGTTGG 1320
 20 ACAGACCTGG CTGAACCTTA GTTCTTTCAT CTATGAAATG GGAATATGAA TTAGTGCAGC 1380
 AGCTTTTAGG GCAGATTGTC CATGGCATAT ACAAGGTAAC TACCATAGTG CTCCTTGGGT 1440
 25 ATTGCCAATA TCCTATTATT TCTGTGTAAG ATGAAGATAC TGATTGTTTT GAG 1493

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AATTGGGCAG AGGNATTATA TACACTATAC TGGCATTTCAC AGCCCGGAAA 60
 40 GTCAGAGATG TATATTGGAA AATTTACAAC TCCATCTACA TTGGTTCCCA GGACGCTCTC 120
 ATAGCACATT ACCCAAGAAT CTACAACGAT GATAAGAACA CCTATATTCG TTATGAACCTT 180
 45 GACTATATCT TATAATTTTA TTGTTTATTT TGTGTTTAAT GCACAGCTAC TTCACACCTT 240
 AAAGTTGCTT TGATTGGTG ATGTAACTT TAAACATTG CAGATCAGTG TAGAACTGGT 300
 CATAGAGGAA GAGCTAGAAA TCCAGTAGCA TGATTTTAA ATAACCTGTC TTTGTTTTTG 360
 50 ATGTTAAACA GTAAATGCCA GTAGTGACCA AGAACACAGT GATTATATAC ACTATACTGG 420
 AGGGATTTC TTTTAATTC ATCTTTATGA AGATTAGAA CTCATTCCCTT GTGTTTAAAG 480
 55 GGAATGTTA ATTGAGAAAT AAACATTGT GWACAAAATG YTAACAAAAA AAAAAAAA 540
 AAAAAAAA AAAAAAAA AAAAAAAA AACTCGA 577

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2860 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

	GTGTNGACCG CTCTCNCAAT ATGGCTCCCC CGGGCTGGCA GRWRKTCRGT CWCKRGTGGC	60
	TAGCCTGTCC TGACAGGGGA GAGTTAAGCT CCCGTTCTCC ACCGTGCCGG CTGGCCAGGT	120
15	GGGCTGAGGG TGACCGAGAG ACCAGAACCT GCTTGCTGGA GCTTAGTGCT CAGAGCTGGG	180
	GAGGGAGGTT CCGCCGCTCC TCTGCTGTCA GCGCCGGCAG CCCCTCCCGG CTTCACTTCC	240
20	TCCCGCAGCC CCGCTACTG AGAAGCTCCG GGATCCAGC AGCCGCCACG CCCTGGCCTC	300
	AGCCTGCCGG GCTTCCAGTC AGGCCAACAC CGACGCGCAC TGGGGAGGAA GACAGGACCC	360
	TTGACATCTC CATCTGCACA GAGGTCCTGG CTGGAACCGA GCAGCCTCCT CTCCTAGGA	420
25	TGACCTCACC CTCCAGCTCT CCAGTTTTC A GGTGGAGAC ATTAGATGGA GGCCAAGAAG	480
	ATGGCTCTGA GCGGACAGA GGAAAGCTGG ATTTTGGGAG CGGGCTGCCT CCCATGGAGT	540
30	CACAGTTCCA GGGCGAGGAC CGGAAATTCG CCCCTTCAGA TAAGAGTCAA CCTCCAATA	600
	CCGAAAGGGA ACAGGTGCCA GTCAGCCGGA TCCAAACCGA TTTGACCGAG ATCGGCTCTT	660
	CAATGCGGTC TCCCGGGGTG TCCCGAGGA TCTGGCTGGA CTTCCAGAGT ACCTGAGCAA	720
35	GACCAGCAAG TACCTCACCG ACTTCGGBAA TACACAGAGG GCTCCACAGG TAAGACGGCC	780
	TGATGAAGGC TGTGCTGAAA CCTTAAGGAC GGGGTCAATG CCTGCATTCT GCCACTGCTG	840
40	CAGATCGACC GGGACTCTGG CAATCCTCAG CCCCTGGTAA ATGCCCAGTG CACAGATGAC	900
	TATTACCGAG GCCACAGCGC TCTGCACATC GCCATTGAGA AAGAGGAGTC TGCAGTGTGT	960
	GAAGCTCCTG GTGGAGAATG GGGCCAATGT GCATGCCCGG GTCTGCGGCG ACTTCTTCCA	1020
45	GAAGGGCCAA GGGACTTGCT TTTATTTTCG TGAGCTACCC CTCTCTTTGG CCGCTTGAC	1080
	CAAGCAGTGG GATGTGGTAA GCTACCTCCT GGAGAACCCA CACCAGCCCG CCAGCCTGCA	1140
50	GGCCACTGAC TCCAGGGCA ACACAGTCCT GCATGCCCTA GTGGATGATC TCGGACAACT	1200
	CAGCTGAGAA CATTGCACTG GTGACCAGCA TGTATGATGG GCTCCTCCAA GCTKGGGSCC	1260
	SCCYTCTGCC CTACCGTGCA GCTTGAGGAC ATCCGCAACC TGCAGGATCT CACGCCTCTG	1320
55	AAGCTGGCCG CCAAGGAGGG CAAGATCGAG ATTTTCAGGC ACATCCTGCA GCGGGAGTTT	1380
	TCAGGACTGA GCCACCTTTC CCGAAAGTTC ACCGAGTGGT GCTATGGGCC TGTCCGGGTG	1440
60	TCGCTGTATG ACCTGGCTTC TGTGGACAGC TGTGAGGAGA ACTCAGTGCT GGAGATCATT	1500

	GCCTTTCATT GCAAGAGCCC GCACCGACAC CGAATGGTCG TTTTGGAGCC CCTGAACAAA	1560
- 5	CTGCTGCAGG CGAAATGGGA TCTGCTCATC CCCAAGTTCT TCTTAACTT CCTGTGTAAT	1620
	CTGATCTACA TGTTTCATCTT CACCGCTGTT GCCTACCATC AGCCTACCCT GAAGAAGCAG	1680
	GCCGCCCTC ACCTGAAAGC GGAGGTGGA AACTCCATGC TGCTGACGGG CCACATCCTT	1740
10	ATCCTGCTAG GGGGATCTA CCTCCTCGTG GGGCCAGCTG TGGTACTTCT GGCGGGCCA	1800
	CGTGTTCATC TGGATCTCGT TCATAGACAG CTACTTTGGA AATCCTCTTC CTGTTCCAGG	1860
15	CCCTGCTTCA CAGTGGTGTC CCAGGTGCTG TGTTCCTGG GCCATCGAGT GGTACCTGCC	1920
	CCTGCTGTG TCTGCGCTGG TGGCTGGGCT GGCTGAACCT GCTTTACTAA TACACGTGGC	1980
	GTTCCAGCAC ACAGGCAGTC TACAGTTTCA TGWTCCCTGA AGCCCTGGTG AGCCTGAGCC	2040
20	AGGAGGCTTG GCGCCCCGAA GCTCCTACAG GCCCCAATGC CACAGAGTCA GTGCAGCCCA	2100
	TGGAGGGACA GGAGGACGAG GGCAACGGGG CCCAGTACAG GGGTATCCTG GAAGCCTCCT	2160
25	TGGAGCTCTT CAAATTCACC ATCGGCATGG GCGAGCTGGC CTTCCAGGAG CAGCTGCACT	2220
	TCCGCGGCAT GGTGCTGCTG CTGCTGCTGG CCTACGTGCT GCTCACCTAC ATCCTGCTGC	2280
	TCAACATGCT CATCGCCCTC ATGAAGCGAA CGTCACAGTG TCGCCACTGA CAGCTGGAGC	2340
30	ATCTGGAAGC TGCAGAAAGC CATCTCTGTC CTGGAGATGG AGAATGGCTA TTGGTGGTGC	2400
	AGGAAAAAGC AGCGGGCAGG TGTGATGCTG ACCGTTGGCA CTAAGCCCAG ATGGCAGCCC	2460
35	CGATGAGCGC TGGTGCTTCA GGGTGGAGGA GGTGAACTGG GCTTCATGGG GAGCAGACGC	2520
	TGCCTACGCT GTGTGAGGAC CCGTCAGGGG CAGGTGTCCC TCGAACTCTC GAGAACCCTG	2580
	TCCTGGCTTC CCCTCCCAAG GAGGATGAGG ATGGTGCCTC TGAGGAAAAC TATGTGCCCCG	2640
40	TCCAGCTCCT CCAGTCCAAC TGATGGCCCA GATGCAGCAG GAGGCCAGAG GACAGAGCAG	2700
	AGGATCTTTC CAACCACATC TGCTGGCTCT GGGGTCCAG TGAATTCTGG TGGCAAATAT	2760
45	ATATTTTCAC TAACTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAVGAGGG GGGGCCGKT	2820
	ASCCAAWTTT GCCCTATAAG TGAGTGCCWA TTACGATAAA	2860

50

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

	CTGCTTGTTGT CTGCGCTGGT GCTGGGCTGG CTGAACCTGC TTTACTATAC ACGTGGCTTC	60
	CAGCACACAG GCATCTACAG TGTCTATGATC CAGAAGCCCT GGTGAGCCTG AGCCAGGANN	120
- 5	TTGGCGCCCC GAAGCTCCTA CAGGCCCCAA TGCCACAGAG TCAGTGCAGC CCATGGAGGG	180
	ACAGGAGGAC GAGGGCAACG GGGCCCAGTA CAGGGGTATC CTGGAAGCCT CCTTGGAGCT	240
10	CTTCAAATTC ACCATCGGCA TGGGCGAGCT GGCCTTCCAG GAGCAGCTGC ACTTCCGCGG	300
	CATGGTGCTG CTGCTGCTGC TGGCCTACGT GCTGCTCACC TACATCCTGC TGCTCAACAT	360
	GCTCATCGCC CTCATGNAGC GAGACCGWCA ACAGTGTGCG CACTGACAGC TGGAGCATCT	420
15	GGAAGCTGCA GAAAGCCATC TCTGTCCTGG AGATGGAGAA TGGCTATTGG TGGTGCAGGA	480
	AGAAGCAGCG GGCAGGTGTG ATGCTGACCG TTGGCACTAA GCCAGATGGC AGCCCCGATG	540
20	AGCGCTGGTG CTTCAGGGTG GAGGAGGTGA ACTGGGCTTC ATGGGAGCAG ACGCTGCCTA	600
	CGCTGTGTGA GGACCCGTCA GGGGCAGGTG TCCCTCGAAC TCTCGAGAAC CCTGTCCTGG	660
	CTTCCCTCC CAAGGAGGAT GAGGATGGTG CCTCTGAGGA AACTATGTG CCCGTCCAGC	720
25	TCCTCCAGTC CAACTGATGG CCCAGATGCA GCAGGAGGCC AGAGGACAGA GCAGAGGATC	780
	TTTCCAACCA CATCTGCTGG CTCTGGGGTC CCACTGAATT CTGGTGGCAA ATATATATTT	840
30	TCACTAAMWM AAAAAAAAAA AAAAAAAAAA ACTCGA	876

(2) INFORMATION FOR SEQ ID NO: 309:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2025 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

45	CATGACCCGC CTGATGCGAT CCCGCACAGC CTCTGGTTCC AGCGTCACTT CTCTGGATGG	60
	CACCCGCAGC CGCTCCCACA CCAGCGAGGG CACCCGAAGC CGCTCCCACA CCAGCGAGGG	120
	CACCCGCAGC CGCTCGCACA CCAGCGAGGG GGCCACCTG GACATCACC CCAACTCGGG	180
50	TGCTGCTGGG AACASGCCG GCCCAAGTCC ATGGAGGTCT CCTGCTAGGC GGCCTGCCA	240
	GCTGCCGCCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC CTCCCCGGCC CCTTTTCGCC	300
	CCCTGCCTGC CATACTGCGC CTAAGTCGGT ATTAATCCAA AGCTTATTTT GTAAGAGTGA	360
55	GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC TCTCCAAAGG CGGGGTGGCG	420
	GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC CTCTTCCATT AACCAGTGGC	480
60	CGGTTGCCAC TCTCTCCCC TCCCTCAGAG ACACCAAAC GCCAAAACA AGACGCGTAC	540

	AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC ATCCTGGTTC AAACGGGTGC	600
- 5	CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCCTCTTT AACTGAGGAG AAGCTGATCC	660
	AGTTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG GGTAAATAGT ACATGCAGGC	720
	ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAGAGGTG GGATTCATGT CGAGGCTAGA	780
10	GGCATTGGA ACAACAAATC TACGTAGTAA ACTTGAAGAA ACCGATTTT AAAGTTGGTG	840
	CATCTAGAAA GCTTTGAATG CAGAAGCAAA CAAGCTTGAT TTTTCTAGCA TCCTCTTAAT	900
15	GTGCAGCAAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG ACAAAAATAT TTCAGCAAAC	960
	GTTGGGCATC ATGGTMTTGT AAGGCTTTAG TTCTGCTTTC TGCCTCTCCT CCACAGCCCC	1020
	AACCTCCAC CCCTGATACA TGAGCCAGTG ATTATCTTG TTCAGGGAGA AGATCATTTA	1080
20	GATTTGTMTT GCATTCCTTA GAATGGAGGG CAACATTCCA CAGCTGCCCT GGCTGTGATG	1140
	AGTGTCCCTG CAGGGGCCGG AGTAGGAGCA CTGGGGTGGG GCGGAATTG GGGTFACTCG	1200
25	ATGTAAGGGA TTCTTGTTG TTGTGTTGAG ATCCAGTGCA GTGTGATTT CTGTGGATCC	1260
	CAGCTTGGTT CCAGGAATTT TGTGTGATTG GCTTAAATCC AGTTTTCAAT CTTGACAGC	1320
	TGGGCTGGAA CGTGAACCTA GTAGCTGAAC CTGTCTGACC CGGTCACGTT CTTGGATCCT	1380
30	CAGAACTCTT TGCTCTTGTC GGGGTGGGGG TGGGAACCTA CGTGGGGAGC GGTGGCTGAG	1440
	AAAATGTAAG GATTCCTGAA TACATATTCC ATGGGACTTT CCTTCCCTCT CCTGCTTCCT	1500
35	CTTTTCTGTC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC CACTGACGTT TCTGGGCGGC	1560
	CAGTGGCGCT GCCAGGTTCC TGTACTACTG CCTTGTACTT TTCATTTTGG CTCACCGTGG	1620
	ATTTTCTCAT AGGAAGTTTG GTCAGAGTGA ATTGAATATT GTAAGTCAGC CACTGGGACC	1680
40	CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG TCCAGCCTTC CAGGTGGCGT	1740
	GAGAGGCAAT GACTCGTTAC CTGCCGCCCA TCACCTTGGA GGCCTTCCCT GGCCTTGAGT	1800
45	AGAAAAGTCG GGGATCGGGG CAAGAGAGGC TGAGTACGGA TGGGAACTA TTGTGCACAA	1860
	GTCTTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA TTCCAGACC AATAAATTTG	1920
	TAACCTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAATC	1980
50	GAGGGGGGCC CGTACCCAAT TCGCCGTATA TGATCGTAAA CAATC	2025

55 (2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3026 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

5	TAGGCAGCAC TGAAATATCC TAACCCCTA AGCTCCAGGT GCCCTGTGGN ACGAGCAACT	60
	GGACTATAGC AGGGCTGGGC TCTGTCTTCC TGGTCATAGG CTCACTCTTT CCCCCAATC	120
10	TTCTCTGGA GCTTTCAGC CAAGGTGCTA AAAGGAATAG GTAGGAGACC TCTTCTATCT	180
	AATCCTTAAA AGCATAATGT TGAACATTCA TTCAACAGCT GATGCCCTAT AACCCCTGCC	240
	TGGATTCTT CCTATTAGGC TATAAGAAGT AGCAAGATCT TTACATAATT CAGAGTGGTT	300
15	TCATTGCCCTT CCTACCTCT CTAAATGGCC CTCCATTTAT TTGACTAAAG CATCACACAG	360
	TGGCACTAGC ATTATACCAA GAGTATGAGA AATACAGTGC TTTATGGCTC TAACATTACT	420
20	GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG GATGGCAGCC TCAGGGCTTC CTTATGTCCT	480
	CCACCACAAG AGCTCCTGA TGAAGGTCAT CTMTTCCCC TATCCTGTTT TCCCCCTCCC	540
	CGCTCCTAAT GGTACGTGGG TACCCAGGCT GGTCTTGGG CTAGGTAGTG GGGACCAAGT	600
25	TCATTACCTC CCTATCAGTT CTAGCATAGT AACTACGGT ACCAGTGTTA GTGGGAAGAG	660
	CTGGGTTTTT CTAGTATACC CACTGCATCC TACTCCTACC TGGTCAACCC GCTGCTTCCA	720
30	GGTATGGGAC CTGCTAAGTG TGAATTACC TGATAAGGGA GAGGGAAATA CAAGGAGGGC	780
	CTCTGGTGTT CCTGGCCTCA GCCAGCTGCC CACAAGCCAT AAACCAATAA AACAAGAATA	840
	CTGAGTCAGT TTTTATCTG GGTCTCTTTC ATTCCCACTG CACTTGGTGC TGCTTGGCT	900
35	GACTGGGAAC ACCCCATAAC TACAGAGTCT GACAGGAAGA CTGGAGACTG TCCACTTCTA	960
	GCTCGGAAC TACTGTGTAA ATAACTTTC AGAACTGCTA CCATGAAGTG AAAATGCCAC	1020
40	ATTTTGCTTT ATAATTTCTA CCCATGTTGG GAAAACTGG CTTTTTCCA GCCCTTCCA	1080
	GGGCATAAAA CTCAACCCCT TCGATAGCAA GTCCCATCAG CCTATTATTT TTTTAAAGAA	1140
	AACTGCACT TGTMTTCTT TTTACAGTTA CTCTCTCTCT GCCCCAAAAT TATAAACTCT	1200
45	AAGTGTAATA AAAAGTCTTA ACAACAGCTT CTGTCTTGTA AAAATATGTA TTATACATCT	1260
	GTATTTTAA ATTCTGCTCC TGAAAAATGA CTGTCCCAT CTCCACTCAC TGCAATTGGG	1320
50	GCCTTTCCA TTGGTCTGCA TGTCTTTTAT CATTCAGGC CAGTGGACAG AGGGAGAAGG	1380
	GAGAACAGGG GTCGCCAACA CTGTGTTGC TTTCTGACTG ATCCTGAACA AGAAAGAGTA	1440
	AACTGAGGC GTCGCTCCC ATGCACAACT CTCCAAAACA CTTATCTCTC TGCAAGAGTG	1500
55	GGCTTTCCAG GGTCTTACT GGAAGCAGT TAAGCCCCCT CTCACCCCT TCCTTTTTC	1560
	TTCTTTACT CCTTTGGCTT CAAAGGATTT TGGAAAAGAA ACAATATGCT TTACTCAT	1620
60	TTCAATTTT TAAATTGCA GGGGACTG AAAAATACGG CAGGTGCCT AAGGCTGCTG	1680

	TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT TACAAGATAA AAAACGAATC CCCTAAACAA	1740
	AAAGAACAAT AGAACTGGTC TTCCATTTTG CCACCTTTCC TGTTCATGAC AGCTACTAAC	1800
5	CTGGAGACAG TAACATTTCA TTAACCAAAG AAAGTGGGTC ACCTGACCTC TGAAGAGCTG	1860
	AGTACTCAGG CCACTCCAAT CACCCTACAA GATGCCAAGG AGGTCCCAGG AAGTCCAGCT	1920
10	CCTTAAACTG ACGCTAGNMA ATAAACCTGG GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT	1980
	CCATCTGTGA GGTGAYAGGC AAGGATGAAA GACAAAGAAG GAAAAGAGTA TCAAAGGCAG	2040
	AAAGGAGATC ATTTAGTTGG GTCTGAAAGG AAAAGTCTTT GCTATCCGAC ATGTACTGCT	2100
15	AGTACCTGTA AGCATTTTGT GTCCAGAAT GGAAAAAAA ATCAGCTATT GGTAATATAA	2160
	TAATGTCTTT TCCCTGGAGT CAGTTTTTTT AAAAAGTTAA CTCTTAGTTT TTAATTGTTT	2220
20	AATTCTAAAA GAGAAGGGAG CTGAGGCCAT TCCCTGTAGG AGTAAAGATA AAAGGATAGG	2280
	AAAAGATTCA AAGCTCTAAT AGAGTCACAG CTTTCCAGG TATAAACCT AAAATTAAGA	2340
	AGTACAATAA GCAGAGGTGG AAAATGATCT AGTTCCTGAT AGCTACCCAC AGAGCAAGTG	2400
25	ATTTATAAAT TTGAAATCCA AACTACTTTC TTAATATCAC TTGGTCTCC ATTTTTCCTA	2460
	GGACAGGAAA TATGTCCCCC CTAACCTTTC TTGCTTCAAA AATTAAAAATC CAGCATCCCA	2520
30	AGATCATTTCT ACAAGTAATT TTGCACAGAC ATCTCCTCAC CCCAGTGCCT GTCTGGAGCT	2580
	CACCCAAGGT CANCCAAACA ACTTGGTTGT GAACCCAACCT GCCTTAACCT TCTGGGGGAG	2640
	GGGGATTAGC TAGACTAGGA GACCCAGAAG TGAATGGGAA AGGGTGAGGA CTTCAACAATG	2700
35	TTGGCCTGTC AGAGCTTGAT TAGAAGCCAA GACAGTGGCA GCAAAGGAAG ACTTGGCCCA	2760
	GGAAAAACCT GTGGGTTGTG CTAATTTCTG TCCAGAAAAT AGGGTGGACA GAAGCTGTG	2820
40	GGGTGCATGG AGGAATTGGG ACCTGGTTAT GTTGTATTTC TCGGACTGTG AATTTTGGTG	2880
	ATGTAAACA GAATATTCTG TAAACCTAAT GTCTGTATAA ATAATGAGCG TTAACACAGT	2940
	AAAATATTCA ATAAGAAGTC AAAAAAAAAA AAAAAAACT CGAGGGGGG CCCGGTACCC	3000
45	AATTNNCAA ATAGAGATNG TATTAC	3026

50 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

60 GCAGGCTTTG TGCTCACCTA CAAGCTGGGT GAGCAGGGTG CCAGCAGCCT GTTTCCTCTT 60

CTCCTGCTGG ACCACGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG TGTGGGTGCT 120
 GTGGTCTGCT CCATCGCTGG CTCTCCCTG GGTGGGACCT TGCTGGCCAA GCACTGGAAA 180
 5 CTGCTGCCTC TGTTGARGTC GGTGCTGCGC TTCCGCCTCG GGGGCCTAGC CTGTCAGACT 240
 GCCTTGGTCT TCCACCTGGA CACCCTGGGG GCCAGCATGG ACGCTGGCAC AATCTTGAGA 300
 10 GGTTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GAGGCCTGGT CACCACAGTC 360
 ACCTTCACTG GGATGATGCG CTGCAGCCAG CTGGCCCCCA GGGCCTGCAG GCCACACACT 420
 ACAGCCTTCT GGCCACGCTG GAGCTGCTGG GGAAGCTGCT GCTGGGCACT CTGCGGAGGC 480
 15 CTGGCTGATG GGTGGGGGCC ACATCCCTGC TTCTTGCTCC TGCTCATCCT CTCTGCCTTT 540
 CCCGTTCTGT ACCTGGACCT AGCACCCAGC ACCTTTCTCT GAGCTGAGTG GCTGGAGTGG 600
 20 TCAATAAAGC CACATGTGCC TGTGGCCCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 660
 AACTGGAGGG GGGGCCCGGT ACCCAAATCG CCGGATATGA TCGTAAACAA TC 712

25

(2) INFORMATION FOR SEQ ID NO: 312:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CAAATTTCA GAACTTTCAG GAGGGCAAGA GAATATCAA CAAAGATTTC TGGAAGTATT 60
 TTGCCAACCT TCTGGTTGAG CTGCAAGAAA ATATTTATGG TGAGAACTTT TCTGTTTCCC 120
 40 GTTATTTGGT TTTTGGTTGG TTTTGTGTTG TTTTTTACTA TGCTTTGGTC TGTA AAAATA 180
 TGCAACTGAA CTACATTTCAG AAGGAAATAT TGTCTACATA GAATATTATA TGAAGTTGGT 240
 45 ACATAATTCT GATGAGGAAA AAAAATCTTT GCAATTCTTT AAGCCATAAT GTTGTTTTTC 300
 TGTGTTGTTT TCCCTGGATG AAAATATCAG TATTAAGTAG ACAGCATATT ATTCAAGTGT 360
 TTAGACTTAT TAATATGTTT TTGTCCTGTA TTTATACATA TGTGTATTTT GGAAAGTATT 420
 50 GCCTTTTTTA AGGGAAGCTA TAATTCGATA CATAGTGAAA AAGGGAATGG TGACCCCTTT 480
 GTGCCTCTTC CACTGAGGAT AACAAACAGC ATTGTAATCC ATTCTCTTGC ACCTTCTTCT 540
 55 TCTTATCTTG TTATTACGGT TTTATTAATT TTGTAGAGGG ACAGGGAGTG GGCAAGGGGA 600
 AGAAGCAGCT TATTTGACTA ACCAGCCCCT CTGTGGTCCA CCAGCGTCTT GGCTTGGTGG 660
 GAGGGCTCTC AATCAGCAGG GCCCCAGGAG GGAAGAAGAA GTGGGGCAAA GCCTGGCCTC 720
 60

GCCGCTCGGG AGCTTTGCCA TCTGAGCCAC GCCTCCTCCA GGCCATGCTC CTTGAACTTG 780
 GAAATGTCAA CCGGAGCCCT TACACCAGCC CTCCAGCATC TAATAGACTT GAATCTACTC 840
 5 TAAACGAATA TTTAATCCAA CCTCACTACA TTGTAGCTCA GTCCAACGAC TAACCCTGAA 900
 ATGGGGGTGT TCCAGCCTTC AGCGAGATGG CCAAGCGGTC CCTTGGGGGC TGTGGCAGCG 960
 10 GGCTTATCCT TCTCTGTTGC CAACCTTGCC GTCCGACCTC CTCCGCCCCC ATGCGGTGAC 1020
 CCCGTCCGTG TCTGTGTCTG TCCATACGTG TGAGTCCAGC TAAAAAGACA AAACAGAACC 1080
 CGTGGGCCCCA GCTCGGAAGG TCGTGGAGA AGGCTCCGAC GTCTCCGAAG TGCAGCCCTT 1140
 15 GGGATGGCAT TCCGTGTGTG GCCTTATTC TGGAGAATCT GTATACGGCT CGCCTATAGA 1200
 AATATAGCCT CTTCATGCTG TATTAAAAGG ACTTTTAAAA GCAAAAAAAA AAAAAAAAAA 1260
 CTTGAGGGGG GGNCCGGTAC CCAATTNTC 1289
 20

25 (2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Ile Leu Phe Ser Ser Ser
 1 5 10 15

35 Leu Pro Phe Leu Trp Leu
 20

40 (2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Met Phe Leu Thr Gln Gly Gly Pro Leu Pro Ser Thr Arg Ala Arg
 1 5 10 15

50 Pro Thr Cys Gln Ala Gly Ala Leu Pro Lys Pro Ser Gly Leu Leu Gly
 20 25 30

55 Val Thr Cys Trp Asn Gly Leu Lys Gly Pro Leu Cys Gly Asn Arg Cys
 35 40 45

Ser Pro Asn Thr Leu Leu Leu Ala Ala Arg Gln Ala Leu Trp Lys Gly
 50 55 60

60 Arg Gly Arg Thr His Gln Asp Leu Pro Gly Pro Leu Gln Gly Arg Gln

	65					70						75					80
	Leu	Gly	Pro	Glu	Pro	Lys	His	Leu	Ala	Leu	Leu	Pro	Pro	Arg	Gly	Gln	
					85					90					95		
-5	Glu	Ala	Ser	Trp	Ala	Ser	Ser	Leu	Pro	Gly	Gln	Gly	Pro	Leu	Pro	Leu	
				100					105					110			
	Pro	His	Ile	Asn	Cys	Thr	Val	Phe	Ser	Leu	Lys	Ala	Ser	Phe	Ile	Lys	
10			115					120					125				

15

(2) INFORMATION FOR SEQ ID NO: 315:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

25 Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15
Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

30

(2) INFORMATION FOR SEQ ID NO: 316:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40

Met Asp Gly Phe Ser Ser Arg Leu Phe Ser Ser Leu Pro Phe Val Ala
1 5 10 15

45 Leu Gln Trp Phe Ile Val Ile Ser His Leu Leu Ser Leu Ser Leu Ser
 20 25 30

Ala Cys Cys Tyr Gln Thr His Cys Ser Leu Xaa Gln Leu Ser Ser Ala
35 40 45

50 Phe Ser Xaa Met Gly Glu Ser Cys Val Gly Glu Arg Glu Tyr Xaa Phe
50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 317:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

- 5

Met Pro Leu Ile Asn Leu Leu Leu Tyr Tyr Val Pro Asn Gly Gly
1 5 10 15

10

Lys Gln Asp Lys Lys
20

15

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Gly Arg His Leu Val Leu Val Met Phe Ile Thr Thr Ser Leu His
1 5 10 15

25

Ser Gly Thr Pro Val Pro Glu Asn Val Ile Cys Gly Val Thr Lys Gly
20 25 30

30

Pro Gln Gly Lys Lys Lys Lys
35

35

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Trp Trp Ser Arg Asp Tyr Thr Met Val Phe Leu Leu Phe Thr
1 5 10 15

45

Met Val Phe Thr Gly Asp Leu Val Ile Arg Gly Arg Thr Glu Leu Ser
20 25 30

Leu

50

(2) INFORMATION FOR SEQ ID NO: 320:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

60

Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe

548

1 5 10 15
 Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu Ile Leu
 20 25 30
 - 5 Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu Leu Pro
 35 40 45
 10 Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala Glu Asn
 50 55 60
 Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val
 65 70 75 80
 15 Gln Thr Ser Glu Pro Ser Gly Thr
 85

20 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 25 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Gln Pro Gly Ala Gly Val Leu Val Leu Gly Leu Leu Leu Pro Pro
 1 5 10 15
 30 Pro Gln Ser Pro Ser Leu Ser
 20

35 (2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 40 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Thr Phe Thr Leu Gly Asp Ser Gln Val Leu Leu Ile Asn Leu Phe
 45 1 5 10 15
 Pro Ser Met Pro Ser Gly Ser Cys Ala Arg Pro
 20 25

50 (2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

60 Met Cys Leu Glu Cys Trp Ala Glu Asn Leu Gly Pro His His Thr Ser


```

      1              5              10              15
Ser Leu Leu Asn Pro Arg His Leu Pro Ser Ile Pro Ala Met Phe Pro
      20              25              30
- 5 Val Ser Ser Gly Cys Phe Gln Glu Gln Gln Glu Met Asn Lys Ser Leu
      35              40              45
10 Val Ser Cys Leu Phe Val Leu His Phe Val Leu His Cys Ile Phe Xaa
      50              55              60

```

15

(2) INFORMATION FOR SEQ ID NO: 324:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEO ID NO: 324:

[illegible]

Lys Lys Lys Lys
195

5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

10

15

Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys
1 5 10 15

Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu
20 25 30

20

Ala Xaa Xaa Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp
35 40 45

25

Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr
50 55 60

Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val
65 70 75 80

30

Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val
85 90 95

Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys
100 105 110

35

Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp
115 120 125

40

Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln
130 135 140

Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala
145 150 155 160

45

Ala Arg Xaa His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg
165 170 175

Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met
180 185 190

50

Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn
195 200 205

55

Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala
210 215 220

Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro
225 230 235 240

60

Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
245 250

(2) INFORMATION FOR SEQ ID NO: 326:

- 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
 1 5 10 15

15 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala
 20 25 30

Val Ile Lys Asn Asn Ser His Tyr Gln Thr Ser Lys Ala Leu Glu Leu
 35 40 45

20

Glu Lys Thr Thr Glu Asn Lys Glu Ser Asn Pro Phe Ile Leu Gln Val
 50 55 60

25

Asn Lys Leu Xaa
 65

(2) INFORMATION FOR SEQ ID NO: 327:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Gly Glu Gly Lys Asn Gly Phe Gly Gly Phe Val His Thr Ala Asp
 1 5 10 15

40 Ala Cys Trp Glu Gly Val His Ser Glu Pro Val Cys Arg Thr Val His
 20 25 30

Thr Val His Thr Cys His His Gln Ala Phe Leu Val Leu Ile Gly Trp
 35 40 45

45

Ser Lys Ser Gly Lys Glu Arg Lys Glu Ala Phe Leu Thr Ala Ile Ile
 50 55 60

50

Leu Asn Ser Arg Ser Ile His Ile Ser Cys Ser Trp Pro Pro Ser Pro
 65 70 75 80

Val Pro Gln Xaa

55

(2) INFORMATION FOR SEQ ID NO: 328:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

552

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

- 5 Met Leu Leu Ile Asn Leu Leu Trp Leu Val Thr Met Ile Lys Ser Val
 1 5 10 15
 Ile Asn Asn Asn Ile Ile Leu Phe Leu Lys Lys Lys Ser Leu Phe Phe
 20 25 30
 10 Ile Asp Ser Val
 35

15

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

25 Met Thr Phe Pro Phe Glu Lys Lys Ile Val Ala Phe Ser Ala Phe Tyr
 1 5 10 15
 Leu Ile Pro Gly Glu Ser Arg Leu Ala Pro Thr Phe Asn Pro Ser Ala
 20 25 30
 30 Asp Met Thr Val Ile Leu Arg Gly Arg Ala Gln His Lys Thr Ala Met
 35 40 45
 Leu Glu Ser Tyr Asn Trp Lys Val Ser Cys Gln Leu Arg Glu Xaa
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 330:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

45

45 Met His Ser Lys Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile
 1 5 10 15
 Leu Ile Leu Pro Val Cys Ala His Leu His Glu Glu Leu Asn Cys Cys
 20 25 30
 Phe His Arg
 35

55

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 amino acids

553

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Gly Ala Leu Val Leu Leu Leu Cys Leu Leu Val Gly Val Gln Gln
 1 5 10 15
 Ser Gly Ser Val Trp Asp Ser
 20
 10

(2) INFORMATION FOR SEQ ID NO: 332:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Gln Ser Ala Glu Ile Leu Ser Trp Thr Asp Val Leu His Asp Phe
 1 5 10 15
 Leu Phe Ser Leu Phe Leu Trp Pro Ala Phe Glu Asp Arg Ala Leu Leu
 25 20 25 30
 Ile Phe Thr Leu Asn Gln Ile Val
 35 40
 30

(2) INFORMATION FOR SEQ ID NO: 333:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

40 Met Gln Ser Leu Val Gln Trp Gly Leu Asp Ser Tyr Asp Tyr Leu Gln
 1 5 10 15
 Asn Ala Pro Pro Gly Phe Phe Pro Arg Leu Gly Val Ile Gly Phe Ala
 20 25 30
 45 Gly Leu Ile Gly Leu Leu Leu Ala Arg Gly Ser Lys Ile Lys Lys Leu
 35 40 45
 Val Tyr Pro Pro Gly Phe Met Gly Leu Ala Ala Ser Leu Tyr Tyr Pro
 50 55 60
 Gln Gln Ala Ile Val Phe Ala Gln Val Ser Gly Glu Arg Leu Tyr Asp
 65 70 75 80
 55 Trp Gly Leu Arg Gly Tyr Ile Val Ile Glu Asp Leu Trp Lys Glu Asn
 85 90 95
 Phe Gln Lys Pro Gly Asn Val Lys Asn Ser Pro Gly Thr Lys Xaa
 100 105 110
 60

(2) INFORMATION FOR SEQ ID NO: 334:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

10

Met Ala Pro Ser Leu Leu Leu Ala Pro Leu Cys Ser Leu Glu Ala
 1 5 10 15

15

Val Leu Ser Ser Pro Leu Glu Lys Gln Cys Gln Leu Pro Gly Ile Phe
 20 25 30

Cys Gln Leu Gln Leu Pro Cys Pro Leu Leu Leu Ser Ala Gln Leu Leu
 35 40 45

20

Lys Gly Ile Val Xaa Pro Arg Cys Pro Ala Ser Leu Pro Gln Pro Pro
 50 55 60

25

His Pro Ala Pro Ser Trp His Leu Pro Leu His Cys Thr Glu Arg Xaa
 65 70 75 80

Pro His His Leu Pro Leu Gln Gly Gly Ser Ser Asn Met Glu Glu Xaa
 85 90 95

30

Asn Tyr Arg Gly Tyr Xaa Asp Ala Gln Leu
 100 105

(2) INFORMATION FOR SEQ ID NO: 335:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Thr Thr Cys Leu Phe Gly Leu Leu Ser Cys Glu Met Ser Ala Gln
 1 5 10 15

45

Val Ser Gln Lys Ser Cys Val Tyr Asp Glu Ser Glu Cys Phe Ser Ser
 20 25 30

50

Val Gly Gln Leu Leu Ala Leu Leu Ile Leu Val Tyr Val Leu Pro Ser
 35 40 45

Ile Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

5 Met Leu Trp Lys Cys Ser Gln Asn Ile Ala Arg Cys Leu Leu Leu Leu
 1 5 10 15

Leu Ala Leu Val Glu Ile Lys Leu Glu Asp Leu Gln Ser Gln Leu His
 20 25 30

10 Pro Thr Trp Lys Ser Ile Pro Gly Pro Ser Pro Arg Asn Gln His Arg
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 337:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

25

Met Leu Ile Pro Leu Gln Cys Leu Phe Ser Ser Asp Arg Met Leu Thr
 1 5 10 15

30

Phe Leu Thr Pro Trp Gln Lys Gly Glu Lys Cys Val Leu Gly Trp Val
 20 25 30

Thr Lys Phe Leu Ser Glu Ile Ser Xaa
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 338:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

45

Met Thr Phe Ser Ser Leu Lys Leu Phe Val Leu Thr Cys Ile Ile Lys
 1 5 10 15

50

Gly Leu Glu Arg Phe Ile Ile Leu Arg Glu Val Cys Asn Gln Glu Ile
 20 25 30

Gln Arg Ser Leu Ser Ser Asn Leu Val His Val Leu Leu Gln Pro Ala
 35 40 45

55

Thr Phe Lys Asp Val Leu Val Thr Glu Ile Ile Cys Leu Cys Met Cys
 50 55 60

Leu Tyr Ser Ile Lys Tyr Met Pro Pro Gln Lys Lys
 65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

5
10 Lys Val Tyr Ile Phe Leu Ile Phe Met Val Leu Ile Leu Pro Ser Leu
1 5 10 15
15 Gly Leu Thr Arg Tyr Met Pro Pro Xaa Ser Xaa Leu Asn Ser Glu
20 25 30

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

20
25 Met Ala Lys Ile Ser Pro Phe Glu Val Val Lys Arg Thr Ser Val Pro
1 5 10 15
30 Val Leu Val Gly Leu Val Ile Val Ile Val Ala Thr Glu Leu Met Val
20 25 30
35 Pro Gly Thr Ala Ala Ala Val Thr Gly Lys
35 40

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

40
45 Met Arg Leu Phe Phe Ile Gly Phe Leu Leu Leu Phe Ser Phe Gly Leu
1 5 10 15
50 Leu Arg Gln Pro Ser Leu Ser Ala Glu His
20 25

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

60

Met Val Phe Ser Val Ser Ser Ala Leu Ala Leu Leu Leu Met Leu Leu
1 5 10 15

Arg Ser Ser Asp Leu Ala Lys Lys Thr Glu
20 25

10 (2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Ser Leu Glu Phe Tyr Gln Lys Lys Lys Ser Arg Trp Pro Phe Ser
1 5 10 15

20 Asp Glu Cys Ile Pro Trp Glu Val Trp Thr Val Lys Val His Val Val
20 25 30

Ala Leu Ala Thr Glu Gln Glu Arg Gln Ile Cys Arg Glu Lys Val Gly
35 40 45

25 Glu Lys Leu Cys Glu Lys Ile Ile Asn Ile Val Glu Val Met Asn Arg
50 55 60

30 His Glu Tyr Leu Pro Lys Met Pro Thr Gln Ser Glu Val Asp Asn Val
65 70 75 80

Phe Asp Thr Gly Leu Arg Asp Val Gln Pro Tyr Leu Tyr Lys Ile Ser
85 90 95

35 Phe Gln Ile Thr Asp Ala Leu Gly Thr Ser Val Thr Thr Thr Met Arg
100 105 110

Arg Leu Ile Lys Asp Thr Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly
115 120 125

40 Ser Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu
130 135 140

45 Gly Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp Xaa
145 150 155

50 (2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Phe Leu Leu Pro Leu Pro Ala Ala Gly Arg Val Val Val Arg Arg
1 5 10 15

60 Leu Ala Val Arg Arg Phe Gly Ser Arg Ser Leu Ser Thr Ala Asp Met

558

	20	25	30
	Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp Asp		
	35	40	45
5	Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu Ala		
	50	55	60
10	Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys Ala		
	65	70	75
	Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser Val		
	85	90	95
15	Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln Glu		
	100	105	110
	Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala Gly		
	115	120	125
20	Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp Pro		
	130	135	140
25	Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu Tyr		
	145	150	155
	Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala Lys		
	165	170	175
30	Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu Phe		
	180	185	190
	Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala Asn		
	195	200	205
35	Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu Lys		
	210	215	220
	Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp Ile		
	225	230	235
40	Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser Asp		
	245	250	255
45	Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn Ala		
	260	265	270
	Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp Ser		
	275	280	285
50	Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg Ala		
	290	295	300
	Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala Ala		
	305	310	315
55	Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys Glu		
	325	330	335
60	Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg Ala		

559

340 345 350
 Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly Arg
 355 360 365
 - 5 Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro Lys
 370 375 380
 10 Xaa Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala Leu
 385 390 395 400
 Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp Asn
 405 410 415
 15 Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg Met
 420 425 430
 Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu Ala
 435 440 445
 20 Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr Ala
 450 455 460
 25 Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His Leu
 465 470 475 480
 Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu Arg
 485 490 495
 30 Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu Leu
 500 505 510
 Arg Phe Ser Gln Asp Asn Ala Xaa
 515 520
 35

(2) INFORMATION FOR SEQ ID NO: 345:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

45

Thr Ile Leu Phe Leu Phe Leu Gln Leu Ser Ala Leu Arg Leu Ile Val
 1 5 10 15

50

Gly Lys Asp Ser Ile Asp Ile Asp Ile Ser Ser Arg Arg Arg Glu Asp
 20 25 30

Gln Ser Leu Arg Leu Asn Ala
 35

55

(2) INFORMATION FOR SEQ ID NO: 346:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

560

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```

- 5  Met Thr Ser Glu Leu Asp Ile Phe Val Gly Asn Thr Thr Leu Ile Asp
      1           5           10           15

      Glu Asp Val Tyr Arg Leu Trp Leu Asp Gly Tyr Ser Val Thr Asp Ala
            20           25           30

10  Val Ala Leu Arg Val Arg Ser Gly Ile Leu Glu Gln Thr Gly Ala Thr
      35           40           45

      Ala Ala Val Leu Gln Ser Asp Thr Met Asp His Tyr Arg Thr Phe His
15  50           55           60

      Met Leu Glu Arg Leu Leu His Ala Pro Pro Lys Leu Leu His Gln Leu
      65           70           75           80

20  Ile Phe Gln Ile Pro Pro Ser Arg Gln Ala Leu Leu Ile Glu Arg Tyr
            85           90           95

      Tyr Ala Phe Asp Glu Ala Phe Val Arg Glu Val Leu Gly Lys Lys Leu
            100          105          110

25  Ser Lys Gly Thr Lys Lys Asp Leu Asp Asp Ile Ser Thr Lys Thr Gly
      115          120          125

      Ile Thr Leu Lys Ser Cys Arg Arg Gln Phe Asp Asn Phe Lys Arg Val
30  130          135          140

      Phe Lys Val Val Glu Glu Met Arg Gly Ser Leu Val Asp Asn Ile Gln
      145          150          155          160

35  Gln His Phe Leu Leu Ser Asp Arg Leu Ala Arg Asp Tyr Ala Ala Ile
      165          170          175
-----
      Val Phe Phe Ala Asn Asn Arg Phe Glu Thr Gly Lys Lys Lys Leu Gln
            180          185          190

40  Tyr Leu Ser Phe Gly Asp Phe Ala Phe Cys Ala Glu Leu Met Ile Gln
      195          200          205

      Asn Trp Thr Leu Gly Pro Val Asp Ser Gln Met Asp Asp Met Asp Met
45  210          215          220

      Asp Leu Asp Arg Asn Phe Ser Arg Thr Xaa
      225          230

```

50

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

60

Met Ala Ala Ala Val Ala Gly Met Leu Arg Gly Gly Leu Leu Pro Gln

561

1 5 10 15
 Ala Gly Arg Leu Pro Thr Leu Gln Thr Val Arg Tyr Gly Ser Lys Ala
 20 25 30
 5 Val Thr Arg His Arg Arg Val Met His Phe Gln Arg Gln Lys Leu Met
 35 40 45
 10 Ala Val Thr Glu Tyr Ile Pro Pro Lys Pro Ala Ile His Pro Ser Cys
 50 55 60
 Leu Pro Ser Pro Pro Ser Pro Pro Gln Glu Glu Ile Gly Leu Ile Arg
 65 70 75 80
 15 Leu Leu Arg Arg Glu Ile Ala Ala Val Phe Gln Asp Asn Arg Met Ile
 85 90 95
 Ala Val Cys Gln Asn Val Ala Leu Ser Ala Glu Asp Lys Leu Leu Ile
 100 105 110
 20 Ala Thr Pro Ala Ala Glu Thr Gln Asp Pro Asp Glu Gly Leu Pro Gln
 115 120 125
 Pro Gly Pro Glu Ser Pro Ser Trp Arg Ile Pro Ser Thr Lys Ile Cys
 130 135 140
 25 Cys Pro Phe Leu Trp Gly Thr Thr Cys Cys Trp Ser Val Lys Ser Pro
 145 150 155 160
 30 Arg Ser Arg Arg Trp Tyr Gly Ser Xaa
 165

35 (2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Lys Arg Ser Phe Leu Leu Pro Leu Leu Val Gly Phe Leu Asp
 1 5 10 15
 45 Thr Ala His Leu Ile Leu Leu Glu Thr Leu Ser Val Cys Leu Trp Leu
 20 25 30
 Pro Ser Leu Ile Asp Ser Arg Cys Val Met Ser
 35 40
 50

55 (2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Lys Glu Gly Pro Pro Cys Lys Arg His His Tyr Tyr Gln Asn Cys
 1 5 10 15
 5 Gly Ala Lys Leu Leu Val Ser Leu Phe Gly Glu Thr Asn Gln Ile His
 20 25 30
 Leu Leu Glu Thr Gln Val Gly Thr Glu Lys Gly Gly Glu Arg Ile Trp
 35 40 45
 10 Glu Glu Lys Trp Arg Ile Ser Ser Thr Val Leu Phe Ile Ser Val Asn
 50 55 60
 Ser Tyr Val Glu Gly Ser Val Leu Glu Ile Lys Leu Phe Tyr
 15 65 70 75

20 (2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Ser Glu Ile Leu Ser Leu Leu Phe Cys Leu Leu Gly Pro Ala Leu
 1 5 10 15
 30 Asp Glu Arg Arg Glu Glu Lys Asp
 20

35 (2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15
 45 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 35 40 45
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 50 55 60
 55 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95
 60

Arg Pro Ala Gly Gly Ala His Leu Cys Ala Met Xaa Val Ile Glu Gly
 100 105 110
 - 5 Leu Val Val Asp Val Gly Glu Arg Ile Leu His Gly Gln Arg Glu Val
 115 120 125
 Gly Gln Val Ser Gln Val Leu Pro Ala Leu Ser Leu Gly Leu Val Phe
 130 135 140
 10 Leu Cys Gln Gly Thr Val Glu Lys Val Ser Gly Ala Ala His Cys Ser
 145 150 155 160
 Ser Leu Leu Cys Cys Leu Pro Trp Gln Cys Ser Gly Gly Gly Phe Pro
 165 170 175
 15 Thr Xaa Arg Cys Ser Arg Pro Tyr Phe Ser Ser His Lys Gly Val Ala
 180 185 190
 20 Ala Thr Leu Ala Leu Thr Cys His Cys Asp Lys Val His Val Ala Gly
 195 200 205
 Leu Gly Lys Asp Trp Ala Ile Glu Gln Arg Arg Arg Thr Cys Glu Ser
 210 215 220
 25 Asp Xaa Glu Xaa Xaa Pro Phe Thr Leu Ala Gly Leu Val Leu Val Leu
 225 230 235 240
 Arg Phe Cys Gln Val Val Leu Val Trp Ile Pro Gln Leu Gly Asp Lys
 245 250 255
 30 His Trp Arg Gly Met Thr Arg Leu Gly Arg Val Ser Leu Thr Ser Ser
 260 265 270
 Ile Xaa
 35

40 (2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Ile Phe Thr Ser Val Thr Lys Gly Ile Leu Leu Ile Ala Leu Trp
 1 5 10 15
 50 Val Pro Leu Phe His Phe Met Leu Ile Asp Ser Ile Leu Gly Pro Ser
 20 25 30
 Arg Leu Leu Thr Asp Gly Val Pro Phe Asn Pro Trp His Val Xaa
 35 40 45
 55

(2) INFORMATION FOR SEQ ID NO: 353:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

- 5

Met Lys Thr
 1

10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

20

Met Ser Ile Ser Gly Thr Asp Gly Leu Ile Leu Leu Val Gly Leu
 1 5 10 15

Glu Ala Xaa Val Arg Ser Ser Lys Lys Trp Ile Pro Lys Ala Leu Xaa
 20 25 30

25

Val Thr Gln Ala Lys Trp Asn Ser Trp Pro Ser Arg Arg Asn Ala Gly
 35 40 45

Phe Ala Leu His
 50

30

(2) INFORMATION FOR SEQ ID NO: 355:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

40

Met Glu His Cys Leu Tyr His Ser Val His Gly Ile Asn Pro Tyr Ile
 1 5 10 15

45

His Lys Asn Thr His Pro Ser Ile Asn Ile Tyr Met Val Trp Asp Glu
 20 25 30

Gln Val Asn Ser Phe Glu Arg Glu Phe Val Pro Phe Phe Phe Leu Ile
 35 40 45

50

Ile Leu Leu Asn Cys Cys Gln Leu Ser Asn Lys Gln Thr Glu Lys Leu
 50 55 60

Phe Gly Lys Thr Leu His Thr Pro Phe Leu Ser Ser Ala Leu Lys Tyr
 65 70 75 80

55

Arg Leu Asn Thr His Ile Leu Pro Val Phe Ser Tyr Ser Asp Ser Ile
 85 90 95

60

Leu Thr Cys His Leu Ile Leu Ala Ser Tyr Phe Ser His Val Tyr Leu
 100 105 110

Pro Val Thr Cys Ile Cys Tyr Leu Asn Arg Lys Lys Asn Ile Gln Lys
 115 120 125

5 Lys Lys Asn Xaa
 130

10 (2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly Ser Arg Asp His Leu Phe Lys Val Leu Val Val Gly Asp Ala
 1 5 10 15
 20 Ala Val Gly Lys Thr Ser Leu Val Gln Asp Tyr Ser Gln Asp Ser Phe
 20 25 30
 25 Ser Lys His Tyr Lys Ser Thr Val Gly Val Asp Phe Ala Leu Lys Val
 35 40 45
 Leu Gln Trp Ser Asp Tyr Glu Ile Val Arg Leu Gln Leu Trp Asp Ile
 50 55 60
 30 Ala Gly Gln Glu Arg Phe Thr Ser Met Thr Arg Leu Tyr Tyr Arg Asp
 65 70 75 80
 Ala Ser Ala Cys Val Ile Met Phe Asp Val Thr Asn Ala Thr Thr Phe
 85 90 95
 35 Ser Asn Ser Gln Arg Trp Lys Gln Asp Leu Asp Ser Lys Leu Thr Leu
 100 105 110
 40 Pro Asn Gly Glu Pro Val Pro Cys Leu Leu Leu Ala Asn Lys Cys Asp
 115 120 125
 Leu Ser Pro Trp Ala Val Ser Arg Asp Gln Ile Asp Arg Phe Ser Lys
 130 135 140
 45 Glu Asn Gly Phe Thr Gly Trp Thr Glu Thr Ser Val Lys Glu Asn Lys
 145 150 155 160
 Asn Ile Asn Glu Ala Met Arg Val Leu Ile Glu Lys Met Met Arg Asn
 165 170 175
 50 Ser Thr Glu Asp Ile Met Ser Leu Ser Thr Gln Gly Asp Tyr Ile Asn
 180 185 190
 55 Leu Gln Thr Lys Ser Ser Ser Trp Ser Cys Cys Xaa
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ile Ser Leu Ile Phe Gln Leu Glu Glu Glu Lys Leu Val Glu Lys
 1 5 10 15

10 Phe Phe Phe Phe Leu Phe Phe Phe Leu Lys Lys Gly Ser Gln Gly Ser
 20 25 30

Asn Leu Lys Ile Val Pro Arg His Met Arg Val Val Leu Arg Gly
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 358:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Thr Tyr Val Thr Cys Leu His Val Cys Leu Leu Val Glu Phe Leu
 1 5 10 15

30 Asn Ser Gln Leu Thr Asn His Arg Lys Tyr Tyr Phe Leu Ser Tyr Gly
 20 25 30

Phe Trp Phe Thr Gly Leu Arg Gly Phe Ser Glu Tyr Leu Trp Pro Gln
 35 40 45

35 Gln His Thr Ser Phe His Pro Asn Arg Asn Glu Ile Asn Phe Val Ser
 50 55 60

Thr Asp Asn Arg Ile Trp Val Thr Xaa
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 359:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ser Asp Gln Glu Ala Lys Pro Ser Thr Glu Asp Leu Gly Asp Lys
 1 5 10 15

55 Lys Glu Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser
 20 25 30

Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys
 35 40 45

60 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe

```

      50              55              60
Leu Phe Glu Gly Gln Arg Ile Ala Asp Asn His Thr Pro Lys Glu Leu
  65              70              75              80
- 5
Gly Met Glu Glu Glu Asp Val Ile Glu Val Tyr Gln Glu Gln Thr Gly
      85              90              95
10
Gly His Ser Thr Val Xaa
      100

```

15

(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20

30

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40

45

50

55

60

Glu Ala Arg Asn Leu Pro Pro Leu Thr Glu Ala Gln Lys Asn Lys Leu
85 90 95

Arg His Leu Ser Val Val Thr Leu Ala Ala Lys Val Lys Cys Ile Pro
 100 105 110

5 Tyr Ala Val Leu Leu Glu Ala Leu Ala Leu Arg Asn Val Arg Gln Leu
 115 120 125

Glu Asp Leu Val Ile Glu Ala Val Tyr Ala Asp Val Leu Arg Gly Ser
 130 135 140

10 Leu Asp Gln Arg Asn Gln Arg Leu Glu Val Asp Tyr Ser Ile Gly Arg
 145 150 155 160

15 Asp Ile Gln Arg Gln Asp Leu Ser Ala Ile Ala Arg Thr Leu Xaa Lys
 165 170 175

Asn His Xaa

20

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

30 Met Lys Ser Ser Ser Leu Phe Phe Phe Phe Leu Ala His Phe Ile His
 1 5 10 15

Ser His Asp Leu Pro Gly Leu Cys Arg
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 363:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

45

Met Lys Phe Ala Ala Ser Gly Xaa Phe Leu His His Met Ala Gly Leu
 1 5 10 15

50

Ser Ser Ser Lys Leu Ser Met Ser Lys Ala Leu Pro Leu Thr Lys Val
 20 25 30

Val Gln Asn Asp Ala Tyr Thr Ala Pro Ala Leu Pro Ser Ser Ile Arg
 35 40 45

55

Thr Lys Ala Leu Thr Asn Met Ser Arg Thr Leu Val Asn Lys Glu Glu
 50 55 60

Pro Pro Lys Glu Leu Pro Ala Ala Glu Pro Val Leu Ser Pro Leu Glu
 65 70 75 80

60

	Gly	Thr	Lys	Met	Thr	Val	Asn	Asn	Leu	His	Pro	Arg	Val	Thr	Glu	Glu
							85									95
- 5	Asp	Ile	Val	Glu	Leu	Phe	Cys	Val	Cys	Gly	Ala	Leu	Lys	Arg	Ala	Arg
				100					105					110		
	Leu	Val	His	Pro	Gly	Val	Ala	Glu	Val	Val	Phe	Val	Lys	Lys	Asp	Asp
				115				120					125			
10	Ala	Ile	Thr	Ala	Tyr	Lys	Lys	Tyr	Asn	Asn	Arg	Cys	Leu	Asp	Gly	Gln
				130			135					140				
	Pro	Met	Lys	Cys	Asn	Leu	His	Met	Asn	Gly	Asn	Val	Ile	Thr	Ser	Asp
15				145			150				155					160
	Gln	Pro	Ile	Leu	Leu	Arg	Leu	Ser	Asp	Ser	Pro	Ser	Met	Lys	Lys	Glu
					165					170					175	
	Ser	Glu	Leu	Pro	Arg	Arg	Val	Asn	Ser	Ala	Ser	Ser	Ser	Asn	Pro	Pro
20				180					185					190		
	Ala	Glu	Val	Asp	Pro	Asp	Thr	Ile	Leu	Lys	Ala	Leu	Phe	Lys	Ser	Ser
				195				200					205			
25	Gly	Ala	Ser	Xaa	Thr	Thr	Gln	Pro	Thr	Glu	Phe	Lys	Ile	Lys	Leu	Xaa
				210			215					220				

30

(2) INFORMATION FOR SEQ ID NO: 364:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

40

Met Ser Lys Asn Cys Ile Lys Leu Leu Cys Glu Asp Pro Val Phe Ala
1 5 10 15

45

Glu Tyr Ile Lys Cys Ile Leu Met Asp Glu Arg Thr Phe Leu Asn Asn
20 25 30

Asn Ile Val Tyr Thr Phe Met Thr His Phe Leu Leu Lys Val Gln Ser
35 40 45

50

Gln Val Phe Ser Glu Ala Asn Cys Ala Asn Leu Ile Ser Thr Leu Ile
50 55 60

Thr Asn Leu Ile Ser Gln Tyr Gln Asn Leu Gln Ser Asp Phe Ser Asn
65 70 75 80

55

Arg Val Glu Ile Ser Lys Ala Ser Ala Ser Leu Asn Gly Asp Leu Arg
85 90 95

60

Ala Leu Ala Leu Leu Leu Ser Val His Thr Pro Lys Gln Leu Asn Pro
100 105 110

570

Ala Leu Ile Pro Thr Leu Gln Glu Leu Leu Ser Lys Cys Arg Thr Cys
 115 120 125

5 Leu Gln Gln Arg Asn Ser Leu Gln Glu Gln Glu Ala Lys Glu Arg Lys
 130 135 140

10 Thr Lys Asp Asp Glu Gly Ala Thr Pro Ile Lys Arg Arg Arg Val Ser
 145 150 155 160

Ser Asp Glu Glu His Thr Val Asp Ser Cys Ile Ser Asp Met Lys Thr
 165 170 175

15 Glu Thr Arg Glu Val Leu Thr Pro Thr Ser Thr Ser Asp Asn Glu Thr
 180 185 190

Arg Asp Ser Ser Ile Ile Asp Pro Gly Thr Glu Gln Asp Leu Pro Ser
 195 200 205

20 Pro Glu Asn Ser Ser Val Lys Glu Tyr Arg Met Glu Val Pro Ser Ser
 210 215 220

25 Phe Ser Glu Asp Met Ser Asn Ile Arg Ser Gln His Ala Glu Glu Gln
 225 230 235 240

Ser Asn Asn Gly Arg Tyr Asp Asp Cys Lys Glu Phe Lys Asp Leu His
 245 250 255

30 Cys Ser Lys Asp Ser Thr Leu Ala Glu Glu Glu Ser Glu Phe Pro Ser
 260 265 270

Thr Ser Ile Ser Ala Val Leu Ser Asp Leu Ala Asp Leu Arg Ser Cys
 275 280 285

35 Asp Gly Gln Ala Leu Pro Ser Gln Asp Pro Glu Val Ala Leu Ser Leu
 290 295 300

40 Ser Cys Gly His Ser Arg Gly Leu Phe Ser His Met Gln Gln His Asp
 305 310 315 320

Ile Leu Asp Thr Leu Cys Arg Thr Ile Glu Ser Thr Ile His Val Val
 325 330 335

45 Thr Arg Ile Ser Gly Lys Gly Asn Gln Ala Ala Ser Xaa
 340 345

(2) INFORMATION FOR SEQ ID NO: 365:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Leu His Gln Asp His Ile Thr Phe Ala Met Leu Leu Ala Arg Ile
 1 5 10 15

60 Lys Leu Lys Gly Thr Val Gly Glu Pro Thr Tyr Asp Ala Glu Phe Gln

	20	25	30
5	His Phe Leu Arg Gly Asn Glu Ile Val Leu Ser Ala Gly Ser Thr Pro 35 40 45		
	Arg Ile Gln Gly Leu Thr Val Glu Gln Ala Glu Ala Val Val Arg Leu 50 55 60		
10	Ser Cys Leu Pro Ala Phe Lys Asp Leu Ile Ala Lys Val Gln Ala Asp 65 70 75 80		
	Glu Gln Phe Gly Ile Trp Leu Asp Ser Ser Ser Pro Glu Gln Thr Val 85 90 95		
15	Pro Tyr Leu Trp Ser Glu Glu Thr Pro Ala Thr Pro Ile Gly Gln Ala 100 105 110		
	Ile His Arg Leu Leu Leu Ile Gln Ala Phe Arg Pro Asp Arg Leu Leu 115 120 125		
20	Ala Met Ala His Met Phe Val Ser Thr Asn Leu Gly Glu Ser Phe Met 130 135 140		
	Ser Ile Met Glu Gln Pro Leu Asp Leu Thr His Ile Val Xaa Thr Glu 145 150 155 160		
25	Val Lys Pro Asn Thr Pro Val Leu Met Cys Ser Val Pro Gly Tyr Asp 165 170 175		
30	Ala Ser Gly His Val Glu Asp Leu Ala Ala Glu Gln Asn Thr Gln Ile 180 185 190		
	Thr Ser Ile Ala Ile Gly Ser Ala Glu Gly Phe Asn Gln Ala Asp Lys 195 200 205		
35	Ala Ile Asn Thr Ala Val Lys Ser Gly Arg Trp Val Met Leu Lys Asn 210 215 220		
40	Val His Leu Ala Pro Gly Trp Leu Met Gln Leu Glu Lys Lys Leu His 225 230 235 240		
	Ser Leu Gln Pro His Ala Cys Phe Arg Leu Phe Leu Thr Met Glu Ile 245 250 255		
45	Asn Pro Lys Val Pro Val Asn Leu Leu Arg Ala Gly Arg Ile Phe Val 260 265 270		
	Phe Glu Pro Pro Pro Gly Xaa Lys Ala Asn Met Leu Arg Thr Phe Ser 275 280 285		
50	Ser Ile Pro Val Ser Arg Ile Cys Lys Ser Pro Asn Glu Arg Ala Arg 290 295 300		
	Leu Tyr Phe Leu Leu Ala Trp Phe His Ala Ile Ile Gln Glu Arg Leu 305 310 315 320		
55	Arg Tyr Ala Pro Leu Gly Trp Ser Lys Lys Tyr Glu Phe Gly Glu Ser 325 330 335		
60	Asp Leu Arg Ser Xaa Cys Asp Thr Val Asp Thr Trp Leu Asp Asp Thr		

572

340 345 350
 Ala Lys Gly Arg Gln Asn Ile Ser Pro Asp Lys Ile Pro Trp Ser Ala
 355 360 365
 5 Leu Lys Thr Leu Met Ala Gln Ser Ile Tyr Gly Gly Arg Val Asp Asn
 370 375 380
 10 Glu Phe Asp Gln Arg Leu Leu Asn Thr Phe Leu Glu Arg Leu Phe Thr
 385 390 395 400
 Thr Arg Ser Phe Asp Ser Glu Phe Lys Leu Ala Cys Lys Val Asp Gly
 405 410 415
 15 His Lys Asp Ile Gln Met Pro Asp Gly Met Gln Ala Arg Gly Val Cys
 420 425 430
 Ala Val Gly Gly Val Ala Pro Arg His Pro Asp Ala Leu Leu Ala Gly
 435 440 445
 20 Pro Ala Gln Gln Arg Arg Glu Ser Pro Pro Tyr His Thr Gly Cys Gly
 450 455 460
 25 His Asp Gln
 465

30 (2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser Glu Ile Pro Val Leu
 1 5 10 15
 40 Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu Trp Val Gln Arg Leu
 20 25 30
 Lys Glu Glu Tyr Gln Ser Leu Ile Arg Tyr Val Glu Asn Asn Lys Asn
 35 40 45
 45 Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn Lys Glu Gly Thr Arg
 50 55 60
 50 Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu Leu Lys Tyr Glu Phe
 65 70 75 80
 Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro Thr Thr Ala Pro Glu
 85 90 95
 55 Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala Lys Met Tyr Arg Gly
 100 105 110
 Gly Lys Ile Cys Leu Thr Asp His Phe Lys Pro Leu Trp Gly Gln Glu
 115 120 125
 60

Cys Ala Gln Ile Trp Thr Ser Ser Ser His Gly Ser Gly Ala Gly Ser
130 135 140

Met Xaa Gly Ser Gly Asn Pro Xaa
145 150

5

10

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr
1 5 10 15

20

Gln Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly
20 25 30

Ser Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu
35 40 45

25

Glu Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile
50 55 60

30

Gln Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro
65 70 75 80

Ala Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val
85 90 95

35

Trp Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile
100 105 110

40

Gln Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met
115 120 125

Thr Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln
130 135 140

45

Thr Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp
145 150 155 160

Leu Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Xaa Leu
165 170 175

50

Glu Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln
180 185 190

Lys Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile
195 200 205

55

Leu Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys
210 215 220

60

Lys Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn
225 230 235 240

[illegible]

30

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

~~(D) TOPOLOGY: linear~~

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

40	Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser 1 5 10 15
	Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe 20 25 30
45	Trp Gly Phe Gly Arg Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr 35 40 45
	Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser 50 55 60
50	His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln 65 70 75 80
55	Pro Asn Xaa

60 (2) INFORMATION FOR SEQ ID NO: 369:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15

10 Tyr Trp Thr Met Xaa
 20

15 (2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
 1 5 10 15

25

Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu
 20 25 30

30

Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
 35 40 45

Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys
 50 55 60

35

Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys
 65 70 75 80

40

Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
 85 90 95

Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
 100 105 110

45

Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
 115 120 125

Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
 130 135 140

50

Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
 145 150 155 160

Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
 165 170 175

55

Glu Asp Gln Thr Lys Pro Val Leu Glu Tyr Tyr Gln Lys Lys Gly Val
 180 185 190

60

Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val
 195 200 205

Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser
 210 215 220

5 Val Thr Pro
 225

10 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Phe Leu Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln
 1 5 10 15
 20 Leu Lys Ile Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu
 25 Lys Ile Ile Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser
 35 40 45
 Trp Ala Ile Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn
 50 55 60
 30 Lys Thr Ala Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr Xaa
 65 70 75

35 (2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ala Val Phe Pro Cys Cys Pro Phe Leu Thr Leu Met Leu Pro
 1 5 10 15
 45 Leu Leu Glu Cys Leu Val Gly Met Ile Met Cys Tyr Leu Gly Ile Ser
 20 25 30
 Phe Thr Asp Thr Arg Lys Thr Ala Gly Leu Lys Lys Lys Lys Lys
 50 35 40 45
 Lys Xaa Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 61 amino acids

577

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

5 Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15
 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Ala Ser Tyr Leu Trp
 20 25 30
 10 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Ser Trp Ala Cys
 35 40 45
 15 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu Xaa
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 374:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15
 30 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30
 Ile Leu Phe Phe Ile Val Phe Xaa
 35 40
 35

(2) INFORMATION FOR SEQ ID NO: 375:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Cys Ser Gly Gln Ser Gln Val Trp Lys Met Ala Leu Gln Ala Leu
 1 5 10 15
 50 Asp Ser Glu Thr Val Val Ile Leu Pro Asp Met His Leu Ile Leu Ser
 20 25 30
 Leu Arg Leu Ile His Asn Ala Arg Pro Cys Leu Xaa
 35 40
 55

(2) INFORMATION FOR SEQ ID NO: 376:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

578

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

5 Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp Pro Arg Asp
1 5 10 15

Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys Pro Arg Arg
20 25 30

10 Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu Ile Lys Val
35 40 45

Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile Arg Glu Asp
15 50 55 60

Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp Asp Lys Ser
65 70 75 80

20 Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln Tyr Val Arg
85 90 95

Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro Arg Tyr Leu
100 105 110

25 Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys Tyr Val Cys
115 120 125

Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys Gln Leu Leu
30 130 135 140

Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile Cys Glu Tyr
145 150 155 160

35 Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met
165 170 175

Ile His Thr Gly Glu Lys His Tyr Asn Val Arg Ser Val Asp Leu Leu
180 185 190

40 Val Asp Lys Arg His Leu Leu Ile Gly Thr Xaa
195 200

45

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

55 Met Leu Pro Arg Arg Thr Phe Tyr Phe Tyr Phe Ile Phe Ile Phe Phe
1 5 10 15

Leu Ala Ser Phe Trp Gly Phe Thr Leu Arg Ala Ser Phe
20 25

60

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

5
 10 Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu Met
 1 5 10 15
 Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val Leu
 20 25 30
 15 Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu Trp
 35 40 45
 20 Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg Met
 50 55 60
 Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val Gln
 65 70 75 80
 25 Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu Asn
 85 90 95
 Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met Pro Ser Phe
 100 105 110
 30 Phe Ser Cys His Leu Phe Cys Thr Leu Arg Trp Lys Tyr Phe Glu Val
 115 120 125
 Phe Tyr Asn His Lys Phe Leu Xaa
 35 130 135

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

40
 45 Met Ala Trp Arg Arg Arg Glu Pro Ala Ser Gly Leu Ala Ala Cys Trp
 1 5 10 15
 50 Leu Trp Arg Cys Ser Pro Trp Pro Cys Ala Cys Pro Gly Pro Gly Ala
 20 25 30
 Gly Leu Ser Ser Gly Ser Arg Pro Trp
 35 40
 55

(2) INFORMATION FOR SEQ ID NO: 380:

60 (i) SEQUENCE CHARACTERISTICS:

580

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

5

Met Glu Phe Leu Lys Val Ala Arg Arg Asn Lys Arg Glu Gln Leu Glu
 1 5 10 15

10

Gln Ile Gln Lys Glu Leu Ser Val Leu Glu Glu Asp Ile Lys Arg Val
 20 25 30

Glu Glu Met Ser Gly Leu Tyr Ser Pro Val Ser Glu Asp Ser Thr Val
 35 40 45

15

Pro Gln Phe Glu Ala Pro Ser Pro Ser His Ser Ser Ile Ile Asp Ser
 50 55 60

Thr Glu Tyr Ser Gln Pro Pro Gly Phe Ser Gly Ser Ser Gln Thr Lys
 65 70 75 80

20

Lys Gln Pro Trp Tyr Asn Ser Thr Leu Ala Ser Arg Arg Lys Arg Leu
 85 90 95

25

Thr Ala His Phe Glu Asp Leu Glu Gln Cys Tyr Phe Ser Thr Arg Met
 100 105 110

Ser Arg Ile Ser Asp Asp Ser Arg Thr Ala Ser Gln Leu Asp Glu Phe
 115 120 125

30

Gln Glu Cys Leu Ser Lys Phe Thr Arg Tyr Asn Ser Val Arg Pro Leu
 130 135 140

Ala Thr Leu Ser Tyr Ala Ser Asp Leu Tyr Asn Gly Ser Ser Ile Val
 145 150 155 160

35

~~Ser Ser Ile Glu Phe Asp Arg Asp Cys Asp Tyr Phe Ala Ile Ala Gly~~
 165 170 175

40

Val Thr Lys Lys Ile Lys Val Tyr Glu Tyr Asp Thr Val Ile Gln Asp
 180 185 190

Ala Val Asp Ile His Tyr Pro Glu Asn Glu Met Thr Cys Asn Ser Lys
 195 200 205

45

Ile Ser Cys Ile Ser Trp Ser Ser Tyr His Lys Asn Leu Leu Ala Ser
 210 215 220

Ser Asp Tyr Glu Gly Thr Val Ile Leu Trp Asp Gly Phe Thr Gly Gln
 225 230 235 240

50

Arg Ser Lys Val Tyr Gln Glu His Glu Lys Arg Cys Trp Ser Val Asp
 245 250 255

55

Phe Asn Leu Met Asp Pro Lys Leu Leu Ala Ser Gly Ser Asp Asp Ala
 260 265 270

Lys Val Lys Leu Trp Ser Thr Asn Leu Asp Asn Ser Val Ala Ser Ile
 275 280 285

60

Glu Ala Lys Ala Asn Val Cys Cys Val Lys Phe Ser Pro Ser Ser Arg

581

290 295 300

5 Tyr His Leu Ala Phe Gly Cys Ala Asp His Cys Val His Tyr Tyr Asp
305 310 315 320

Leu Arg Asn Thr Lys Gln Pro Ile Met Val Phe Lys Gly His Arg Lys
325 330 335

10 Ala Val Ser Tyr Ala Lys Phe Val Ser Gly Glu Glu Ile Val Ser Ala
340 345 350

Ser Thr Asp Ser Gln Leu Lys Leu Trp Asn Val Gly Lys Pro Tyr Cys
355 360 365

15 Leu Arg Ser Phe Lys Gly His Ile Asn Glu Lys Asn Phe Val Gly Leu
370 375 380

Ala Ser Asn Gly Asp Tyr Ile Ala Cys Gly Ser Glu Asn Asn Ser Leu
385 390 395 400

20 Tyr Leu Tyr Tyr Lys Gly Leu Ser Lys Thr Leu Leu Thr Phe Lys Phe
405 410 415

Asp Thr Val Lys Ser Val Leu Asp Lys Asp Arg Lys Glu Asp Asp Thr
420 425 430

Asn Glu Phe Val Ser Ala Val Cys Trp Arg Ala Leu Pro Asp Gly Glu
435 440 445

30 Ser Asn Val Leu Ile Ala Ala Asn Ser Gln Gly Thr Ile Lys Val Leu
450 455 460

Glu Leu Val Xaa
465

35

(2) INFORMATION FOR SEQ ID NO: 381:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Lys Glu Asp Gly Phe Trp Phe Phe Phe Phe Leu Phe Phe Phe
1 5 10 15

50

Val Val Gly Ser Lys Phe Val Asn Gly Asn Lys Leu Val
20 25

55

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Pro Leu Ala Pro Tyr Cys Asp Leu Leu Val Ala Leu Ser Phe Ala
1 5 10 15

5 Leu Val Leu Glu Ser Pro Val Asp Ser Ser Asp Phe Thr
20 25

10 (2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Asn Ser Leu Val Ser Trp Gln Leu Leu Leu Phe Leu Cys Ala Thr
1 5 10 15

20 His Phe Gly Glu Pro Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg
20 25 30

25 Pro Thr Gly Gln Gln Leu Glu Ser Leu Gly Leu Leu Ala Pro Gly Glu
35 40 45

Gln Ser Leu Pro Cys Thr Glu Arg Lys Pro Ala Ala Thr Ala Arg Leu
50 55 60

30 Ser Arg Arg Gly Thr Ser Leu Ser Pro Pro Pro Glu Ser Ser Gly Ser
65 70 75 80

Pro Gln Gln Pro Gly Leu Ser Ala Pro His Ser Arg Gln Ile Pro Ala
85 90 95

35 Pro Gln Gly Ala Val Leu Val Gln Arg Glu Lys Asp Leu Pro Asn Tyr
100 105 110

40 Asn Trp Asn Ser Phe Gly Leu Arg Phe Gly Lys Arg Glu Ala Ala Pro
115 120 125

Gly Asn His Gly Arg Ser Ala Gly Arg Gly
130 135

45

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

55 Met Ser Cys Phe Ile Asp Ser Xaa Asp Ser Lys Ile Leu His Leu Leu
1 5 10 15

Val Val Ser Phe Ile Cys Xaa Leu Phe Leu Leu Ile Leu Thr His Gly
20 25 30

60

Ile Leu Ile Leu Arg Xaa Phe Phe Ser Val Xaa Xaa His Ser Leu Lys
 35 40 45

5 Asn Asn Leu Glu Glu Tyr Leu Ile Leu Met Asn Lys Ala Leu Leu Thr
 50 55 60

Arg Glu Asp Phe Phe Val Leu Pro Xaa Ala
 65 70

10

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 521 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

20 Met Ser Ala Gly Glu Val Glu Arg Leu Val Ser Glu Leu Ser Gly Gly
 1 5 10 15

Thr Gly Gly Asp Glu Glu Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu
 20 25 30

25

Val Glu Arg Pro Glu Glu Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly
 35 40 45

30 Ile Glu Asp Glu Thr Ala Glu Asn Gly Val Pro Lys Pro Lys Val Thr
 50 55 60

Glu Thr Glu Asp Asp Ser Asp Ser Asp Ser Asp Asp Glu Asp Asp
 65 70 75 80

35 Val His Val Thr Ile Gly Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly
 85 90 95

40 Ser Tyr Gly Thr Ala Pro Val Asn Leu Asn Ile Lys Thr Gly Gly Arg
 100 105 110

Val Tyr Gly Thr Thr Gly Thr Lys Val Lys Gly Val Asp Leu Asp Ala
 115 120 125

45 Pro Gly Ser Ile Asn Gly Val Pro Leu Leu Glu Val Asp Leu Asp Ser
 130 135 140

Phe Glu Asp Lys Pro Trp Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr
 145 150 155 160

50 Phe Asn Tyr Gly Phe Asn Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys
 165 170 175

Gln Lys Arg Ile Arg Met Gly Leu Glu Val Ile Pro Val Thr Ser Thr
 180 185 190

55

Thr Asn Lys Ile Thr Val Gln Gln Gly Arg Thr Gly Asn Ser Glu Lys
 195 200 205

60 Glu Thr Ala Leu Pro Ser Thr Lys Ala Glu Phe Thr Ser Pro Pro Ser
 210 215 220

Leu Phe Lys Thr Gly Leu Pro Pro Ser Arg Arg Leu Pro Gly Ala Ile
 225 230 235 240
 5 Asp Val Ile Gly Gln Thr Ile Thr Ile Ser Arg Val Glu Gly Arg Arg
 245 250 255
 Arg Ala Asn Glu Asn Ser Asn Ile Gln Val Leu Ser Glu Arg Ser Ala
 260 265 270
 10 Thr Glu Val Asp Asn Asn Phe Ser Lys Pro Pro Pro Phe Phe Pro Pro
 275 280 285
 Gly Ala Pro Pro Thr His Leu Pro Pro Pro Pro Phe Leu Pro Pro Pro
 15 290 295 300
 Pro Thr Val Ser Thr Ala Pro Pro Leu Ile Pro Pro Pro Gly Phe Pro
 305 310 315 320
 20 Pro Pro Pro Gly Ala Pro Pro Pro Ser Leu Ile Pro Thr Ile Glu Ser
 325 330 335
 Gly His Ser Ser Gly Tyr Asp Ser Arg Ser Ala Arg Ala Phe Pro Tyr
 340 345 350
 25 Gly Asn Val Ala Phe Pro His Leu Pro Gly Ser Ala Pro Ser Trp Pro
 355 360 365
 Ser Leu Val Asp Thr Ser Lys Gln Trp Asp Tyr Tyr Ala Arg Arg Glu
 30 370 375 380
 Lys Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 385 390 395 400
 35 Arg Asp Arg Glu Arg Glu Arg Thr Arg Glu Arg Glu Arg Glu Arg Asp
 405 410 415
 His Ser Pro Thr Pro Ser Val Phe Asn Ser Asp Glu Glu Arg Tyr Arg
 420 425 430
 40 Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr Glu Arg His Arg Ala Ser Arg
 435 440 445
 Glu Lys Glu Glu Arg His Arg Glu Arg Arg His Arg Glu Lys Glu Glu
 45 450 455 460
 Thr Arg His Lys Ser Ser Arg Ser Asn Ser Arg Arg Arg His Glu Ser
 465 470 475 480
 50 Glu Glu Gly Asp Ser His Arg Arg His Lys His Lys Lys Ser Lys Arg
 485 490 495
 Ser Lys Glu Gly Lys Glu Ala Gly Ser Glu Pro Ala Pro Glu Gln Glu
 500 505 510
 55 Ser Thr Glu Ala Thr Pro Ala Glu Xaa
 515 520
 60

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

5 Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu
 10 1 5 10 15
 Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val
 20 25 30
 15 Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu
 35 40 45
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 50 55 60
 20 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr
 65 70 75 80
 Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu
 25 85 90 95
 Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr
 100 105 110
 30 Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly
 115 120 125
 Val Arg Val Phe Gly Ile Asn Lys Tyr
 35 130 135

(2) INFORMATION FOR SEQ ID NO: 387:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

45

50

55

60

Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 1 5 10 15
 Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 20 25 30
 Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45
 Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60
 Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
85 90 95

5 Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr Leu
100 105 110

Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser Pro
115 120 125

10 Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe Trp
130 135 140

Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr Leu
145 150 155 160

15 Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val Asp
165 170 175

Gly Glu Glu Leu Gln Met Glu Pro Val Xaa
20 180 185

25 (2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met
1

35

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

45 Met Leu Ser Ile Phe Tyr Phe Ala Ile Pro Val Gly Ser Gly Leu Gly
1 5 10 15

Tyr Ile Ala Gly Ser Lys Val Lys Asp Met Ala Gly Asp Trp His Trp
20 25 30

50 Ala Leu Arg Val Thr Pro Gly Leu Gly Val Val Ala Val Leu Leu Leu
35 40 45

Phe Leu Val Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser
55 50 55 60

Asp Leu Pro Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala
65 70 75 80

60 Leu Ala Arg Asn Pro Ser Phe Val Leu Ser Ser Leu Gly Phe Thr Ala

587

85 90 95
 Val Ala Phe Val Thr Gly Ser Leu Ala Leu Trp Ala Pro Ala Phe Leu
 100 105 110
 5 Leu Arg Ser Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly
 115 120 125
 10 Asp Ser Cys Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys
 130 135 140
 Leu Thr Gly Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg
 145 150 155 160
 15 Leu Arg His Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly
 165 170 175
 Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg
 180 185 190
 20 Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu
 195 200 205
 Leu Ser Met Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val
 25 210 215 220
 Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser
 225 230 235 240
 30 His Leu Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser
 245 250 255
 Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg
 260 265 270
 35 Ala Leu Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly
 275 280 285

40 Gly Ala Leu Pro Gly His Arg His Leu His Xaa
 290 295

(2) INFORMATION FOR SEQ ID NO: 390:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Gly Pro Gln Gly Trp Val Arg Pro Leu Lys Thr Ala Pro Lys Leu
 1 5 10 15

55 Gly Glu Ala Ile Arg Leu Ile Leu Phe Leu Asn Phe Val Lys Gln Cys
 20 25 30

Ile Ala Ser Val Asn Leu Cys Ile Leu Arg Leu Asn Ile Thr Pro Leu
 35 40 45

60

Leu

- 5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

10 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

15 Met Tyr Val Asn Tyr Gly Thr Arg Asn Tyr Ser Thr Glu Gly Pro Ala
1 5 10 15

Ala Leu Leu Asp Gln Ala Lys Leu Ser Leu Leu Val Trp Val Leu Cys
20 25 30

20 Phe Val Leu Leu Phe Val Cys Phe Cys Gly Leu Ser Tyr Val Val Ile
35 40 45

Ala Gln Val Pro Val Gly Leu Leu Cys Ile Thr Glu Xaa
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 392:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

35

Met Leu Trp Phe Ala Asn Phe Phe Thr Tyr Leu Phe Leu Ser Gln Ser
1 5 10 15

40 Val Ala Phe Val His Ile Ser His Ile Gly Val Arg Gln Val Asn Thr
20 25 30

Asn Cys Tyr Phe Ser Arg Lys Ser Tyr Cys Tyr Gly Ile Leu Asn Pro
35 40 45

45 Ile Asn Cys Ile Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys
50 55 60

Lys Lys Lys Lys Ile Pro Ala Gly Arg Xaa Leu Phe Pro Phe Gly
65 70 75

50

(2) INFORMATION FOR SEQ ID NO: 393:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

60

Met Pro Gly Ala Phe Ser Glu Thr Val Ile Asn Asp Leu Leu Ser Leu
1 5 10 15

5 Phe Leu Val Leu Pro Ala Glu Leu Ser Tyr Ser Thr Leu Ser Gly Val
20 25 30

Tyr Arg Asn Ala
35

10

(2) INFORMATION FOR SEQ ID NO: 394:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

20 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
1 5 10 15

Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
20 25 30

25

Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
35 40 45

30

Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
50 55 60

Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
65 70 75 80

35

Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
85 90 95

Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
100 105 110

40

Leu Asp Arg Arg Ser Glu Ser Cys Ser Met Leu Pro Trp Xaa Ala Gln
115 120 125

45

Leu Leu Asp Arg Thr Ile Gly Pro Leu Tyr Leu Leu Phe Val Gln Phe
130 135 140

Ser Pro Ala Phe Ser Arg Thr Ser Pro Trp Arg Ser Pro Lys Asn Phe
145 150 155 160

50

Arg Arg Leu Tyr Pro Pro Cys Thr Thr Ser Gly Cys Ala Ala Arg Trp
165 170 175

Xaa Phe Ser Xaa
180

55

(2) INFORMATION FOR SEQ ID NO: 395:

60

(i) SEQUENCE CHARACTERISTICS:

590

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

- 5

Met Pro Thr Pro Cys Thr Ser Leu Pro Ser Cys Cys Gln His Arg Ser
 1 5 10 15

10

Ile Thr Met Thr Leu
 20

(2) INFORMATION FOR SEQ ID NO: 396:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Pro Leu Phe Ile Pro Leu Ile Phe Phe Leu Ser Leu Leu His Cys
 1 5 10 15

25

Gln Ser Lys His Pro Ile Gln Met Ser Leu Cys Met Cys Val Asn Ile
 20 25 30

Ser Leu Val Trp Ser Pro Val Arg Trp Ile Phe Gly Ser Lys Gly Leu
 35 40 45

30

Phe Ser Val His Leu Gln Ser Ser Gln Arg Pro Ser
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

45

Met Ala Gly Pro Arg Pro Xaa Trp Arg Asp Gln Leu Leu Phe Met Ser
 1 5 10 15

Ile Ile Val Leu Val Ile Val Val Ile Cys Leu Met Leu Tyr Ala Leu
 20 25 30

50

Leu Trp Glu Ala Gly Asn Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly
 35 40 45

55

Phe Tyr Asn Phe Cys Leu Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys
 50 55 60

His Gln Phe Pro Glu Leu Glu Ala Leu Gly Val Pro Arg Val Gly Leu
 65 70 75 80

60

Gly Leu Ala Arg Leu Gly Val Tyr Gly Ser Leu Val Leu Thr Leu Phe
 85 90 95

Ala Pro Gln Pro Leu Leu Leu Ala Gln Cys Asn Xaa Asp Glu Arg Ala
100 105 110

5 Trp Arg Leu Ala Val Gly Phe Leu Ala Val Ser Ser Val Leu Leu Ala
115 120 125

Gly Gly Leu Gly Leu Phe Leu Ser Tyr Val Trp Asn Gly Ser Xaa Ser
130 135 140

10 Pro Ser Arg Gly Leu Gly Phe Xaa
145 150

15 (2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Asp Gly Phe Asp Arg Ala Pro Gly Ala Gly Arg Gly Arg Xaa
25 1 5 10 15

Arg Gly Leu Gly Arg Gly Gly Gly Gly Pro Xaa Gly Gly Gly Phe Pro
20 25 30

30 Xaa Gly Xaa Xaa Pro Ala Glu Arg Xaa Arg His Gln Pro Pro Gln Pro
35 35 40 45

Lys Ala Pro Gly Phe Leu Gln Pro Xaa Pro Leu Arg Gln Pro Arg Thr
50 55 60

35 Thr Pro Pro Pro Gly Ala Gln Cys Glu Val Pro Ala Ser Pro Gln Arg
65 70 75 80

Pro Ser Arg Pro Gly Ala Leu Pro Glu Gln Thr Arg Pro Leu Arg Ala
40 85 90 95

Pro Pro Ser Ser Gln Asp Lys Ile Pro Gln Gln Asn Ser Glu Ser Ala
100 105 110

45 Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
115 120 125

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
130 135 140

50 Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
145 150 155 160

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
55 165 170 175

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
180 185 190

60 Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala

	195	200	205
- 5	Thr Ser Ile Pro Asn Phe 210	Ser Tyr Met Gly Ala Arg 215	Leu Cys Asn Tyr 220
	Leu Ser His His Leu Thr 225	Ile Ser Pro Gln Ser Gly 230	Asn Phe Arg Gln 235 240
10	Leu Leu Leu Gln Arg Cys 245	Arg Thr Glu Tyr Glu Val 250	Lys Asp Gln Ala 255
	Ala Lys Gly Asp Glu Val Thr 260	Arg Lys Arg Phe His Ala 265	Phe Val Leu 270
15	Phe Leu Gly Glu Leu Tyr 275	Leu Asn Leu Glu Ile 280	Lys Gly Thr Asn Gly 285
	Gln Val Thr Arg Ala Asp 290	Ile Leu Gln Val Gly 295	Leu Arg Glu Leu Leu 300
20	Asn Ala Leu Phe Ser Asn 305	Pro Met Asp Asp Asn 310	Leu Ile Cys Ala Val 315 320
	Lys Leu Leu Lys Leu Thr 325	Gly Ser Val Leu Glu Asp 330	Ala Trp Lys Glu 335
25	Lys Gly Lys Met Asp Met 340	Glu Glu Ile Ile Gln Arg 345	Ile Glu Asn Val 350
	Val Leu Asp Ala Asn Cys 355	Ser Arg Asp Val Lys Gln 360	Met Leu Leu Lys 365
	Leu Val Glu Leu Arg Ser 370	Ser Asn Trp Gly Arg 375	Val His Ala Thr Ser 380
35	Thr Tyr Arg Glu Ala Thr 385	Pro Glu Asn Asp Pro 390	Asn Tyr Phe Met Asn 395 400
	Glu Pro Thr Phe Tyr Thr 405	Ser Asp Gly Val Pro Phe 410	Thr Ala Ala Asp 415
40	Pro Asp Tyr Gln Glu Lys 420	Tyr Gln Glu Leu Leu Glu 425	Arg Glu Asp Phe 430
	Phe Pro Asp Tyr Glu Glu 435	Asn Gly Thr Asp Leu Ser 440	Gly Ala Gly Asp 445
	Pro Tyr Leu Asp Asp Ile 450	Asp Asp Glu Met Asp 455	Pro Glu Ile Glu Glu 460
50	Ala Tyr Glu Lys Phe Cys 465	Leu Glu Ser Glu Arg 470	Lys Arg Lys Gln Xaa 475 480

55

(2) INFORMATION FOR SEQ ID NO: 399:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

	Met	Glu	Pro	Lys	Thr	Ile	Thr	Asp	Ala	Leu	Ala	Ser	Ser	Ile	Ile	Lys	
	1				5					10					15		
10	Ser	Val	Leu	Pro	Asn	Phe	Leu	Pro	Tyr	Asn	Val	Met	Leu	Tyr	Ser	Asp	
				20					25					30			
	Ala	Pro	Val	Ser	Glu	Leu	Ser	Leu	Glu	Leu	Leu	Leu	Gln	Val	Val		
				35				40					45				
15	Leu	Pro	Ala	Leu	Leu	Glu	Gln	Gly	His	Thr	Arg	Gln	Trp	Leu	Lys	Gly	
		50				55					60						
	Leu	Val	Arg	Ala	Trp	Thr	Val	Thr	Ala	Gly	Tyr	Leu	Leu	Asp	Leu	His	
20		65				70				75					80		
	Ser	Tyr	Leu	Leu	Gly	Asp	Gln	Glu	Glu	Asn	Glu	Asn	Ser	Ala	Asn	Gln	
				85						90					95		
25	Gln	Val	Asn	Asn	Asn	Gln	His	Ala	Arg	Asn	Asn	Asn	Ala	Ile	Pro	Val	
				100					105					110			
	Val	Gly	Glu	Gly	Leu	His	Ala	Ala	His	Gln	Ala	Ile	Leu	Gln	Gln	Gly	
		115					120					125					
30	Gly	Pro	Val	Gly	Phe	Gln	Xaa	Tyr	Arg	Arg	Pro	Leu	Asn	Phe	Pro	Leu	
		130				135					140						
	Arg	Ile	Phe	Leu	Leu	Ile	Val	Phe	Met	Cys	Ile	Thr	Leu	Leu	Ile	Ala	
35		145				150				155					160		
<hr/>																	
	Ser	Leu	Ile	Cys	Leu	Thr	Leu	Pro	Val	Phe	Ala	Gly	Arg	Trp	Leu	Met	
				165						170					175		
40	Ser	Phe	Trp	Thr	Gly	Thr	Ala	Lys	Ile	His	Glu	Leu	Tyr	Thr	Ala	Ala	
				180					185					190			
	Cys	Gly	Leu	Tyr	Val	Cys	Trp	Leu	Thr	Ile	Arg	Ala	Val	Thr	Val	Met	
		195					200					205					
45	Val	Ala	Trp	Met	Pro	Gln	Gly	Arg	Arg	Val	Ile	Phe	Gln	Lys	Val	Lys	
		210				215					220						
	Glu	Trp	Ser	Leu	Met	Ile	Met	Lys	Thr	Leu	Ile	Val	Ala	Val	Leu	Leu	
50		225				230				235					240		
	Ala	Gly	Val	Val	Pro	Leu	Leu	Leu	Gly	Leu	Leu	Phe	Glu	Leu	Val	Ile	
				245				250					255				
55	Val	Ala	Pro	Leu	Arg	Val	Pro	Leu	Asp	Gln	Thr	Pro	Leu	Phe	Tyr	Pro	
				260				265					270				
	Trp	Gln	Asp	Trp	Ala	Leu	Gly	Val	Leu	His	Ala	Lys	Ile	Ile	Ala	Ala	
		275				280						285					
60																	

Ile Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln
290 295 300

5 Val Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg
305 310 315 320

Lys Leu Ala Ala Pro Val Ile Ser Val Leu Leu Leu Ser Leu Cys Val
325 330 335

10 Pro Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala
340 345 350

Glu Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met
355 360 365

15 Val Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys
370 375 380

20 Arg Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Val Gly Gln Arg
385 390 395 400

Leu Val Asn Tyr Glu Arg Lys Ser Gly Lys Gln Gly Ser Ser Pro Pro
405 410 415

25 Pro Pro Gln Ser Ser Gln Glu
420

30 (2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
1 5 10 15

40 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
20 25 30

Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
35 40 45

45 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro
50 55 60

50 Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu Xaa
65 70 75

55 (2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
 1 5 10 15
 His Cys Trp Gly Leu Pro Leu His Val Ala Pro Leu Cys Arg Gly His
 20 25 30
 Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala Trp
 35 40 45
 Asn Arg Asn Leu Ala Asn Gln Arg His Phe Phe Cys Pro Ser Ile Phe
 50 55 60
 His Thr Cys Pro Thr Val Leu Phe Phe Xaa
 65 70

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Ala Arg Thr Ile Leu Val Leu Tyr Leu Ser Leu Gln Arg Leu Glu Asn
 1 5 10 15
 Leu Ala Tyr His
 20

35

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Pro Leu Pro Ser Val Pro Ile Leu Gly Ile Phe Ser Phe Leu Ile
 1 5 10 15
 Pro Ser Ser Gln Gly Val Ser Tyr Thr Lys Leu Pro Ile Ser Ser Pro
 20 25 30
 Gln Tyr Ser Pro Phe Val Asn Asp His Phe Ser Phe Leu Asn Pro Phe
 35 40 45
 Pro Val Gln Ile His Thr Gly Phe Ala Arg Val Gly Ser Tyr Met Gln
 50 55 60
 Met Pro Leu Val His Leu Cys Leu Leu Gln Thr Ser Leu Met Lys Asn
 65 70 75 80
 Ser Gly Val Gln Gln Gly Ser
 85

60

(2) INFORMATION FOR SEQ ID NO: 404:

- 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile Ile
 1 5 10 15

15

Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala Val
 20 25 30

20

Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile Thr
 35 40 45

Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val Tyr
 50 55 60

25

Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg Asp
 65 70 75 80

Gln Thr Lys Ser Ile Val Glu Lys Ile Pro Ser Lys
 85 90

30

(2) INFORMATION FOR SEQ ID NO: 405:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

~~(B) TYPE: amino acid~~

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

40

Met Ala Cys Ser Cys Leu Met Ile Gln Ser Phe Ser Thr Ser Ala Leu
 1 5 10 15

Val Leu Phe Tyr Gly
 20

45

(2) INFORMATION FOR SEQ ID NO: 406:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

55

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 1 5 10 15

60

Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 20 25 30

597

Ser Gly Phe Pro Ala Phe Pro Lys Pro Ser Pro Thr Tyr Leu Arg Thr
 35 40 45

5 Ser Ala Glu Gln Thr Leu Pro Leu Leu Leu Pro His Leu His Gly Leu
 50 55 60

10 Cys Leu His Gln Pro Leu His Leu Gly Phe Thr Ala Cys Leu Gly Ser
 65 70 75 80

Ala His Ile Leu Gly Gly Gln Pro Ala Leu Pro Ala Val Pro Glu Pro
 85 90 95

15 Tyr Ala Gly His Cys Gln Arg Pro Leu Ala Gly Thr Pro His His Ser
 100 105 110

Cys His Val Gly Pro Ala Asn Arg Gly Arg Arg Ser Glu Ala Trp Val
 115 120 125

20 Gly Arg Tyr Gln Ala Ala Asn Arg Phe Pro Ile Leu Asn Ala Xaa Cys
 130 135 140

Glu Arg Arg Thr Pro Ser Thr Val Leu Ser Ala Arg Ile Ser Ser Ala
 145 150 155 160

25 Thr Met Gly Cys Pro Leu Phe Ala Ile Trp Ala Ala Ser Xaa
 165 170

30

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

40

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15

Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30

45

Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45

Thr Glu Gly Ile Pro Cys Gln Arg Tyr Gln Asn Gly Leu His Ile Xaa
 50 55 60

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55

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

5 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30
 10 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 15 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 20 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 25 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
 130 135 140
 30 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
 145 150 155 160
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
 165 170 175

 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
 180 185 190
 40 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
 195 200 205
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
 210 215 220
 45 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255
 50 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270
 55 Ile Ala Lys Val Lys Ala Asn Xaa
 275 280

60 (2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

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Met Xaa Leu Trp Pro Gln Thr Cys Ser Gly Lys Phe Asp Gly Thr Leu
1 5 10 15

Ala Phe Ser Ile His Xaa Leu Ala Val Ile Leu Gly Asp Gln Leu Thr
20 25 30

Ala Ala Asp Leu Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp
35 40 45

Glu Val Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu
50 55 60

Leu His Ile Asp Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe
65 70 75 80

Leu Val Thr Asp Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala
85 90 95

Glu Gln Leu Ile Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr
100 105 110

Asp Tyr Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser
115 120 125

Ser Val Arg Trp Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys
130 135 140

Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu
145 150 155 160

Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala
165 170 175

Phe Val Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met
180 185 190

Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn
195 200 205

Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln
210 215 220

Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln
225 230 235 240

Glu Ala Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser
245 250 255

Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile Ser
260 265 270

Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr Xaa
275 280

(2) INFORMATION FOR SEQ ID NO: 410:

-5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu Phe Leu Phe Phe Val Ile Ile Phe Leu Phe Val Phe Leu Ile
1 5 10 15

15

Leu Ile Ile Gln Phe Ser Lys Pro Leu Thr Asn Pro His Pro Pro Ala
20 25 30

Gly Xaa Ser Asp Arg Arg Arg Arg Tyr Ser Ser Tyr Arg Ser His Asp
35 40 45

20

His Tyr Gln Arg Gln Arg Val Leu Gln Lys Glu Arg Ala Ile Glu Glu
50 55 60

25

Arg Arg Val Val Phe Ile Gly Lys Ile Pro Gly Arg Met Thr Arg Ser
65 70 75 80

Glu Leu Lys Gln Arg Phe Ser Val Phe Gly Glu Ile Glu Glu Cys Thr
85 90 95

30

Ile His Phe Arg Val Gln Gly Asp Asn Tyr Gly Phe Val Thr Tyr Arg
100 105 110

Tyr Ala Glu Glu Ala Phe Ala Ala Ile Glu Ser Gly His Lys Leu Arg
115 120 125

35

Gln Ala Asp Glu Gln Pro Phe Asp Leu Cys Phe Gly Gly Arg Arg Xaa
130 135 140

40

Xaa Cys Lys Arg Ser Tyr Ser Asp Leu Asp Ser Asn Arg Glu Asp Phe
145 150 155 160

Asp Pro Ala Pro Val Lys Ser Lys Phe Asp Ser Leu Asp Phe Asp Thr
165 170 175

45

Leu Leu Lys Gln Ala Gln Lys Asn Leu Arg Arg
180 185

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(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Lys Leu Pro Gly Lys Phe Arg Arg Ala His Gln Gly Asn Leu Glu
1 5 10 15

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601

Ser Gln Leu Thr Ser Glu Ser Tyr Tyr Lys Glu Thr Leu Ser Val Pro
 20 25 30
 5 Thr Val Glu His Ile Ile Gln Glu Leu Lys Asp Ile Phe Ser Glu Gln
 35 40 45
 His Leu Lys Ala Leu Lys Cys Leu Ser Leu Val Pro Ser Val Met Gly
 50 55 60
 10 Gln Leu Lys Phe Asn Thr Ser Glu Glu His His Ala Asp Met Tyr Arg
 65 70 75 80
 Ser Asp Leu Pro Asn Pro Asp Thr Leu Ser Ala Glu Leu His Cys Trp
 85 90 95
 15 Arg Ile Lys Trp Lys His Arg Gly Lys Asp Ile Glu Leu Pro Ser Thr
 100 105 110
 Ile Tyr Glu Ala Leu His Leu Pro Asp Ile Lys Phe Phe Pro Asn Val
 115 120 125
 Tyr Ala Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu
 130 135 140
 25 Asn Glu Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg
 145 150 155 160
 Asn Thr Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile
 165 170 175
 30 Asn Phe Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile
 180 185 190
 Lys Leu Tyr Thr Xaa Xaa Ser Xaa Leu Xaa Thr Xaa Xaa Ser Xaa Xaa
 195 200 205
 Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
 210 215 220
 40 Asp Xaa Xaa Xaa Arg Glu Lys Ala Val Arg Cys Met Xaa
 225 230 235

45 (2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Lys Pro Met Ala Val Val Ala Ser Thr Val Leu Gly Leu Val Gln
 1 5 10 15
 55 Asn Met Arg Ala Phe Gly Gly Ile Leu Val Val Val Tyr Tyr Val Phe
 20 25 30
 60 Ala Ile Ile Gly Ile Asn Leu Phe Arg Gly Val Ile Val Ala Leu Pro
 35 40 45

Gly Asn Ser Ser Leu Ala Pro Ala Asn Gly Ser Ala Pro Cys Gly Ser
 50 55 60
 5 Phe Glu Gln Leu Glu Tyr Trp Ala Asn Asn Phe Asp Asp Phe Ala Ala
 65 70 75 80
 Ala Leu Val Thr Leu Trp Asn Leu Met Val Val Asn Asn Trp Gln Val
 85 90 95
 10 Phe Leu Asp Ala Tyr Arg Arg Tyr Ser Gly Pro Trp Ser Lys Ile Tyr
 100 105 110
 Phe Val Leu Trp Trp Leu Val Ser Ser Val Ile Trp Val Asn Leu Phe
 115 120 125
 Leu Ala Leu Ile Leu Glu Asn Phe Leu His Lys Trp Asp Pro Arg Ser
 130 135 140
 20 His Leu Gln Pro Leu Ala Gly Thr Pro Glu Ala Thr Tyr Gln Met Thr
 145 150 155 160
 Val Glu Leu Leu Phe Arg Asp Ile Leu Glu Glu Pro Gly Glu Asp Glu
 165 170 175
 25 Leu Thr Glu Arg Leu Ser Gln His Pro His Leu Trp Leu Cys Arg Xaa
 180 185 190

30

35 (2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Asn Val Val Val Val Ala Phe Gly Leu Ile Leu Ile Ile Glu Ser Leu
 1 5 10 15

45 Gly Glu Gln Cys Pro
 20

50 (2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
 1 5 10 15

60

Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
 20 25 30
 Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
 5 35 40 45
 Ala Pro Xaa
 50

10

(2) INFORMATION FOR SEQ ID NO: 415:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

20 Met Leu Ile Ile Ser Leu Arg Pro Gln Phe Pro Ser Leu Ile Val Gln
 1 5 10 15
 Leu Glu Cys Ser Val Leu Phe Leu Pro Ile Ser Leu Asn Leu Leu Leu
 25 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 416:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
 1 5 10 15
 Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
 20 25 30
 45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
 35 40 45
 Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
 50 50 55 60
 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
 65 70 75 80
 55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
 85 90 95
 Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
 100 105 110
 60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Ile Gly Arg Pro
145 150 155 160

Gln Val Xaa

10

15 (2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
1 5 10 15

25 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
20 25 30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
35 40 45

30 Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
50 55 60

35 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
65 70 75 80

Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
85 90 95

40 Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
100 105 110

Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu
115 120 125

45 Ala Pro Gly Arg Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro
130 135 140

50 Trp Phe Thr Ala Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys
145 150 155 160

Arg Gln Arg Arg Gln Glu Arg Arg Gln Met Lys Arg Leu Xaa
165 170

55

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids

60

605

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

5 Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Val Ala Met Met
 1 5 10 15
 Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala Leu Arg
 20 25 30
 10 Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Cys Cys Leu
 35 40 45
 Ala Xaa
 15 50

(2) INFORMATION FOR SEQ ID NO: 419:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Leu Gly Lys Gly Gly Gly Arg Ala Gly Leu Leu Arg Tyr Arg Leu
 1 5 10 15
 30 Leu Tyr Phe Thr Leu Val Val Gly Glu Gly Glu Pro Gly Glu Asn Lys
 20 25 30
 Val Thr Ile Pro Phe Phe Glu Thr Gly Lys Lys Ile Ile Phe Cys Ser
 35 40 45
 35 Val Lys Met Val Glu Asn Ser Asn Val Pro Ser His Lys Gly Pro Val
 50 55 60
 40 Pro Leu Arg Ser Glu Gln Trp Glu Leu Lys Ile Ser Glu Thr Leu Gly
 65 70 75 80
 Glu Gly Lys Ile Gly Phe Leu Leu Ile Gly Arg Cys Ser Ser Gly Xaa
 85 90 95
 45 Gly Gly Leu Cys Phe Cys Trp Asp Val Leu Cys Cys Met Tyr Ala Tyr
 100 105 110
 Met Asp Arg Ser Leu Leu Ser Leu
 115 120
 50

(2) INFORMATION FOR SEQ ID NO: 420:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

606

Met Thr His Leu Leu Leu Thr Ala Thr Val Thr Pro Ser Glu Gln Asn
 1 5 10 15

5 Ser Ser Arg Glu Pro Gly Trp Glu Thr Ala Met Ala Lys Asp Ile Leu
 20 25 30

Gly Glu Ala Gly Leu His Phe Asp Glu Leu Asn Lys Leu Arg Val Leu
 35 40 45

10 Asp Pro Glu Val Thr Gln Gln Thr Ile Glu Leu Lys Glu Glu Cys Lys
 50 55 60

Asp Phe Val Asp Lys Ile Gly Gln Phe Gln Lys Ile Val Gly Gly Leu
 65 70 75 80

15 Ile Glu Leu Val Asp Gln Leu Ala Lys Glu Ala Glu Asn Glu Lys Met
 85 90 95

Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys Ser Ile Ala Lys Gln Arg
 100 105 110

Glu Ala Gln Gln Gln Gln Leu Gln Ala Leu Ile Ala Glu Lys Lys Met
 115 120 125

25 Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu Ala Leu Cys Lys Val Glu
 130 135 140

Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe Ile Phe Gln Lys Xaa
 145 150 155

30

(2) INFORMATION FOR SEQ ID NO: 421:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15

45 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45

50 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80

55 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95

60 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110

607

Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125

5 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr Xaa
 145 150

10

(2) INFORMATION FOR SEQ ID NO: 422:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

20

Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala Leu
 1 5 10 15

25

Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile Ala Ala
 20 25 30

Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val Val Gly Val
 35 40 45

30

Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala Leu Val Gly Leu
 50 55 60

Ile Gly Ala Val Lys His His Gln Val Leu Leu Phe Phe Tyr Met Ile
 65 70 75 80

35

Ile Leu Leu Leu Val Phe Ile Val Gln Phe Ser Val Ser Cys Ala Cys
 85 90 95

40

Leu Ala Leu Asn Gln Glu Gln Gln Gly Gln Leu Leu Glu Val Gly Trp
 100 105 110

Asn Asn Thr Ala Ser Ala Arg Asn Asp Ile Gln Arg Asn Leu Asn Cys
 115 120 125

45

Cys Gly Phe Arg Ser Val Asn Pro Asn Asp Thr Cys Leu Ala Ser Cys
 130 135 140

Val Lys Ser Asp His Ser Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu
 145 150 155 160

50

Tyr Ala Gly Glu Val Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe
 165 170 175

55

Ser Phe Thr Glu Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn
 180 185 190

Gln Lys Asp Pro Arg Ala Asn Pro Ser Ala Phe Leu
 195 200

60

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

5
 10 Met Leu Gln Ser Ile Ile Lys Asn Ile Trp Ile Pro Met Lys Pro Tyr
 1 5 10 15
 Tyr Thr Lys Val Tyr Gln Glu Ile Trp Ile Gly Met Gly Leu Met Gly
 20 25 30
 15 Phe Ile Val Tyr Lys Ile Arg Ala Ala Asp Lys Arg Ser Lys Ala Leu
 35 40 45
 20 Lys Ala Ser Ala Pro Ala Pro Gly His His Asn Gln Ile Tyr Leu Glu
 50 55 60
 Tyr Met Xaa
 65

25

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

30
 35 Met Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val
 1 5 10 15
 Ala Val Asn Asn Pro Lys Lys Gln Glu
 20 25
 40

(2) INFORMATION FOR SEQ ID NO: 425:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

50

Met Ala Ala Xaa Glu Pro Ala Val Leu Ala Leu Pro Asn Ser Gly Ala
 1 5 10 15
 Gly Gly Ala Gly Ala Pro Ser Gly Thr Val Pro Val Leu Phe Cys Phe
 20 25 30
 Ser Val Phe Ala Arg Pro Ser Ser Val Pro His Gly Ala Gly Tyr Glu
 35 40 45

60

Leu Leu Ile Gln Lys Phe Leu Ser Leu Tyr Gly Asp Gln Ile Asp Met

609

[illegible]

50 (2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Arg Asp Leu Gly Thr Leu Leu Ser Pro Val Cys Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 427:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

10

Met Phe Gly Cys Leu Val Ala Gly Arg Leu Val Gln Thr Ala Ala Gln
 1 5 10 15

15

Gln Val Ala Glu Asp Lys Phe Val Phe Asp Leu Pro Asp Tyr Glu Ser
 20 25 30

Ile Asn His Val Val Val Phe Met Leu Gly Thr Ile Pro Phe Pro Glu
 35 40 45

20

Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro Asp Ser Asn Gly Met
 50 55 60

25

Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn Gly Lys Pro Ser Ala
 65 70 75 80

Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu Gly Ser Gln His Pro
 85 90 95

30

Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser Val Ala Gln Ile Gly
 100 105 110

Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln Gln Thr Pro Val Gly
 115 120 125

35

Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr Gln Phe Thr Gln Lys
 130 135 140

40

Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser Phe Ala Val Ser Gln
 145 150 155 160

Ala Gln Met Thr Pro Ser Pro Ser Glu Met Phe Ile Pro Ala Asn Val
 165 170 175

45

Val Leu Lys Trp Tyr Glu Asn Phe Gln Arg Arg Leu Ala Gln Asn Pro
 180 185 190

Xaa Phe Trp Xaa Thr Xaa
 195

50

(2) INFORMATION FOR SEQ ID NO: 428:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

60

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser

611

1 5 10 15

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Leu Leu Trp Lys
20 25 30

5

Asn Arg Gly Gly Val Gly Arg Ser Val Met Ser Ala Val Glu Xaa
35 40 45

10

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Lys Lys Val Glu Glu Lys Arg Val Asp Val Asn Ser Ala Val Ala
1 5 10 15

Met Gly Glu Val Ile Leu Ala Val Cys His Pro Asp Cys Ile Thr Thr
20 25 30

25

Ile Lys His Trp Ile Thr Ile Ile Arg Ala Arg Phe Glu Glu Val Leu
35 40 45

Thr Trp Ala Lys Gln His Gln Gln Arg Leu Glu Thr Ala Leu Ser Glu
50 55 60

30

Leu Val Ala Asn Ala Glu Leu Leu Glu Glu Leu Leu Ala Trp Ile Gln
65 70 75 80

Trp Ala Glu Thr Thr Leu Ile Gln Arg Asp Gln Glu Pro Ile Pro Gln
85 90 95

35

Asn Ile Asp Arg Val Lys Ala Leu Ile Ala Glu His Gln Thr Phe Met
100 105 110

40

Glu Glu Met Thr Arg Lys Gln Pro Asp Val Asp Arg Val Thr Lys Thr
115 120 125

Tyr Lys Arg Lys Asn Ile Glu Pro Thr His Ala Pro Phe Ile Glu Lys
130 135 140

45

Ser Arg Ser Gly Gly Arg Lys Ser Leu Ser Gln Pro Thr Pro Pro Pro
145 150 155 160

Met Pro Ile Leu Ser Gln Ser Glu Ala Lys Asn Pro Arg Ile Asn Gln
165 170 175

50

Leu Ser Ala Arg Trp Gln Gln Val Trp Leu Leu Ala Leu Glu Arg Gln
180 185 190

Arg Lys Leu Asn Asp Ala Leu Asp Arg Leu Glu Glu Leu Lys Glu Phe
195 200 205

55

Ala Asn Phe Asp Phe Asp Val Trp Arg Lys Lys Tyr Met Arg Trp Met
210 215 220

Asn His Lys Lys Ser Arg Val Met Asp Phe Phe Arg Arg Ile Asp Lys
 225 230 235 240
 5 Asp Gln Asp Gly Lys Ile Thr Arg Gln Glu Phe Ile Asp Gly Ile Leu
 245 250 255
 Ala Ser Lys Phe Pro Thr Thr Lys Leu Glu Met Thr Ala Val Ala Asp
 260 265 270
 10 Ile Phe Asp Arg Asp Gly Asp Gly Tyr Ile Asp Tyr Tyr Glu Phe Val
 275 280 285
 Ala Ala Leu His Pro Asn Lys Asp Ala Tyr Arg Pro Thr Thr Asp Ala
 290 295 300
 15 Asp Lys Ile Glu Asp Glu Val Thr Arg Gln Val Ala Gln Cys Lys Cys
 305 310 315 320
 20 Ala Lys Arg Phe Gln Val Glu Gln Ile Gly Glu Asn Lys Tyr Arg Phe
 325 330 335
 Phe Leu Gly Asn Gln Phe Gly Asp Ser Gln Gln Leu Arg Leu Val Arg
 340 345 350
 25 Ile Leu Arg Asn Arg Asp Gly Ser Arg Trp Trp Arg Met Asp Gly Leu
 355 360 365
 Gly Xaa
 30 370

(2) INFORMATION FOR SEQ ID NO: 430:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Asn Val Lys Thr Phe Ser Xaa Asp His Met His Phe Leu Cys Cys
 1 5 10 15
 45 Leu Tyr Leu Arg Tyr Val Thr Phe Val Tyr Leu Asn Leu Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 431:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Glu Pro His Leu Arg Cys Arg Val Thr Arg Val Arg Gly Ser Leu
 1 5 10 15
 60 Gly Asn Thr Gly Arg Trp Leu Leu

5 (2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met His Tyr Leu Val Leu Gly Gly Leu Gly Val Phe Leu Phe Phe Ser
 1 5 10 15
 Cys Phe Val Phe Leu Phe Phe Xaa Phe Ser Phe Ala Phe Phe Pro Phe
 20 25 30
 Tyr Leu Glu Gly Met Gly Gly Ser Gly Asn Arg Glu Val Gly Gly Gly
 35 40 45
 Phe Cys Leu Phe Phe
 50

25

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Val Ser Lys Ala Leu Leu Arg Leu Val Ser Ala Val Asn Arg Arg
 1 5 10 15
 Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
 20 25 30
 Val Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu
 35 40 45
 Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu
 50 55 60
 Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val
 65 70 75 80
 Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Ile Thr Gly Gly
 85 90 95
 Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu Met Met Asp Gly
 100 105 110
 His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly Arg Lys Arg Asn
 115 120 125
 Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu Ile Asn His Asp
 130 135 140

60

Val Trp Ser Pro Ser Thr Ser Arg Leu Thr Arg Tyr Thr Ile Trp His
145 150 155 160

5 Leu Gln Pro Pro Leu Gln Thr Thr Cys Ile Ile Leu Ser Arg His Xaa
165 170 175

10

(2) INFORMATION FOR SEQ ID NO: 434:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

20

Met Leu Arg Cys Trp Pro Leu Phe Trp Leu Pro Leu Val Ser Pro Phe
1 5 10 15

25

Cys Ser Leu Phe Trp Leu Leu Val Glu Trp Phe Gly Thr Asn Ile Asp
20 25 30

Arg Glu Ser Tyr Asp Ala Ile Gly Gly Pro Ser Trp Met Thr Ala Ser
35 40 45

30

Ser Phe Cys Leu Ser Asn Ser Asn Ile Trp Ser Leu Glu Ile Ser Ser
50 55 60

35

Gly Ser Thr Ser Val Val His Ser Gln Gln Ala Met Asp
65 70 75

(2) INFORMATION FOR SEQ ID NO: 435:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

45

Met Arg Ser Cys Glu Ile Gln Leu Cys Val Trp Leu Leu Val Ser Ser
1 5 10 15

50

His Val Asp Met Val Leu Gly Gly Ser Pro Ser Thr Leu Tyr Met Met
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 436:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

615

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

5 Met Val Val Asn Ser Leu Cys Phe Leu Ser Leu Leu Val Ile Leu
 1 5 10 15
 Glu Leu Ser Thr Asp Ser Ser Ala Arg Leu Leu Tyr His Glu
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 437:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

20

Met Asp Lys Gln Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile
 1 5 10 15

25

Gln Gly Lys Ile Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser
 20 25 30

Pro Thr Ile Phe Ser His Ser Ile Leu Leu Leu Leu Pro His His Val
 35 40 45

30

Leu Pro Cys Thr Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg
 50 55 60

Glu Phe Gly Asp Gln
 65

35

(2) INFORMATION FOR SEQ ID NO: 438:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

45

Met Pro Leu Cys Phe Phe Ser Phe Leu Cys Cys Trp Val Leu Val Phe
 1 5 10 15

Lys Leu Ile

50

(2) INFORMATION FOR SEQ ID NO: 439:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15
 5 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30
 Arg Val Met Val Asn Leu Asn Ile Leu Phe Xaa
 35 40
 10

(2) INFORMATION FOR SEQ ID NO: 440:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

20 Met Leu Leu Phe Pro Ser Leu Leu Phe Ala Ala Thr Tyr Asn Val Ala
 1 5 10 15
 25 Asn Pro Ser Arg Leu Ile Leu Tyr Met Ile Ser Ala Gly Ala Asp Ser
 20 25 30
 Gln

30

(2) INFORMATION FOR SEQ ID NO: 441:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

40 Met Trp Gln Val Arg Gly Leu Pro Pro Val Pro Leu Leu Leu Thr Met
 1 5 10 15
 Ser Pro Pro Pro Cys Leu Ser Ser Pro Phe Pro Phe Ile Ser Val Pro
 20 25 30
 45 Leu Phe Glu Ala Val Pro Ile Ser Val Ser Asp Gln Pro Ser Pro Xaa
 35 40 45
 Leu Thr Thr Leu Leu
 50 50

55 (2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ile Thr Ser Val Leu Val Phe Leu Ile Phe Phe Phe Pro Tyr Leu
 1 5 10 15

5 Ser Leu Val Thr Leu Leu Gln Ala Arg Asn Leu Trp Val Ile His Arg
 20 25 30

Ala Ala Leu Cys Glu Ser Gly Leu Phe His Trp Arg Lys Gly Ile Glu
 35 40 45

10 Asn Gln Leu Glu Pro Met Tyr Phe Leu Pro His Gly Thr Leu Phe Leu
 50 55 60

15

- (2) INFORMATION FOR SEQ ID NO: 443:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Leu Tyr Ser Cys Glu Pro Tyr Leu Ile Ile Leu Asn Ile Tyr Ser
 1 5 10 15

30 Gln Lys Ala Phe Tyr Phe Tyr Phe Phe Glu Gly Ser Phe Ser Val Cys
 20 25 30

Thr Leu

35

- (2) INFORMATION FOR SEQ ID NO: 444:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

40 Met Arg Gln Arg Gln Ala Ala Cys Gln Pro Pro Pro Ser Arg Asn Gly
 1 5 10 15

50 Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 20 25 30

Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Ser Ser Pro Leu
 35 40 45

55 Asn Leu Leu Leu Leu Val Ser Ile Ser Trp Asp Leu Gly Leu Lys Leu
 50 55 60

Asn Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr
 65 70 75 80

60

Lys Lys Phe Asn Lys Lys Lys Lys Lys
85

-5

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

15 Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

20 Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

25 Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

30 Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

35 Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

40 Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

45 Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

50 Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
210 215 220

55 Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

60 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
 260 265 270

-5 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Pro Pro Gly Pro Glu Lys Ser
 290 295 300

10 Gly Asn Pro Arg Thr Pro Ser Thr Leu Thr Ser Gln Gly Gln Gly Arg
 305 310 315 320

Glu Ala Ala Leu Leu Gly Leu Leu Thr Leu Gln Gly Thr Val Ala Phe
 15 325 330 335

Val Glu Thr Leu Met Glu Ile Cys Leu Thr Ser Gly Lys Asp
 340 345 350

20

(2) INFORMATION FOR SEQ ID NO: 446:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Val Phe Leu Pro Arg Gly Val Val Val Ser Gly Gly Ala Ala Cys
 1 5 10 15

Leu Trp Leu Thr Phe Ile Leu Glu Thr Glu Val Tyr Leu Asp Leu Ala
 20 25 30

35 Thr Glu Ala Arg Ala His Ser Arg Met Gly Leu Gly Leu Trp Pro Pro
 35 40 45

40 Asn

45 (2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Ser Ala Glu Leu Asp Tyr Thr Ile Glu Ile Pro Asp Gln Pro
 1 5 10 15

55 Cys Trp Ser Gln Lys Asn Ser Pro Ser Pro Gly Gly Lys Glu Ala Glu
 20 25 30

Thr Arg Gln Pro Val Val Ile Leu Leu Gly Trp Gly Gly Cys Lys Asp
 35 40 45

60

620

Lys Asn Leu Ala Lys Tyr Ser Ala Ile Tyr His Lys Arg Gly Cys Ile
 50 55 60
 - 5 Val Ile Arg Tyr Thr Ala Pro Trp His Met Val Phe Phe Ser Glu Ser
 65 70 75 80
 Leu Gly Ile Pro Ser Leu Arg Val Leu Ala Gln Lys Leu Leu Glu Leu
 85 90 95
 10 Leu Phe Asp Tyr Glu Ile Glu Lys Glu Pro Leu Leu Phe His Val Phe
 100 105 110
 Ser Asn Gly Gly Val Met Leu Tyr Arg Tyr Val Leu Glu Leu Leu Gln
 115 120 125
 15 Thr Arg Arg Phe Cys Arg Leu Arg Val Val Gly Thr Ile Phe Asp Ser
 130 135 140
 Ala Pro Gly Asp Ser Asn Leu Val Gly Ala Leu Arg Ala Leu Ala Ala
 145 150 155 160
 Ile Leu Glu Arg Arg Ala Ala Met Leu Arg Leu Leu Leu Leu Val Ala
 165 170 175
 25 Phe Ala Leu Val Val Val Leu Phe His Val Leu Leu Ala Pro Ile Thr
 180 185 190
 Ala Xaa Phe His Thr His Phe Tyr Asp Arg Leu Gln Asp Ala Gly Ser
 195 200 205
 30 Arg Trp Pro Glu Leu Tyr Leu Tyr Ser Arg Ala Asp Glu Val Val Leu
 210 215 220
 Ala Arg Asp Ile Glu Arg Met Val Glu Ala Arg Leu Ala Arg Arg Val
 225 230 235 240
 Leu Ala Arg Ser Val Asp Phe Val Ser Ser Ala His Val Ser His Leu
 245 250 255
 40 Arg Asp Tyr Pro Thr Tyr Tyr Thr Ser Leu Cys Val Asp Phe Met Arg
 260 265 270
 Asn Cys Val Arg Cys Xaa
 275
 45

(2) INFORMATION FOR SEQ ID NO: 448:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

55

Met Ser Phe Ile Phe Asp Trp Ile Tyr Ser Gly Phe Ser Ser Val Leu
 1 5 10 15

60

Gln Phe Leu Gly Leu Tyr Lys Lys Thr Gly Lys Leu Val Phe Leu Gly
 20 25 30

Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
 35 40 45
 5 Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
 50 55 60
 Thr Ile Ala Gly Met Thr Phe Thr Thr Phe Asp Leu Gly Gly His Val
 65 70 75 80
 10 Gln Ala Arg Arg Val Trp Lys Asn Tyr Leu Pro Ala Ile Asn Gly Ile
 85 90 95
 15 Val Phe Leu Val Asp Cys Ala Asp His Glu Arg Leu Leu Glu Ser Lys
 100 105 110
 Glu Glu Leu Asp Ser Leu Met Thr Asp Glu Thr Ile Ala Asn Val Pro
 115 120 125
 20 Ile Leu Ile Leu Gly Asn Lys Ile Asp Arg Pro Glu Ala Ile Ser Glu
 130 135 140
 Glu Arg Leu Arg Glu Met Phe Gly Leu Tyr Gly Gln Thr Thr Gly Lys
 145 150 155 160
 25 Gly Ser Ile Ser Leu Lys Glu Leu Asn Ala Arg Pro Leu Glu Val Phe
 165 170 175
 30 Met Cys Ser Val Leu Lys Arg Gln Gly Tyr Gly Glu Gly Phe Arg Trp
 180 185 190
 Met Ala Gln Tyr Ile Asp Xaa
 195

35

(2) INFORMATION FOR SEQ ID NO: 449:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

45 Met Thr Leu Ser Arg Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser
 1 5 10 15
 Tyr Asn Ile Leu Asp Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys
 20 25 30
 50 Glu Leu Thr Ala Leu Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro
 35 40 45
 55 His Arg Thr Val Lys Glu Lys Leu Pro His Met Val Glu Trp Trp Thr
 50 55 60
 Lys Ala His Asn Leu Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile
 65 70 75 80
 60 Ala Gln Val Val Arg Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys

622

85 90 95

Thr Phe Phe Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe
100 105 110

-5 Ser Ala Gly Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys
115 120 125

10 Val Phe His Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn
130 135 140

Glu Asp Gly Phe Leu Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr
145 150 155 160

15 Asn Lys Asn Ser Ser Val Cys Glu Asn Xaa Gly Tyr Phe Gln Gln Leu
165 170 175

Glu Gly Lys Thr Asn Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu
180 185 190

20 Thr Met Ala Asp Gly Val Pro Gly Val Gln Asn Ile Leu Lys Ile Gly
195 200 205

25 Phe Leu Asn Asp Lys Val Glu Glu Arg Arg Xaa Arg Tyr Met Asp Ser
210 215 220

Tyr Asp Ile Val Leu Glu Lys Asp Glu Thr Leu Asp Val Val Asn Gly
225 230 235 240

30 Leu Leu Gln His Ile Leu Cys Gln Gly Val Gln Leu Glu Met Gln Gly
245 250 255

Pro Xaa

35

(2) INFORMATION FOR SEQ ID NO: 450:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

45

Met Ser His Val Leu Leu Cys Pro Ser Leu Ser Cys Ser Asn Leu Leu
1 5 10 15

50

Pro Pro Ser His Ser Leu Gly Thr Met Gly Ser Leu Ser Pro His Leu
20 25 30

Cys Gly His Thr Met Cys Pro Val Asn Pro Glu Leu Pro Leu Ser Ser
35 40 45

55

Arg Leu Thr Thr Asp Gln Pro Gln Pro Asp Ala Cys Ser Pro Thr Leu
50 55 60

Leu Thr Leu Pro Leu Pro Ser Ser Phe Leu Pro His Ser Lys Pro Thr
65 70 75 80

60

Phe Xaa His Pro Cys Ser Pro
85

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(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

15

Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser
1 5 10 15

Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Xaa Pro Met Ala Ile
20 25 30

20

Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser
35 40 45

Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp
50 55 60

25

Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn
65 70 75 80

30

Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala
85 90 95

Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile
100 105 110

35

Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly
115 120 125

Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln
130 135 140

40

Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe
145 150 155 160

45

Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His
165 170 175

Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro
180 185 190

50

Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr
195 200 205

Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp
210 215 220

55

Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys
225 230 235 240

60

Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val
245 250 255

624

Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met His
260 265 270

-5 Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr Ala
275 280 285

Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu Phe
290 295 300

10 Cys Pro Glu Lys Val Ala Leu Ala Glu Ala Xaa
305 310 315

15

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

20 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

25 Met Pro Gly Leu Ser Leu Ala Leu Leu Pro Phe Gly Pro Gly Cys Thr
1 5 10 15

Glu Ala Leu His Ala Gly Cys Phe Pro Ala Phe Ala Ser Ala Thr Arg
20 25 30

30 Val Asn Gly Glu Ala Ala Leu Ser Pro Gly Leu Cys Asp Pro Ile Ser
35 40 45

Val Pro Tyr Val
50

35

(2) INFORMATION FOR SEQ ID NO: 453:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

45

Met Ala Val Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys
1 5 10 15

50 Gly Phe Ile Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val
20 25 30

Leu Leu Trp Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala
35 40 45

55 Gly Leu Lys Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys
50 55 60

Asp Thr Glu Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys
65 70 75 80

60

625

Asp Ser Asn Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala
 85 90 95
 - 5 Ser Gln Met Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser
 100 105 110
 Tyr Tyr Asn Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu
 115 120 125
 10 Tyr Met Thr Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr
 130 135 140
 Thr Gln Gly Leu Ser Gly Phe His Pro Gln Tyr Phe Asp Gly Ser Ile
 15 145 150 155 160
 Ser Tyr Asn Trp Asn Asn Gly Asn Cys Ser Phe Tyr Leu Ala Thr Ser
 165 170 175
 20 Lys Met Trp Phe Gly Ser Ala Gly Leu Ile Ser Gly Leu Ala Gln Leu
 180 185 190
 Ser Cys Leu Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro
 195 200 205
 25 Leu Asp Leu Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile
 210 215 220
 Gln Gly Glu Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu
 30 225 230 235 240
 Ile Tyr Met Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr
 245 250 255
 35 Ser Pro Glu Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly
 260 265 270
 Val Ile Ala Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr
 275 280 285
 40 Gln Leu Leu Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn
 290 295 300
 Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile
 45 305 310 315 320
 Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu
 325 330 335
 50 Ile Ser Val Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe
 340 345 350
 Ala Gln Asn Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala
 355 360 365
 55 Lys Glu Val Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val Xaa
 370 375 380

60 (2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

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Met Arg Ser Ile Gly Asn Lys Asn Thr Ile Leu Leu Gly Leu Gly Phe
1 5 10 15

Gln Ile Leu Gln Leu Ala Trp Tyr Gly Phe Gly Ser Glu Pro Trp Met
20 25 30

Met Trp Ala Ala Gly Ala Val Ala Ala Met Ser Ser Ile Thr Phe Pro
35 40 45

Ala Val Ser Ala Leu Val Ser Arg Thr Ala Asp Ala Asp Gln Gln Gly
50 55 60

Val Val Gln Gly Met Ile Thr Gly Ile Arg Gly Leu Cys Asn Gly Leu
65 70 75 80

Gly Pro Ala Leu Tyr Gly Phe Ile Phe Tyr Ile Phe His Val Glu Leu
85 90 95

Lys Glu Leu Pro Ile Thr Gly Thr Asp Leu Gly Thr Asn Thr Ser Pro
100 105 110

Gln His His Phe Glu Gln Asn Ser Ile Ile Pro Gly Pro Pro Phe Leu
115 120 125

Phe Gly Ala Cys Ser Val Leu Leu Ala Leu Val Ala Leu Phe Ile
130 135 140

Pro Glu His Thr Asn Leu Ser Leu Arg Ser Ser Ser Trp Arg Lys His
145 150 155 160

Cys Gly Ser His Ser His Pro His Asn Thr Gln Ala Pro Gly Glu Ala
165 170 175

Lys Glu Pro Leu Leu Gln Asp Thr Asn Val
180 185

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
1 5 10 15

Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
20 25 30

Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

35 40 45

Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
50 55 60

-5 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
65 70 75 80

10 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
85 90 95

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
100 105 110

15 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
115 120 125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
130 135 140

20 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
145 150 155 160

25 Arg Arg Xaa

30 (2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Arg Ile Gln Val Phe Ile Leu Leu Leu Gly Ala Gly Gly Thr Ser
1 5 10 15

40 Gln Phe Thr Lys Pro Pro Ser Leu Pro Leu Glu Pro Glu Pro Ala Val
20 25 30

Glu Ser Ser Pro Thr Glu Thr Ser Glu Gln Ile Arg Glu Lys
35 40 45

45

(2) INFORMATION FOR SEQ ID NO: 457:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ser Tyr Leu Ala Phe Leu Tyr Met Thr Phe Asp Phe Cys Cys Leu
1 5 10 15

60 Tyr Phe Ser Thr Val Tyr Ala Pro Ser Phe Lys Tyr Ile Cys Val His
20 25 30

Thr Asp Thr His Ile Cys Val Cys Val Cys Ile Tyr Leu Ser Ser Val
 35 40 45
 -5 Val Ser Lys Ser Ser Ala Glu Ala Asp Gly Val Leu Gln Pro Arg Arg
 50 55 60
 His Pro Ala Ser Leu Leu Ile Val Phe Ala Thr Ser Ile Ser Glu Ser
 65 70 75 80
 10 Ser Leu Leu Ile Phe Ser Phe Gln Lys Thr Glu Ala Lys Leu Ile Val
 85 90 95
 Phe Ala Val Ser Leu Ala Ala Lys Xaa
 15 100 105

(2) INFORMATION FOR SEQ ID NO: 458:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
 1 5 10 15
 30 Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
 20 25 30
 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
 35 40 45
 35 Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
 50 55 60
 Ala His Thr Val Ala Xaa
 40 65 70

(2) INFORMATION FOR SEQ ID NO: 459:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
 1 5 10 15
 55 Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
 20 25 30
 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 35 40 45
 60

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 50 55 60
 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Val Met Gly Pro
 5 65 70 75 80
 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 85 90 95
 10 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 100 105 110
 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
 115 120 125
 15 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 130 135 140
 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
 20 145 150 155

(2) INFORMATION FOR SEQ ID NO: 460:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
 1 5 10 15
 35 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 40 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 45 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 50 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 55 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 60 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175

- 5 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190

Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205

10 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220

Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 15 225 230 235 240

Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255

20 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270

Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285

25 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300

Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 30 305 310 315 320

Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

35

(2) INFORMATION FOR SEQ ID NO: 461:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

45

Met Leu Lys Cys Ile
 1 5

50

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

55

Met Ile Leu Thr Leu Leu Ser Val Val Ser Thr Met Ala Ser
 1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 463:

-5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

10

Met Lys Leu His Pro Pro Pro Pro Ser Pro Val Thr Gln Asp His Arg
 1 5 10 15

15

Ser Lys Ser Ser His Ser Asn Trp Met Pro Arg Met Gly Ala Cys Ser
 20 25 30

Met Ser Arg Thr Ser Ser Ser Gly Pro Pro Ser Leu Cys Lys Ser Thr
 35 40 45

20

Ser Gly Arg Ser Cys Thr Arg Pro His Cys Trp Pro Ser Leu Pro Ala
 50 55 60

Trp Val Ser Val Phe Thr Arg Thr Asn Thr Gly Ser Trp Cys Tyr Pro
 65 70 75 80

25

Ala Trp Gly Gly Ala Phe Ser Arg Pro Trp Met Ser Ala Gln Ser Met
 85 90 95

30

Cys Cys Ala Glu Arg Ser Val Leu Gln Val Ala Cys Arg Leu Leu Asp
 100 105 110

Ala Leu Glu Phe Leu His Glu Asn Glu Tyr Val His Gly Asn Val Thr
 115 120 125

35

Ala Glu Asn Ile Phe Val Asp Pro Glu Asp Gln Ser Gln Val Thr Leu
 130 135 140

Ala Gly Tyr Gly Phe Ala Phe Arg Tyr Cys Pro Ser Gly Lys His Val
 145 150 155 160

40

Ala Tyr Val Glu Gly Ser Arg Ser Pro His Glu Gly Asp Leu Glu Phe
 165 170 175

45

Ile Ser Met Asp Leu His Lys Gly Cys Gly Pro Ser Arg Arg Xaa Asp
 180 185 190

Leu Gln Ser Leu Gly Tyr Cys Met Leu Lys Trp Leu Tyr Gly Phe Leu
 195 200 205

50

Pro Trp Thr Asn Cys Leu Pro Xaa Xaa Glu Asp Ile Met Lys Gln Lys
 210 215 220

Gln Lys Phe Val Asp Lys Pro Gly Pro Phe Val Gly Pro Cys Gly His
 225 230 235 240

55

Trp Ile Arg Pro Ser Glu Thr Leu Gln Lys Tyr Leu Lys Val Val Met
 245 250 255

60

Ala Leu Thr Tyr Glu Glu Lys Pro Pro Tyr Ala Met Leu Arg Asn Asn
 260 265 270

Leu Glu Ala Leu Leu Gln Asp Leu Arg Val Ser Pro Tyr
 275 280 285

-5

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

15

Met Thr Ser Pro Pro Pro His Gln Gly Trp Glu Gln Arg Gly Cys Gly
 1 5 10 15

Glu Ser Gln Val Pro Leu Ala Leu Ser Arg Val Phe Ser Thr Ser His
 20 25 30

20

Tyr Cys Leu Leu Leu Val Ala Asn Gln Ser Ile Phe Phe Pro Cys Leu
 35 40 45

25

Trp Ala Val Glu Arg Leu Leu Gly Val Arg Cys Thr Cys Pro Leu Ser
 50 55 60

Trp Gly Lys Arg Ile Ile Ser Glu His Cys Ser Ala Gln Ser Ser Xaa
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met His Thr Trp Tyr Asn Asp Arg Arg Gln Asn Cys His Cys Leu Leu
 1 5 10 15

45

Phe Phe Leu Ile Tyr Leu Arg Lys Ile Tyr Gln Val Val Pro His Val
 20 25 30

50

Pro Leu Leu Val Lys Cys Arg Gly Arg Leu Lys Gly Val Asn Ile
 35 40 45

55

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val
 1 5 10 15
 5 Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr
 20 25 30
 Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu
 35 40 45
 10 Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser
 50 55 60
 Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu
 15 65 70 75 80
 Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro Gln Lys Ala Glu Asn Xaa
 85 90 95

20

25 (2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Ala Ser Gly Ala Asp Ser Lys Gly Asp Asp Leu Ser Thr Ala Ile
 1 5 10 15
 35 Leu Lys Gln Lys Asn Arg Pro Asn Arg Leu Ile Val Asp Glu Ala Ile
 20 25 30
 Asn Glu Asp Asn Ser Val Val Ser Leu Ser Gln Pro Lys Met Asp Glu
 40 35 40 45
 Leu Gln Leu Phe Arg Gly Asp Thr Val Leu Leu Lys Gly Lys Lys Arg
 50 55 60
 45 Arg Glu Ala Val Cys Ile Val Leu Ser Asp Asp Thr Cys Ser Asp Glu
 65 70 75 80
 Lys Ile Arg Met Asn Arg Val Val Arg Asn Asn Leu Arg Val Arg Leu
 85 90 95
 50 Gly Asp Val Ile Ser Ile Gln Pro Cys Pro Asp Val Lys Tyr Gly Lys
 100 105 110
 Arg Ile His Val Leu Pro Ile Asp Asp Thr Val Glu Gly Ile Thr Gly
 55 115 120 125
 Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg
 130 135 140
 60 Pro Ile Arg Lys Gly Asp Ile Phe Leu Val Arg Gly Gly Met Arg Ala

634

145 150 155 160

Val Glu Phe Lys Val Val Glu Thr Asp Pro Ser Pro Tyr Cys Ile Val
165 170 175

-5 Ala Pro Asp Thr Val Ile His Cys Glu Gly Glu Pro Ile Lys Arg Glu
180 185 190

10 Asp Glu Glu Glu Ser Leu Asn Glu Val Gly Tyr Asp Asp Ile Gly Gly
195 200 205

Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu Met Val Glu Leu Pro Leu
210 215 220

15 Arg His Pro Ala Leu Phe Lys Ala Ile Gly Val Lys Pro Pro Arg Gly
225 230 235 240

Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Ile Ala Arg
245 250 255

20 Ala Val Ala Asn Glu Thr Gly Ala Phe Phe Phe Leu Ile Asn Gly Pro
260 265 270

Glu Ile Met Ser Lys Leu Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys
275 280 285

25 Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro Ala Ile Ile Phe Ile Asp
290 295 300

30 Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu Lys Thr His Gly Glu Val
305 310 315 320

Glu Arg Arg Ile Val Ser Gln Leu Leu Thr Leu Met Asp Gly Leu Lys
325 330 335

35 Gln Arg Ala His Val Ile Val Met Ala Ala Thr Asn Arg Pro Asn Ser
340 345 350

Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg Phe Asp Arg Glu Val Asp
355 360 365

Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu Glu Ile Leu Gln Ile His
370 375 380

45 Thr Lys Asn Met Lys Leu Ala Asp Asp Val Asp Leu Glu Gln Xaa
385 390 395

50 (2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Leu
1

60

(2) INFORMATION FOR SEQ ID NO: 469:

-5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

10

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
 1 5 10 15

15

Pro Pro Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
 20 25 30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
 35 40 45

20

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
 50 55 60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
 65 70 75 80

25

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
 85 90 95

30

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
 100 105 110

Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125

35

Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140

Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160

40

Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
 165 170 175

45

Ile Val Ile Phe Xaa Ser Lys Pro Arg Asn Pro Arg Tyr Ala Pro His
 180 185 190

Leu Glu Pro Gly Ala Leu Pro Asn Leu Xaa Xaa Xaa Ser Leu Ser Lys
 195 200 205

50

Met Ser Xaa Xaa Ser Xaa Met Arg Asn Ser Gln Ala His Arg Asn Phe
 210 215 220

Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn
 225 230 235 240

55

Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu
 245 250 255

60

Leu Trp Ile Cys Cys Ala Thr Cys Cys Tyr Thr Leu Leu Asp Ala Val
 260 265 270

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

10

15

Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser
 1 5 10 15

Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro
 20 25 30

20

Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala
 35 40 45

25

Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly
 50 55 60

Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu Ser
 65 70 75 80

30

Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu Asp
 85 90 95

Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His Asp
 100 105 110

35

Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala Gly
 115 120 125

40

Xaa Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu Ala
 130 135 140

Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe Pro
 145 150 155 160

45

Gly Ser Val Leu Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly Met
 165 170 175

Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr Ser
 180 185 190

50

55

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

-5 Met Arg Lys Thr Arg Leu Trp Gly Leu Leu Trp Met Leu Phe Val Ser
1 5 10 15

Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
20 25 30

10 Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
35 40 45

Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
50 55 60

15 Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
65 70 75 80

20 Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
85 90 95

Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln
100 105 110

25 Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
115 120 125

Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn
130 135 140

30 Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
145 150 155 160

35 Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
165 170 175

Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
180 185 190

40 Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile
195 200 205

Leu Leu Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu
210 215 220

45 Phe Ala Val Thr Leu Arg Ser Phe Val Pro
225 230

50

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

60 Met Leu His Ile Leu Pro Leu Lys Ser Tyr Asp Phe Pro His Phe Ser
1 5 10 15

Leu Met Gly Arg Tyr Arg Cys Ala Ser Leu Leu Phe Cys Phe Leu Leu
 20 25 30
 - 5 Leu Phe Phe Phe Phe Cys Ser Val Leu Trp Thr Phe Ser Asp Met His
 35 40 45
 Arg Ser Gly Glu Asp Gly Pro Trp Thr Pro Cys Val His His Leu Ala
 50 55 60
 10 Ala Ser Leu Ile Ser Tyr Gly Gln Pro Gly Phe Ile Cys Ile Ser Leu
 65 70 75 80
 15 Phe Ser Pro Val Leu Phe Ile Glu Asn Pro Arg His Tyr Ala Asn Ala
 85 90 95
 Thr Val Thr Thr Leu Gly Asp Trp Xaa
 100 105

20

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

30 Met Val Phe Leu Lys Tyr Arg Phe Leu Phe Phe Leu Val Phe Leu Ala
 1 5 10 15
 Asn Cys Ile Tyr Ser Leu His Tyr Lys Pro Ser Leu Met Tyr Pro Lys
 20 25 30

35

40

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 571 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

50 Met Ala Leu Ser Arg Gly Leu Pro Arg Glu Leu Ala Glu Ala Val Ala
 1 5 10 15
 Gly Gly Arg Val Leu Val Val Gly Ala Gly Gly Ile Gly Cys Glu Leu
 20 25 30

55 Leu Lys Asn Leu Val Leu Thr Gly Phe Ser His Ile Asp Leu Ile Asp
 35 40 45

Leu Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Gln
 50 55 60

60

Lys Lys His Val Gly Arg Ser Lys Ala Gln Val Ala Lys Glu Ser Val
 65 70 75 80
 5 Leu Gln Phe Tyr Pro Lys Ala Asn Ile Val Ala Tyr His Asp Ser Ile
 85 90 95
 Met Asn Pro Asp Tyr Asn Val Glu Phe Phe Arg Gln Phe Ile Leu Val
 100 105 110
 10 Met Asn Ala Leu Asp Asn Arg Ala Ala Arg Asn His Val Asn Arg Met
 115 120 125
 Cys Leu Ala Ala Asp Val Pro Leu Ile Glu Ser Gly Thr Ala Gly Tyr
 130 135 140
 15 Leu Gly Gln Val Thr Thr Ile Lys Lys Gly Val Thr Glu Cys Tyr Glu
 145 150 155 160
 Cys His Pro Lys Pro Thr Gln Arg Thr Phe Pro Gly Cys Thr Ile Arg
 165 170 175
 20 Asn Thr Pro Ser Glu Pro Ile His Cys Ile Val Trp Ala Lys Tyr Leu
 180 185 190
 25 Phe Asn Gln Leu Phe Gly Glu Glu Asp Ala Asp Gln Glu Val Ser Pro
 195 200 205
 Asp Arg Ala Asp Pro Glu Ala Ala Trp Glu Pro Thr Glu Ala Glu Ala
 210 215 220
 30 Arg Ala Arg Ala Ser Asn Glu Asp Gly Asp Ile Lys Arg Ile Ser Thr
 225 230 235 240
 Lys Glu Trp Ala Lys Ser Thr Gly Tyr Asp Pro Val Lys Leu Phe Thr
 245 250 255
 35 Lys Leu Phe Lys Asp Asp Ile Arg Tyr Leu Leu Thr Met Asp Lys Leu
 260 265 270
 40 Trp Arg Lys Arg Lys Pro Pro Val Pro Leu Asp Trp Ala Glu Val Gln
 275 280 285
 Ser Gln Gly Glu Glu Thr Asn Ala Ser Asp Gln Gln Asn Glu Pro Gln
 290 295 300
 45 Leu Gly Leu Lys Asp Gln Gln Val Leu Asp Val Lys Ser Tyr Ala Arg
 305 310 315 320
 Leu Phe Ser Lys Ser Ile Glu Thr Leu Arg Val His Leu Ala Glu Lys
 325 330 335
 50 Gly Asp Gly Ala Glu Leu Ile Trp Asp Lys Asp Asp Pro Ser Ala Met
 340 345 350
 55 Asp Phe Val Thr Ser Ala Ala Asn Leu Arg Met His Ile Phe Ser Met
 355 360 365
 Asn Met Lys Ser Arg Phe Asp Ile Lys Ser Met Ala Gly Asn Ile Ile
 370 375 380
 60

Pro Ala Ile Ala Thr Thr Asn Ala Val Ile Ala Gly Leu Ile Val Leu
 385 390 395 400

5 Glu Gly Leu Lys Ile Leu Ser Gly Lys Ile Asp Gln Cys Arg Thr Ile
 405 410 415

Phe Leu Asn Lys Gln Pro Asn Pro Arg Lys Lys Leu Leu Val Pro Cys
 420 425 430

10 Ala Leu Asp Pro Pro Asn Pro Asn Cys Tyr Val Cys Ala Ser Lys Pro
 435 440 445

Glu Val Thr Val Arg Leu Asn Val His Lys Val Thr Val Leu Thr Leu
 450 455 460

15 Gln Asp Lys Ile Val Lys Glu Lys Phe Ala Met Val Ala Pro Asp Val
 465 470 475 480

Gln Ile Glu Asp Gly Lys Gly Thr Ile Leu Ile Ser Ser Glu Glu Gly
 20 485 490 495

Glu Thr Glu Ala Asn Asn His Lys Lys Leu Ser Glu Phe Gly Ile Arg
 500 505 510

25 Asn Gly Ser Arg Leu Gln Ala Asp Asp Phe Leu Gln Asp Tyr Thr Leu
 515 520 525

Leu Ile Asn Ile Leu His Ser Glu Asp Leu Gly Lys Asp Val Glu Phe
 530 535 540

30 Glu Val Val Gly Asp Ala Pro Glu Lys Val Gly Xaa Lys Gln Ala Glu
 545 550 555 560

Asp Ala Ala Lys Ser Ile Thr Asn Gly Gln Xaa
 35 565 570

(2) INFORMATION FOR SEQ ID NO: 475:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu Thr His Cys
 1 5 10 15

50 Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu Arg Thr Pro
 20 25 30

Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe Gly Asn Lys
 35 40 45

55 Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser Ser Arg Val
 50 55 60

Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu Thr Phe Thr
 60 65 70 75 80

Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala Leu Ser Ile
85 90 95

5 Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro Pro Gly Cys
100 105 110

Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr Ser Ser Glu
115 120 125

10 Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu Pro Glu Phe
130 135 140

15 Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp Asp Gly Arg
145 150 155 160

Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln Thr Tyr Pro
165 170 175

20 Gln Pro Ser Pro Ser Ser Ser Met Thr Cys Lys Val Met Thr Ser Trp
180 185 190

Ala Val Ser Pro Trp Thr Thr Leu Gly Arg Cys Gln Val Ala Arg Leu
195 200 205

25 Glu Pro Ala Arg Ala Val Lys Ser Ser Gly Arg Cys Leu Ser Pro Val
210 215 220

30 Leu Arg Ala Glu Arg Ser Ser Ser Arg Cys Trp Leu Ala Ser Gly Arg
225 230 235 240

Pro Cys Val Ala Val Ser Cys Leu Ser Ser Ser Pro Ala Ser Pro Gly
245 250 255

35 His Ser Gln Pro Val Val Ser Ser Leu Thr Pro Thr Gly Ala Gly Gln
260 265 270

Gln Ala Phe Val Phe Ser Lys Asn Val Leu Ser Ser Leu Trp Tyr Leu
275 280 285

40 Asn Leu Thr Val Leu Ala Glu Asn Val Asn Met Cys Val Cys Cys Val
290 295 300

45 Asn Ser Phe Ser Cys Trp Glu Xaa
305 310

- 50 (2) INFORMATION FOR SEQ ID NO: 476:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Gln His His Leu Trp Ile Leu Leu Leu Cys Leu Gln Thr Trp
1 5 10 15

60 Pro Glu Ala Ala Gly Lys Asp Ser Glu Ile Phe Thr Val Asn Gly Ile

20 25 30
 Leu Gly Glu Ser Val Thr Phe Pro Val Asn Ile Gln Glu Pro Arg Gln
 35 40 45
 5 Val Lys Ile Ile Ala Trp Thr Ser Lys Thr Ser Val Ala Tyr Val Thr
 50 55 60
 10 Pro Gly Asp Ser Glu Thr Ala Pro Val Val Thr Val Thr His Arg Asn
 65 70 75 80
 Tyr Tyr Glu Arg Ile His Ala Leu Gly Pro Asn Tyr Asn Leu Val Ile
 85 90 95
 15 Ser Asp Leu Arg Met Glu Asp Ala Gly Asp Tyr Lys Ala Asp Ile Asn
 100 105 110
 20 Thr Gln Ala Asp Pro Tyr Thr Thr Thr Lys Arg Tyr Asn Leu Gln Ile
 115 120 125
 Tyr Arg Arg Leu Gly Lys Pro Lys Ile Thr Gln Ser Leu Met Ala Ser
 130 135 140
 25 Val Asn Ser Thr Cys Asn Val Thr Leu Thr Cys Ser Val Glu Lys Glu
 145 150 155 160
 Glu Lys Asn Val Thr Tyr Asn Trp Ser Pro Leu Gly Glu Glu Gly Asn
 165 170 175
 30 Val Leu Gln Ile Phe Gln Thr Pro Glu Asp Gln Glu Leu Thr Tyr Thr
 180 185 190
 Cys Thr Ala Gln Asn Pro Val Ser Asn Asn Ser Asp Ser Ile Ser Ala
 195 200 205
 35 Arg Gln Leu Cys Ala Asp Ile Ala Met Gly Phe Arg Thr His His Thr
 210 215 220
 40 Gly Leu Leu Ser Val Leu Ala Met Phe Phe Leu Leu Val Leu Ile Leu
 225 230 235 240
 Ser Ser Val Phe Leu Phe Arg Leu Phe Lys Arg Arg Gln Asp Ala Ala
 245 250 255
 45 Ser Lys Lys Thr Ile Tyr Thr Tyr Ile Met Ala Ser Arg Asn Thr Gln
 260 265 270
 Pro Ala Glu Ser Arg Ile Tyr Asp Glu Ile Leu Gln Ser Lys Val Leu
 275 280 285
 50 Pro Ser Lys Glu Glu Pro Val Asn Thr Val Tyr Ser Glu Val Gln Phe
 290 295 300
 55 Ala Asp Lys Met Gly Lys Ala Ser Thr Gln Asp Ser Lys Pro Pro Gly
 305 310 315 320
 Thr Ser Ser Tyr Glu Ile Val Ile Xaa
 325

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

-5

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

10 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
 1 5 10 15
 Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
 20 25 30
 15 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
 35 40 45
 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
 20 50 55 60
 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
 65 70 75 80
 25 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
 85 90 95
 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
 100 105 110
 30 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
 115 120 125
 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
 35 130 135 140
 Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
 145 150 155 160
 40 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
 165 170 175

Ala Xaa

45

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

55

Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val
 1 5 10 15
 Ile Leu Gly Leu Leu Cys Leu Leu Leu Cys Gly Gly Gly Glu Gly Lys
 20 25 30

60

Val Ala Gly Arg Gln Ala Val Thr Ser Asp Gln Gln Ser Val Gly Arg
 35 40 45

-5 Arg Asp Val Tyr
 50

10 (2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Gln Lys Lys Asn Ser Leu Phe Phe Phe Phe Ala Phe Tyr Tyr Glu
 1 5 10 15

20 Asn Lys Thr Asn Ala Pro Gly Glu Gly Ser Met Ile Thr Arg Asn Ile
 20 25 30

25 Lys Glu Tyr Phe Leu Pro Phe Leu Phe Cys Cys Val Glu Ala Ser Ile
 35 40 45

Ala Ile Asn Lys Leu Asn Tyr Leu His Trp Thr His Phe Gln
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

40 Met Pro Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
 1 5 10 15

Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
 20 25

45

(2) INFORMATION FOR SEQ ID NO: 481:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
 1 5 10 15

60 Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
 20 25 30

645

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
 35 40 45
 - 5 His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
 50 55 60
 Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
 65 70 75 80
 10 His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
 85 90 95
 15 Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
 100 105 110
 Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
 115 120 125
 20 Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Xaa Glu Gln
 130 135 140
 Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
 145 150 155 160
 25 Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
 165 170 175
 30 Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
 180 185 190
 Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
 195 200 205
 35 Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
 210 215 220
 Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
 225 230 235 240
 40 Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
 245 250 255
 45 Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
 260 265 270
 Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
 275 280 285
 50 Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
 290 295 300
 Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
 305 310 315 320
 55 Gly Arg Tyr Leu Gln Met Lys Ala Lys Xaa Gln Gly His Ala Xaa Xaa
 325 330 335
 60 Gln Pro Xaa

(2) INFORMATION FOR SEQ ID NO: 482:

-5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Leu Asn Ser Asn Ile Asn Asp Leu Leu Met Val Thr Tyr Leu Ala
1 5 10 15
Asn Leu Thr Gln Ser Gln Ile Ala Leu Asn Glu Lys Leu Val Asn Leu
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 483:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
1 5 10 15
Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr Arg Ile Gly
20 25 30
Cys Phe Lys Thr Ile Thr Cys Trp Pro Thr Ser Leu Thr Gln Arg Xaa
35 40 45

40

45

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Tyr Met Tyr Ser Leu Asn Val Phe Leu Ser Phe Ile Phe Leu Ala
1 5 10 15
Leu Val Phe Lys Cys Val His Val Cys Gln Gly Ala Asn Ala Phe Leu
20 25 30
Phe Leu Lys Leu Val Phe
35

60

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Gly Leu Arg Leu Ile Cys Leu Glu Leu Thr Met Val Lys Ala Leu
 1 5 10 15
 Val Cys Glu Met Phe Leu Phe Phe Leu Met Thr Gln Lys Leu Ile Trp
 20 25 30
 Gln Glu Cys Thr Glu Lys Phe Ala Lys Leu Leu Val Gln Leu Ile Ser
 35 40 45
 Leu Val Phe Ala Trp Glu Phe Phe Ser Glu Asp Thr Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
 1 5 10 15
 Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
 20 25 30
 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
 35 40 45
 Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
 50 55 60
 Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met
 65 70 75 80
 Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu
 85 90 95
 Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys
 100 105 110
 Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr
 115 120 125
 Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala
 130 135 140

648

Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp
 145 150 155 160
 Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu
 -5 165 170 175
 Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala
 180 185 190
 10 Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr
 195 200 205
 Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly
 210 215 220
 15 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys
 225 230 235 240
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe
 20 245 250 255
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly
 260 265 270
 25 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser
 275 280 285
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val
 290 295 300
 30 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu
 305 310 315 320
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met
 35 325 330 335
 Leu Ala Thr Gly Gly Asn Arg Lys Lys Xaa
 340 345

40

(2) INFORMATION FOR SEQ ID NO: 487:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

50 Met Glu Glu Val Leu Leu Leu Gly Leu Lys Asp Arg Glu Gly Tyr Thr
 1 5 10 15
 Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Cys Met Leu
 20 25 30
 55 Ile Glu Leu Ala Leu Arg Gly Arg Leu Gln Leu Glu Ala Cys Gly Met
 35 40 45
 60 Arg Arg Lys Ser Leu Leu Thr Arg Lys Val Ile Cys Lys Ser Asp Ala
 50 55 60

Pro Thr Gly Asp Val Leu Leu Asp Glu Ala Leu Lys His Val Lys Glu
65 70 75 80

- 5 Thr Gln Pro Pro Glu Thr Val Gln Asn Trp Ile Glu Leu Leu Ser Gly
85 90 95

Glu Thr Trp Asn Pro Leu Lys Leu His Tyr Gln Leu Arg Asn Val Arg
100 105 110

10 Glu Arg Leu Ala Lys Asn Leu Val Glu Lys Gly Val Leu Thr Thr Glu
115 120 125

Lys Gln Asn Phe Leu Leu Phe Asp Met Thr Thr His Pro Leu Thr Asn
15 130 135 140

Asn Asn Ile Lys Gln Arg Leu Ile Lys Lys Val Gln Glu Ala Val Leu
145 150 155 160

20 Asp Lys Trp Val Asn Asp Pro His Arg Met Asp Arg Arg Leu Leu Ala
165 170 175

Leu Ile Tyr Leu Ala His Ala Ser Asp Val Leu Glu Asn Ala Phe Ala
180 185 190

25 Pro Leu Leu Asp Glu Gln Tyr Asp Leu Ala Thr Lys Arg Val Arg Gln
195 200 205

Leu Leu Asp Leu Asp Pro Glu Val Glu Cys Leu Lys Ala Asn Thr Asn
30 210 215 220

Glu Val Leu Trp Ala Val Val Ala Ala Phe Thr Lys Xaa
225 230 235

35

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

45 Met Ala Gln Arg Met Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp
1 5 10 15

Ile Glu Lys Asp Gln Ile Ile Glu Met Ala Cys Leu Ile Thr Asp Ser
20 25 30

50 Asp Leu Asn Ile Leu Ala Glu Gly Pro Asn Leu Ile Ile Lys Gln Pro
35 40 45

Asp Glu Leu Leu Asp Ser Met Ser Asp Trp Cys Lys Glu His His Gly
55 50 55 60

Lys Ser Gly Leu Thr Lys Ala Val Lys Glu Ser Thr Ile Thr Leu Gln
65 70 75 80

60 Gln Ala Glu Tyr Glu Phe Leu Ser Phe Val Arg Gln Gln Thr Pro Pro

650

85 90 95

Gly Leu Cys Pro Leu Ala Gly Asn Ser Val His Glu Asp Lys Lys Phe
100 105 110

- 5 Leu Asp Lys Tyr Met Pro Gln Phe Met Lys His Leu His Tyr Arg Ile
115 120 125

10 Ile Asp Val Ser Thr Val Lys Glu Leu Cys Arg Arg Trp Tyr Pro Glu
130 135 140

Glu Tyr Glu Phe Ala Pro Lys Lys Ala Ala Ser His Arg Ala Leu Asp
145 150 155 160

15 Asp Ile Ser Glu Ser Ile Lys Glu Leu Gln Phe Tyr Arg Asn Asn Ile
165 170 175

Phe Lys Lys Lys Ile Asp Glu Lys Lys Arg Lys Ile Ile Glu Asn Gly
180 185 190

20 Glu Asn Glu Lys Thr Val Ser Xaa
195 200

25

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

35 Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly
1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala
20 25 30

40 Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu
35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala
50 55 60

45 Asp Ala Ala Asp Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu
65 70 75 80

50 Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln
85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
100 105 110

55 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
115 120 125

60 Val Arg Thr Gly Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
130 135 140

651

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
 145 150 155 160
 5 Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
 165 170 175
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
 180 185 190
 10 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
 195 200 205
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
 210 215 220
 15 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
 225 230 235 240
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
 20 245 250 255
 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
 260 265 270
 25 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
 275 280 285
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
 290 295 300
 30 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
 305 310 315 320
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
 35 325 330 335
 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His Xaa
 340 345 350

40

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

50

Met Arg Gly Ser Arg Gly Gly Trp Ala Gly Glu Met Ala Ala Ser Gly
 1 5 10 15

Glu Ser Gly Thr Ser Gly Gly Gly Gly Ser Thr Glu Glu Ala Phe Met
 20 25 30

55

Thr Phe Tyr Ser Glu Val Lys Gln Ile Glu Lys Arg Asp Ser Val Leu
 35 40 45

60

Thr Ser Lys Asn Gln Ile Glu Arg Leu Thr Arg Pro Gly Ser Ser Tyr
 50 55 60

652

Phe Asn Leu Asn Pro Phe Glu Val Leu Gln Ile Asp Pro Glu Val Thr
 65 70 75 80
 5 Asp Glu Glu Ile Lys Lys Arg Phe Arg Gln Leu Ser Ile Leu Val His
 85 90 95
 Pro Asp Lys Asn Gln Asp Asp Ala Asp Arg Ala Gln Lys Ala Phe Glu
 100 105 110
 10 Ala Val Asp Lys Ala Tyr Lys Leu Leu Leu Asp Gln Glu Gln Lys Lys
 115 120 125
 Arg Ala Leu Asp Val Ile Gln Ala Gly Lys Glu Tyr Val Glu His Thr
 15 130 135 140
 Val Lys Glu Arg Lys Lys Gln Leu Lys Lys Glu Gly Lys Pro Thr Ile
 145 150 155 160
 20 Val Glu Glu Asp Asp Pro Glu Leu Phe Lys Gln Ala Val Tyr Lys Gln
 165 170 175
 Thr Met Lys Leu Phe Ala Glu Leu Glu Ile Lys Arg Lys Glu Arg Glu
 180 185 190
 25 Ala Lys Glu Met His Glu Arg Lys Arg Gln Arg Glu Glu Glu Ile Glu
 195 200 205
 Ala Gln Glu Lys Ala Lys Arg Glu Arg Glu Trp Gln Lys Asn Phe Glu
 30 210 215 220
 Glu Ser Arg Asp Gly Arg Val Asp Ser Trp Arg Asn Phe Gln Ala Asn
 225 230 235 240
 35 Thr Lys Gly Lys Lys Glu Lys Lys Asn Arg Thr Phe Leu Arg Pro Pro
 245 250 255
 Lys Val Lys Met Glu Gln Arg Glu Xaa
 260 265
 40

(2) INFORMATION FOR SEQ ID NO: 491:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

50 Asp Ser Met Pro Thr Cys Pro Leu Xaa Ala Ser Leu Glu Cys Gly Pro
 1 5 10 15
 Leu Leu Pro Val Arg Leu Cys Cys Leu
 55 20 25

(2) INFORMATION FOR SEQ ID NO: 492:

60

653

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Asn Glu Tyr Arg Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu
 1 5 10 15

10 Lys Ser Leu Ser Phe Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp
 20 25 30

Tyr Ile Tyr Ala Val Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg
 35 40 45

15 Asp Leu Val His Arg Gln Thr Ala Ser Ala Val Val Gln His Met Ser
 50 55 60

20 Leu Gly Val Tyr Gly Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu
 65 70 75 80

Asn Tyr Val Trp Pro Asn Val Phe Glu Thr Ser Pro His Val Ile Gln
 85 90 95

25 Ala Val Met Gly Ala Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys
 100 105 110

Arg Met Leu Gln Tyr Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys
 115 120 125

30 Val Arg Asp Val Tyr Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser
 130 135 140

35 Gln Asp Ala Leu Ile Ala His Tyr Pro Arg Ile Tyr Gln Arg Xaa
 145 150 155

40 (2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ile Ser Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met
 1 5 10 15

50 Tyr Asp Gly Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln
 20 25 30

Leu Glu Asp Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala
 35 40 45

55 Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu
 50 55 60

60 Phe Ser Gly Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr
 65 70 75 80

654

Gly Pro Val Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys
 85 90 95
 5 Glu Glu Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro
 100 105 110
 His Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln
 115 120 125
 10 Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys
 130 135 140
 Asn Leu Ile Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro
 15 145 150 155 160
 Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn
 165 170 175
 20 Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr
 180 185 190
 Leu Leu Val Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile
 195 200 205
 25 Trp Ile Ser Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln
 210 215 220
 Ala Leu Leu Thr Val Val Ser Gln Val Leu Cys Phe Leu Xaa Ile Glu
 30 225 230 235 240
 Trp Tyr Leu Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn
 245 250 255
 35 Leu Leu Tyr Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val
 260 265 270
 Met Ile Gln Lys Pro Trp Xaa
 275
 40

(2) INFORMATION FOR SEQ ID NO: 494:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:
 50 Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1 5 10 15
 55 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
 20 25 30
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
 35 40 45
 60 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

655

[illegible]

30

(2) INFORMATION FOR SEQ ID NO: 495:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

[illegible]

656

Xaa Pro Gly Pro Ser Pro Trp Arg Ser Pro Ala Arg Arg Pro Ala Gln
 115 120 125

5 Leu Pro Pro Pro Asp Ser Asp Leu Cys Ser Gly Pro Leu Leu Pro Gly
 130 135 140

Pro Phe Ser Pro Pro Ala Cys His Thr Ala Pro Asn Ser Val Leu Ile
 145 150 155 160

10 Gln Ser Leu Phe Cys Lys Ser Glu Leu Trp Trp Arg Gln Met Arg Ser
 165 170 175

Ile Thr Trp Val Pro Ser Pro Lys Ala Gly Trp Arg Trp Thr Lys Gly
 180 185 190

15 Arg Lys Gln Ala Ser Pro His Arg Ile Leu Phe His Xaa
 195 200 205

20 (2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

30 Met Ala Leu Thr Leu Leu Pro Ser Val Ser Arg Leu Pro Gly Glu Arg
 1 5 10 15

Met Ala Ala Ser Gly Leu Pro Tyr Val Leu His His Lys Ser Ser Leu
 20 25 30

35 Met Lys Val Ile Phe Phe Pro Tyr Pro Val Leu Pro Leu Pro Ala Pro
 35 40 45

Asn Gly Thr Trp Val Pro Arg Leu Val Leu Gly Leu Gly Ser Gly Asp
 50 55 60

40 Gln Val His Tyr Leu Pro Ile Ser Ser Ser Ile Val Asn Tyr Gly Thr
 65 70 75 80

Ser Val Ser Gly Lys Ser Trp Val Phe Leu Val Tyr Pro Leu His Pro
 85 90 95

Thr Pro Thr Trp Ser Thr Arg Cys Phe Gln Val Trp Asp Leu Leu Ser
 100 105 110

50 Val Glu Leu Pro Asp Lys Gly Glu Gly Asn Thr Arg Arg Ala Ser Gly
 115 120 125

Val Pro Gly Leu Ser Gln Leu Pro Thr Ser His Lys Pro Ile Lys Gln
 130 135 140

55 Glu Tyr Xaa
 145

60

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
 1 5 10 15

Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys Glu Val Gly
 20 25 30

Ala Ala Leu Pro Pro Arg Gly Pro Ser Leu Ser Asp Cys Leu Gly Leu
 35 40 45

Pro Pro Trp Thr Pro Trp Gly Pro Ala Trp Thr Leu Ala Gln Ser Xaa
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Ser Thr Gly Ala Leu Asn Thr Ser Pro Pro Ala Ser Asn Arg Leu
 1 5 10 15

Glu Ser Thr Leu Asn Glu Tyr Leu Ile Gln Pro Gln Leu His Cys Ser
 20 25 30

Ser Val Gln Arg Leu Thr Leu Lys Trp Gly Cys Ser Ser Leu Gln Arg
 35 40 45

Asp Gly Gln Ala Val Pro Trp Gly Leu Trp Gln Arg Ala Tyr Pro Ser
 50 55 60

Leu Leu Pro Thr Leu Pro Ser Asp Leu Leu Arg Pro His Ala Val Thr
 65 70 75 80

Pro Ser Val Ser Val Ser Val His Thr Cys Glu Ser Ser Xaa
 85 90

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

658

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Xaa Leu Phe Ser Ser Ser
1 5 10 15

5 Leu Pro Phe Leu Trp Leu
20

10 (2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Arg Gly Gly Leu Cys Pro Leu Leu Val Pro Gly Pro Leu Ala Arg Gln
1 5 10 15

Glu Pro Ser Pro Ser Leu Gln Gly Cys Ser Glu Ser Pro Val Gly Met
20 25 30

Asp

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15

Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Pro Gly Lys Pro Gln Ala Cys Pro Glu Leu Thr Ser Val Leu Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

659

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

5 Asn Lys Ser Leu Xaa Ser Cys Leu Phe Val Leu His Phe Val Leu His
1 5 10 15

10 Cys Xaa Phe

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

15 Met Glu Lys Thr His Arg Leu Arg Ile Arg Asn Pro Cys Leu Gln Phe
1 5 10 15

20 Ser Ile Leu Asn Leu Phe Leu Leu Lys Met Ile Val Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

35 Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln
1 5 10 15

40 Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu
20 25 30

45 Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly
35 40 45

Pro Ser Ser Phe Gln Asn Pro Ala Ser Ser Pro Ser Ser Trp Thr His
50 55 60

50 Glu Glu Glu Pro Gly Tyr Phe Pro Gln Tyr Xaa
65 70 75

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Leu Pro Leu Ala Glu Leu Lys Asn Trp Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Leu Trp Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu
 1 5 10 15

Ser Asp Thr Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr
 20 25 30

Gly Asp Val Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys
 35 40 45

Thr Gly Val Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val
 50 55 60

Ala Arg Lys Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe
 65 70 75 80

Met Met Asp Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg
 85 90 95

Val Leu Gln Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu
 100 105 110

Ser His Ala Ala Arg Arg His Gln Arg Xaa Leu Leu Ala Ala Ile Asn
 115 120 125

Ala Phe Arg Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val
 130 135 140

Asn Ser Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu
 145 150 155 160

Gln Gln Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp
 165 170 175

Thr Leu Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala
 180 185 190

Leu Gly Pro Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

661

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

5 Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
 1 5 10 15
 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala
 20 25 30
 10 Val Xaa Lys Lys
 35

15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

25 Met Ala Leu Val Ala Leu Phe Thr Gln Leu Met Arg Xaa Leu Gly Arg
 1 5 10 15
 Cys Pro Gln

30

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

40 Met Thr Phe Pro Phe Glu Lys Glu Asn Ser Cys Phe Gln Cys Leu Leu
 1 5 10 15
 Phe Asp Ser Trp Arg Glu Gln Thr Arg Thr Asn Ile Gln Pro Gln Arg
 20 25 30
 45

50

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

60 Met His Leu Leu Asp Phe Phe Arg Asp Leu Val Leu Leu Val Leu Leu
 1 5 10 15

662

Ala Leu Leu Asp Ser Phe Trp Leu Glu Val Gln Lys
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

10

Met Cys Leu Ile His Phe Ile Lys Ile Ile Leu Val Phe Ile Leu Lys
 1 5 10 15

Leu Trp Leu Tyr Ser Gln Lys Cys Pro Lys
 20 25

20

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

25

30

Met Ile His Val His Glu Trp Asn Asp Gln Met Leu Met Val Tyr Ile
 1 5 10 15

Phe Leu Tyr Pro Val Ser Ile Thr Phe Leu Asn Leu Cys Ser Leu Thr
 20 25 30

35

Cys

40

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

45

Leu Asn Glu Ser Tyr Val Ser Arg Ala Gly Gly Trp Phe Ser Met Phe
 1 5 10 15

Xaa Leu Ile Phe Phe Leu Leu Ala Leu Gly Ser Xaa Leu Cys Leu Leu
 20 25 30

55

Leu Cys Leu Pro Ser Phe Asn Lys Thr Arg Arg Lys Gln Lys Pro
 35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5 Ser Ser Lys Thr Pro Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly Ser
 10 1 5 10 15
 Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu Gly
 20 25 30
 15 Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp
 35 40

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

25 Leu Asn Trp
 30 1

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

35 Phe Ala Phe Cys Ala Glu Leu Met Ile Gln Asn Trp Thr Leu Gly Ala
 1 5 10 15
 40 Val Asp Ser Gln Met Asp Asp Met Asp Met Asp Leu Asp Lys Glu Phe
 20 25 30
 Leu Gln Asp Leu Lys Glu Leu Lys Val Leu Val Ala Asp Lys Asp Leu
 35 40 45
 50 Leu Asp Leu His Lys Ser Leu Val Cys Thr Ala Leu Arg Gly Lys Leu
 50 55 60
 Gly Val Phe Ser Glu Met Glu Ala Asn Phe Lys Asn Leu Ser Arg Gly
 65 70 75 80
 55 Leu Val Asn Val Ala Ala Lys Leu Thr His Asn Lys Asp Val Arg Asp
 85 90 95
 60 Leu Phe Val Asp Leu Val Glu Lys Phe Val Glu Pro Cys Arg Ser Asp
 100 105 110

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His Trp Pro Leu Ser Asp Val Arg Phe Phe Leu Asn Gln Tyr Ser Ala
115 120 125

5 Ser Val His Ser Leu Asp Gly Phe Arg His Gln Ala Ser Gly Thr Ala
130 135 140

Thr Trp Ala Pro Ser Ala Ala Ala Ser Cys Ala Cys Ile Met Thr Glu
145 150 155 160

10 Val Pro Pro Asn Ala Pro Pro Thr Leu Thr Ile Lys Leu Leu
165 170

15

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

20 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

25 Met Trp Lys Asn Leu Gly Ser Gly Ser Val Phe Val Thr Trp Phe Ser
1 5 10 15

Leu Val Met Ile Leu Ser Gly Ile Gly Pro Leu Gly Asp Ala Glu Asp
20 25 30

30 Ser Ile Ser Asp Val Ser His Arg Leu Arg Pro
35 40

35 (2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Phe Gln Phe Pro Leu Leu Thr Ile Ala Leu Gln Phe Leu
1 5 10

45

(2) INFORMATION FOR SEQ ID NO: 520:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

55

Met His Tyr Val Ile Val Leu Ser Leu Phe Val Val Leu Glu Lys Lys
1 5 10 15

60 Asn Lys Met Gly Ser Asp Gly Cys Leu Arg Lys Asn Gly Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Arg Ser Ile Val Leu Arg Gly Ser Leu Phe Leu Phe Phe Ser
1 5 10 15
His Tyr Thr Leu Lys Leu Leu Ser Val Ile Lys Gln Thr Asn Arg Lys
20 25 30
Ile Val Trp Glu Lys Pro Cys Ile Arg Leu Phe Tyr Xaa Val Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Leu Pro Val Leu Leu Cys Leu Thr Leu Pro Met Pro Leu Pro
1 5 10 15
Ser Ala Thr Ala Arg Gly Gly Asn Arg Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Ser Ser Ile Pro Val Ser Ile Leu Ile Gly Met Lys Leu Ile Leu Tyr
1 5 10 15
Leu Leu Ile Thr Glu Ser Gly Ser His Glu Lys Lys Ser Phe Tyr Pro
20 25 30
Ser Phe Lys Tyr Met Phe Lys Ile Ile Ile Tyr Val Ser Ala Tyr Cys
35 40 45
Arg Thr Ala Leu Arg Ala Thr Val Ser His
50 55

666

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Asn Arg Thr Leu Leu Phe Leu Ile Leu Phe Val Leu Phe Gly Leu Gly
 1 5 10 15

Tyr Gly Phe

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Phe Leu Leu Val Leu Ser Val Phe Cys Asp Phe Met Cys Ser Ile
 1 5 10 15

Ala Pro Arg Cys His Ala Leu Ser Leu Val Ser Leu Arg Ala Gln His
 20 25 30

Leu Ser Leu Phe Ile Thr Cys His
 35 40

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Leu Leu Phe Ile Leu Leu Thr Leu Ser Ser Gly Cys Arg Leu Leu
 1 5 10 15

Val Ser Ser Trp Lys Thr Phe Leu Pro His Phe Ser Leu Pro Gly Pro
 20 25 30

Arg Glu His Pro Glu Gly Ser Arg Thr Trp Phe Phe Arg Tyr Trp Glu
 35 40 45

Pro Gly Ala His Cys Leu His Cys Ala
 50 55

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

667

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

5 -
 Ala Arg Leu Leu Leu Phe Leu Ser Ser Val His Pro Ser Ile Met Pro
 1 5 10 15
 Ser Cys Asn Gln Leu
 10 20

(2) INFORMATION FOR SEQ ID NO: 528:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

20 Met Ser Leu Thr Ser Ser Leu Thr Phe Leu Ser His Ile Leu Leu Leu
 1 5 10 15
 25 Pro Gln Lys Leu Gln Phe Leu Ser Trp Met Glu Arg Gln Gln Arg Cys
 20 25 30
 Thr Gly Val Ala Lys Tyr Ala
 30 35

(2) INFORMATION FOR SEQ ID NO: 529:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

40 Met Val Leu Arg Leu Ile Gln Leu Ile Phe Leu Ile Phe Phe Ile His
 1 5 10 15
 45 Ile Ile Ile Leu Leu Ile Pro Gly Ser Arg Pro Cys Gly Ser Trp Val
 20 25 30
 Asn Asp Arg Xaa Leu Gly Leu Arg Asp Val Thr His Leu Ile Tyr Leu
 35 40 45
 50 His Trp Val His Gly His Leu Pro Trp Cys His Pro Tyr Ile Gln Val
 50 55 60
 Glu Phe Ser Ala Leu Ile Glu Ser Thr Ala Gln Leu Gly Leu Pro Phe
 65 70 75 80
 55 Ser Trp Val Arg Val Ile His Pro Phe Leu Val Leu Pro Cys Leu Tyr
 85 90 95
 60 Ser Pro Gly Leu Lys Asn Gly Ile Phe Leu Phe Leu Leu Arg Ala Met
 100 105 110

Pro Gly Gly Met Phe Pro Gly Asn Leu Glu Ala Phe Arg Val Pro Val
115 120 125

5 -

10 (2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
1 5 10 15

20 Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
20 25 30

25 Trp Gly Phe Gly Xaa Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
35 40 45

Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
50 55 60

30 His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
65 70 75 80

Pro Asn

35

(2) INFORMATION FOR SEQ ID NO: 531:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
1 5 10 15

50 Tyr Trp Thr Met
20

55 (2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

669

Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln Leu Lys Ile
 1 5 10 15

5 Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu Lys Ile Ile
 20 25 30

Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser Trp Ala Ile
 35 40 45

10 Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn Lys Thr Ala
 50 55 60

15 Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 533:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15

30 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Xaa Ser Tyr Leu Trp
 20 25 30

Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Xaa Trp Ala Cys
 35 40 45

35 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu
 50 55 60

40

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15

Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30

55 Ile Leu Phe Phe Ile Val Phe
 35

60 (2) INFORMATION FOR SEQ ID NO: 535:

670

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Leu

1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Asp Gln Phe Lys Ile Phe Tyr Phe Leu Lys Ala Phe Phe Ala Cys
1 5 10 15

Cys Asn Val Gln Asp Pro Ser Pro Phe Met Gly Glu Thr Gly Ser Tyr
20 25 30

Leu Asn Ile Gly
35

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Asp Phe Leu Ser Tyr Phe Lys Asp Leu Leu Ser Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Gly Phe Gly Phe Val Leu Asn Ile Phe Ser Phe Phe Leu Xaa Pro
1 5 10 15

Pro Leu

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

Leu Leu Leu Trp Thr Leu Leu Ala Xaa Tyr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 1 5 10 15

Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 20 25 30

Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45

Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60

Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
 85 90 95

Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Xaa
 100 105

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Phe Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met
 1 5 10 15

Leu Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr
 20 25 30

Leu Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser
 35 40 45

672

Pro Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe
 50 55 60

5 -Trp Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr
 65 70 75 80

Leu Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val
 85 90 95

10 Asp Gly Glu Glu Leu Gln Met Glu Pro Val
 100 105

15 (2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

20 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

25 Met Asp Arg Phe Thr Val Ala Gly Val Leu Pro Asp Ile Glu Gln Phe
 1 5 10 15

Phe Asn Ile Gly Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile
 20 25 30

30 Ser Ser Tyr Met Val Leu Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg
 35 40 45

Tyr Asn Arg Lys Tyr Leu Met Cys Gly Gly Ile Ala Phe Trp Ser Leu
 50 55 60

35 Val Thr Leu Gly Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu
 65 70 75 80

40 Leu Leu Thr Arg Gly Leu Val Gly Val Gly Glu Ala Ser Tyr Ser Thr
 85 90 95

Ile Ala Pro Thr Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Thr
 100 105 110

45 Gly Cys Ser Ala Ser Ser Thr Leu Pro Phe Arg Trp Ala Val Val Trp
 115 120 125

Ala Thr Leu Gln Ala Pro Lys Xaa
 130 135

50

(2) INFORMATION FOR SEQ ID NO: 543:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

60

Met Ala Gly Asp Trp His Trp Ala Leu Arg Val Thr Pro Gly Leu Gly
 1 5 10 15
 Val Val Ala Val Leu Leu Leu Phe Leu Val Val Arg Glu Pro Pro Arg
 5 20 25 30
 Gly Ala Val Glu Arg His Ser Asp Leu Pro Pro Leu Asn Pro Thr Ser
 35 40 45
 10 Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg Asn Pro Ser Phe Val Leu
 50 55 60
 Ser Ser Leu Gly Phe Thr Ala Val Ala Phe Val Thr Gly Ser Leu Ala
 65 70 75 80
 15 Leu Trp Ala Pro Ala Phe Leu Leu Arg Ser Arg Val Val Leu Gly Glu
 85 90 95
 Thr Pro Pro Cys Leu Pro Gly Asp Ser Cys Ser Ser Ser Asp Ser Leu
 20 100 105 110
 Ile Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val Gly Leu
 115 120 125
 25 Gly Val Glu Ile Ser Arg Arg Xaa Arg His Ser Asn Pro Arg Ala Asp
 130 135 140
 Pro Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe Leu Phe
 145 150 155 160
 30 Leu Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr Ile Phe
 165 170 175
 Ile Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile Val Ala
 35 180 185 190
 Asp Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr Ala Glu
 195 200 205
 40 Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly Ser Pro
 210 215 220
 Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp Pro Pro
 225 230 235 240
 45 Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met Leu Cys
 245 250 255
 Ala Phe Val Gly Ala Leu Gly Gly Ala Leu Ser Trp Ala Pro Xaa Ser
 50 260 265 270
 Ser Leu Arg Pro Thr Ala Gly Gly His Ser Cys Thr Cys Arg Ala Cys
 275 280 285
 55 Cys Thr Lys Gln Gly Pro Gln Thr Thr Gly Leu Trp Cys Pro Ser Gly
 290 295 300
 Ala Ala Pro Pro Ala Cys Pro Trp Pro Val Cys Ser Ser Glu Arg Leu
 305 310 315 320
 60

674

Pro Leu Thr Tyr Leu His Ile Cys His Ser Xaa Pro Trp Ala His Pro
325 330 335

Thr Lys Gly Leu Gly Leu Thr Pro Trp Pro Gly Pro Ala Ser Arg Gly
340 345 350

Thr Leu Gly Arg Val Pro Ala Pro Arg His Tyr Xaa Gly Ser Ser Gly
355 360 365

10 Glu Glu Val Gly Val Gln Glu Gly Asp Pro Ser Pro Gln Gly Xaa Pro
370 375 380

Gln Gly Leu Gly Ala Ile Cys Asn Gly Ile Lys Phe Val Ala Arg Pro
385 390 395 400

15 Gln Val Pro Ala Leu Val Phe Leu Trp Val Ala Ser Asp Leu Ala Pro
405 410 415

20 Arg Leu His Pro Arg Ala Pro Glu
420

25 (2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Phe Arg Phe Val Ile Cys Leu Phe Leu Trp Leu Val Leu Cys Arg
1 5 10 15

35 Asp Ser Thr Ser Ala Ser Arg Ile Ala Leu Tyr Tyr Arg Ile Val Phe
20 25 30

Leu Ile His Gln Cys Ser Ser
35

40

(2) INFORMATION FOR SEQ ID NO: 545:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Pro Trp Xaa Ala Gln Leu Leu Asp Arg Thr Ile Gly Pro Leu
1 5 10 15

55 Tyr Leu Leu Phe Val Gln Phe Ser Pro Ala Phe Ser Arg Thr Ser Pro
20 25 30

Trp Arg Ser Pro Lys Asn Phe Arg Arg Leu Tyr Pro Pro Cys Thr Thr
35 40 45

60 Ser Gly Cys Ala Ala Arg Trp Leu Phe Ser

50

55

5 (2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Gly Leu Ser Val Leu Leu Pro Leu Cys Leu Leu Gly Pro Gly Arg

1

5

10

15

15

Phe Thr Ser Gly Gln Lys Pro Leu Asp Thr Pro Gly Leu Gly Val Pro

20

25

30

Phe

20

(2) INFORMATION FOR SEQ ID NO: 547:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu

1

5

10

15

35

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr

20

25

30

Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu

35

40

45

40

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe

50

55

60

45

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr

65

70

75

80

Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala

85

90

95

50

Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr

100

105

110

Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln

115

120

125

55

Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala

130

135

140

60

Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu

145

150

155

160

676

Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly
 165 170 175
 5 Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu
 180 185 190
 Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val
 195 200 205
 10 Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu
 210 215 220
 Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val
 225 230 235 240
 15 Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys
 245 250 255
 20 Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser
 260 265 270
 Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn
 275 280 285
 25 Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp
 290 295 300
 Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe
 305 310 315 320
 Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp
 325 330 335
 35 Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu
 340 345 350
 Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln
 355 360 365
 40

(2) INFORMATION FOR SEQ ID NO: 548:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

50 Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15
 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 20 25 30
 Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45
 60 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro

677

50

55

60

Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
 65 70 75

5

(2) INFORMATION FOR SEQ ID NO: 549:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

15

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
 1 5 10 15

20

His Cys Trp Gly Leu Pro Leu Ala Cys Gly Thr Phe Val Gln Gly His
 20 25 30

Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala
 35 40 45

25

(2) INFORMATION FOR SEQ ID NO: 550:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

35

Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr
 1 5 10 15

40

Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys
 20 25 30

Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys
 35 40 45

45

Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn
 50 55 60

Tyr Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile
 65 70 75 80

50

Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala
 85 90 95

Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile
 100 105 110

55

Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val
 115 120 125

60

Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg
 130 135 140

678

Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln Ala Lys Leu Pro Gly
 145 150 155 160

5 -Ile Ala Lys Lys Lys Ala Glu Xaa
 165

10 (2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Ser Val Pro Phe His Leu Leu Val Val Leu Arg Ser Arg Ala Val Arg
 1 5 10 15

20 Ala Arg Arg Arg Arg Glu Pro Arg Ser Leu Pro Arg Pro Gly Asp Glu
 20 25 30

25 Glu Leu Gln Leu Leu Leu Cys Gly Ala Arg Ser Asp Phe Leu Glu Arg
 35 40 45

Cys Glu Glu Asp Trp Val Cys Leu Trp His His Ala Asp His Ala Ala
 50 55 60

30 Phe Pro Gly Ser Phe Gln Cys His Gln Cys Gly Phe Leu Pro His Pro
 65 70 75 80

Gly Ser Ser Leu Cys His His Gln Leu Gln Asp Leu Gln Val Arg His
 85 90 95

35 Pro Ser Cys Thr Glu Val Arg Arg Arg Pro Ser Ile Gln Ser Leu Pro
 100 105 110

40 Gly Arg Arg His Tyr Ser Val Leu Arg Ser Phe Pro
 115 120

45 (2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp
 1 5 10 15

55 Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His
 20 25 30

Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile
 35 40 45

60

679

Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His
 50 55 60

Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu
 5 65 70 75 80

Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro
 85 90 95

Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg
 10 100 105 110

Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr
 115 120 125

Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn
 130 135 140

Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val
 145 150 155 160

Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser
 165 170 175

25 Leu

30 (2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15

Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30

Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45

Thr Glu Gly Ile Pro Cys Ala Lys Ile Pro Glu Trp Val Thr His Leu
 50 55 60

Thr Trp Gln Thr Leu Lys Asn Ser
 65 70

55 (2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Val Leu Arg Ile Ile Cys Leu Trp Pro Cys Gly Thr Thr Leu Pro Leu
 1 5 10 15
 Val Glu Lys Ala His Asp Ser His Ser Ala Asp Pro Val Cys Pro Gly
 20 25 30
 10 Leu Thr Ala His Leu Pro Val Leu Leu Tyr Val Gln Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

15 Met Lys His Ala Asp Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser
 1 5 10 15
 25 Pro Leu Leu Met Thr Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu
 20 25 30
 Ser Leu Gly Pro Arg Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg
 35 40 45
 30 Gly Phe Met Ile Val Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr
 50 55 60
 35 Ile Val Tyr Glu Phe Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp
 65 70 75 80
 Arg Cys Asp Pro Gln Asp Cys Thr Leu Gly Gln Cys Pro Ser Val Pro
 85 90 95
 40 Ser Pro Xaa Thr Pro Val Thr Lys Ala Tyr Val Val Arg Thr Glu Gln
 100 105 110
 Gly Thr Gly Pro Pro Leu Pro Thr Ala Ala Leu Gln Gly Pro Arg Leu
 115 120 125
 45 Trp Phe Leu Thr His Phe Pro Arg Ala Ala Pro Gly Met Trp Pro His
 130 135 140
 50 Cys Cys Leu Pro Leu Gln Ser Trp Gly Leu Lys Gly Leu Tyr Ser Tyr
 145 150 155 160
 Phe Pro Leu Pro Ala Leu Lys Leu Gly Arg Gly Ala Leu Arg Ala Gly
 165 170 175
 55 Pro Thr Lys Gly Leu Val Ala Phe Phe Leu Thr Gln Lys Arg Ser Ala
 180 185 190
 Ile Met Ser Leu Trp Thr Gln Ser His Ser Ser Thr Pro His Thr Glu
 195 200 205
 60

681

Ala Val Ala Ser Gly Pro Lys Val Arg Val Gly Gly Gly Leu Gly Ile
 210 215 220

5 Gln Pro Val Glu Ala Ala Tyr Ser Thr Cys Val Leu Ile Lys Ser Asp
 225 230 235 240

Arg Gly Asn His Glu Lys Lys Lys Lys Lys Lys
 245 250

10

(2) INFORMATION FOR SEQ ID NO: 556:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

20 Gly Leu Ala Gly Leu Cys Gly Gln Leu Ser Ser Pro Ala Leu Cys Val
 1 5 10 15

Asn Arg Leu

25

(2) INFORMATION FOR SEQ ID NO: 557:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

35

Met Ile Thr Glu Lys Trp Gly Leu Asn Met Glu Tyr Cys Arg Gly Gln
 1 5 10 15

40 Ala Tyr Ile Xaa Ser Ser Gly Phe Ser Ser Lys Met Lys Val Val Ala
 20 25 30

Ser Arg Leu Leu Glu Lys Tyr Pro Gln Ala Ile Tyr Thr Leu Cys Ser
 35 40 45

45 Ser Cys Ala Leu Asn Met Trp Leu Ala Lys Ser Val Pro Val Met Gly
 50 55 60

Val Ser Val Ala Leu Gly Thr Ile Glu Glu Val Cys Ser Phe Phe His
 65 70 75 80

50

Arg Ser Pro Gln Leu Leu Glu Leu Asp Asn Val Ile Ser Val Leu
 85 90 95

55 Phe Gln Asn Ser Lys Glu Arg Gly Lys Glu Leu Lys Glu Ile Cys His
 100 105 110

Ser Gln Trp Thr Gly Arg His Asp Ala Phe Glu Ile Leu Val Glu Leu
 115 120 125

60

Leu Gln Ala Leu Val Leu Cys Leu Asp Gly Ile Asn Ser Asp Thr Asn

130 135 140

Ile Arg Trp Asn Asn Tyr Ile Ala Gly Arg Ala Phe Val Leu Cys Ser.
 145 150 155 160

5 -

Ala Val Ser Asp Phe Asp Phe Ile Val Thr Ile Val Val Leu Lys Asn
 165 170 175

10 Val Leu Ser Phe Thr Arg Ala Phe Gly Lys Asn Leu Gln Gly Gln Thr
 180 185 190

Ser Asp Val Phe Phe Ala Ala Gly Ser Leu Thr Ala Val Leu His Ser
 195 200 205

15 Leu Asn Glu Val Ile Gly Lys Tyr Xaa
 210 215

20 (2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu Asn Glu
 1 5 10 15

30 Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg Asn Thr
 20 25 30

Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile Asn Phe
 35 40 45

Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile Lys Leu
 50 55 60

40 Tyr Thr Ser Lys Ser Glu Leu Pro Thr Asp Asn Ser Glu Thr Val Glu
 65 70 75 80

Asn Thr

45

(2) INFORMATION FOR SEQ ID NO: 559:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Val Leu Ile Leu Leu Asn Leu Leu Leu Gly Gln Phe Ser Cys Met
 1 5 10 15

60 Ser Pro Ala Ser His His Cys His Pro Leu Pro Thr Glu Met Pro Cys
 20 25 30

Ser Ser Asp Trp Gly Phe Asp Ser His Thr Val Tyr Pro Ser Cys Val
 35 40 45

5 Asp Ala Leu Leu Pro Lys Pro Ser Ala Asn Ser Phe Pro Asn Gly Ser
 50 55 60

Cys His Cys Gln Gly Leu Tyr Asn Gln Gln Gln Gln Asn Leu His Ala
 65 70 75 80

10 Ala Glu Gly Pro Ala Ser Leu Arg Cys Asn Lys Tyr Val Ser Thr
 85 90 95

15

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

25

Met Ile Pro Ala Tyr Ser Lys Asn Arg Ala Tyr Ala Ile Phe Phe Ile
 1 5 10 15

Val Phe Thr Val Ile Gly Asp Ala Pro Gly Ala Val Leu Ser Cys Ala
 20 25 30

30

Gly His Pro Cys Val Gly Phe Ala Ala Val Leu Val Ala Pro Leu Thr
 35 40 45

Val Ala Val Ser Ser Xaa
 50

35

(2) INFORMATION FOR SEQ ID NO: 561:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

45

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 1 5 10 15

50

Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro
 35 40 45

55

Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys
 50 55 60

Asp Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu
 65 70 75 80

60

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg Ile
 85 90 95

5 Asn Val Gly Leu Arg Gly Trp Trp Leu Val Ala Xaa
 100 105

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
 1 5 10 15

20 Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
 20 25 30

Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
 35 40 45

25 Ala Pro
 50

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
 1 5 10 15

Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
 20 25 30

45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
 35 40 45

Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
 50 55 60

50 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
 65 70 75 80

55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
 85 90 95

Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
 100 105 110

60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

685

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg.
130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Leu Glu Asp Arg
145 150 155 160

10 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Thr
165 170 175

Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr
180 185 190

15 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val
195 200 205

Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
210 215 220

20 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys
225 230 235 240

25 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn Xaa
245 250

30 (2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Ser Phe Leu Met Trp Leu Met Ser Leu Ala Ile Thr Ser Gln Pro
1 5 10 15

40 Pro Met

45 (2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
1 5 10 15

55 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
20 25 30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
35 40 45

60

Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

5 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Phe
 65 70 75 80

10

(2) INFORMATION FOR SEQ ID NO: 566:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

20

His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln Val Leu Ser
 1 5 10 15

25

Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu Ala Pro Gly Arg
 20 25 30

Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro Trp Phe Thr Ala
 35 40 45

30

Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys Arg Gln Arg Arg
 50 55 60

Gln Glu Arg Arg Gln Met Lys Arg Leu
 65 70

35

(2) INFORMATION FOR SEQ ID NO: 567:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

45

Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys Lys Glu Glu Val Ile
 1 5 10 15

50

Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp Val Tyr Tyr Phe Ser
 20 25 30

Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu
 35 40 45

55

Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met
 50 55 60

Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro
 65 70 75 80

60

687

Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile
 85 90 95
 5 Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn
 100 105 110
 His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln
 115 120 125
 10 Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser
 130 135 140
 Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu
 15 145 150 155 160
 Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val
 165 170 175
 Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser
 20 180 185 190
 Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro
 195 200 205
 25 Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu
 210 215 220
 Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala
 30 225 230 235 240
 Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met
 245 250 255
 35 Asp Ser Gly Asp Glu Ala Xaa
 260

(2) INFORMATION FOR SEQ ID NO: 568:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Met Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala
 1 5 10 15
 50 Leu Arg Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Leu
 20 25 30
 Leu Phe Gly Leu Thr His Leu Asn Pro Ser Ala Lys Leu Leu Ser
 35 40 45
 55 Gln Met Lys Thr Ser Gly Asn Arg Lys Ser Glu Tyr Ser Lys Tyr Ala
 50 55 60
 60 Arg Asn Trp Lys Lys His
 65 70

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Pro Val Thr Ser Lys Arg Thr Leu Phe Phe Pro Asp Pro Cys Ser
 1 5 10 15

Tyr Asp Thr Pro Pro Pro Asp Cys His Cys His Ser Phe Arg Ala Glu
 20 25 30

Leu Leu

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 1 5 10 15

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 20 25 30

Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 35 40 45

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ser
 50 55 60

Lys Ala Pro Asn Ser Leu Gly Thr Thr Gly Leu Trp Ser Thr Val Tyr
 65 70 75 80

Ile Phe Thr Glu Val Phe His Asn Phe Ser Asn Asn Ser Ile Phe Ser
 85 90 95

Gly Lys Phe Leu Tyr Glu Val Xaa
 100

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

689

Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu Leu His Ile Val Leu
 1 5 10 15

5 Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala Trp Thr Leu Thr Asn
 20 25 30

Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu His Ala Val Lys Gly
 35 40 45

10 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His
 50 55 60

Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr Ser Ser Arg Lys Phe
 15 65 70 75 80

Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu Ala Ser Phe Tyr Thr
 85 90 95

20 Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr Ala Ser Leu Leu Ser
 100 105 110

Val Leu Ile Pro Lys Met Pro Gln Leu His Gly Val Arg Ile Phe Gly
 115 120 125

25 Ile Asn Lys Tyr
 130

30

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

40 Met Asn Lys Trp Ile Cys Glu Met His Cys Tyr Leu Val Leu Leu Ser
 1 5 10 15

Val Cys Ser Pro Ser Ala Leu Arg Arg Val Arg His Thr Leu Ser Arg
 20 25 30

45

50

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

60 Met Pro Val Leu Ser Leu Leu Cys Thr Leu Ile Val Ser Phe Gln Ser
 1 5 10 15

690

Ala Asp Ser Cys Glu Val Phe Leu Asn Cys Ser Leu
20 25

5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

10

15

Met Lys Val Ser Thr Met Leu Trp Phe Leu Cys Trp Glu Gln Ser His
1 5 10 15

Phe Leu Arg Glu Trp Glu Asp Leu Ser Thr Phe Leu Ile Leu Ile Gln
20 25 30

20

Met Glu Cys Gln Tyr Gly Asn Ser
35 40

25

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

30

35

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser
1 5 10 15

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Xaa Leu
20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

45

50

Met Lys Arg Gly Cys Leu Gly Leu Leu Phe Phe Ser Cys Cys Ser Ser
1 5 10 15

Ala Pro Thr Met Leu Leu Cys Asp Tyr Leu Asn Trp Phe
20 25

55

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

60

691

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

5 Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val
 1 5 10 15

Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu
 20 25 30

10 Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys
 35 40 45

Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys
 15 50 55 60

Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Xaa Asn Arg Arg Arg
 65 70 75 80

20 Xaa Val Arg Gly Leu Pro Ser Xaa Leu Thr Asn Ser
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15

35 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30

Arg Val Met Val Asn Leu Asn Ile Leu Phe
 40 35 40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 1 5 10 15

55 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Pro Pro Leu Ser
 20 25 30

Thr Phe Thr Ser Asp Phe Tyr Phe Met Glu Phe Gly Ile Glu Val Lys
 35 40 45

60

Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr Lys
 50 55 60

5 Lys Phe Asn Lys Lys Lys
 65 70

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Leu Arg Leu Leu Leu Val Ala Phe Ala Leu Val Val Val Leu
 1 5 10 15

20 Phe His Val Leu Leu Ala Pro Ile Thr Ala Leu Phe His Thr His Phe
 20 25 30

Tyr Asp Arg Leu Gln Asp Ala Gly Ser Arg Trp Pro Glu Leu Tyr Leu
 35 40 45

25 Tyr Ser Arg Ala Asp Glu Val Val Leu Ala Arg Asp Ile Glu Arg Met
 50 55 60

30 Val Glu Ala Arg Leu Ala Arg Arg Val Leu Ala Arg Ser Val Asp Phe
 65 70 75 80

Val Ser Ser Ala His Val Ser His Leu Arg Asp Tyr Pro Thr Tyr Tyr
 85 90 95

35 Thr Ser Leu Cys Val Asp Phe Met Arg Asn Cys Val Arg Cys
 100 105 110

40 (2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Met Phe Lys Leu Glu Glu Cys Gly Lys Thr Thr Phe Leu Leu Ser Met
 1 5 10 15

50 Ala Leu Tyr Phe Trp Trp Ile Val Gln Thr Thr Lys Gly Cys
 20 25 30

55 (2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

5 Met Glu Ser Asp Ala Leu Leu Leu Thr Ile Phe Trp Ile Ile Ala Arg
 - 1 5 10 15
 Ser Ser Val Arg Ser Val Gly Lys Ser Ser Gln Arg Ser Phe Thr Thr
 20 25 30
 10 Ile Thr Gln Leu Arg Ser Thr His Thr Gly Pro Ser Arg Arg Ser Tyr
 35 40 45
 Leu Ile Trp Trp Asn Gly Gly Pro Lys Arg Thr Ile Ser Tyr Val Ser
 50 55 60
 15 Arg Arg Phe Arg Ser Phe Arg
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

30 Val Gly Leu Phe Gln Pro Lys Thr Phe Gln Val Pro Val Thr Asp Leu
 1 5 10 15
 Tyr Ile Phe Ile Lys Ile Tyr Ser Glu Ile Gly Pro Ile Met His Val
 20 25 30
 35 Leu Cys Pro Gly Tyr Ser Gln Ser Pro Ser Thr Pro Pro Trp Thr
 35 40 45

40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

50 Met Trp Phe Gly Ser Asp Arg Ser Asp Leu Arg Ile Gly Thr Ala Phe
 1 5 10 15
 Leu Phe Asp Leu Val Cys Asp Leu Cys Ile His Ala Trp Lys Pro Pro
 20 25 30
 55 Gly Leu Val Arg Phe Ser Phe
 35

60

(2) INFORMATION FOR SEQ ID NO: 585:

694

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Leu Asn Thr Ala Ser Leu Asn Leu Pro Trp Lys Val Gln Leu Phe
 1 5 10 15

10 Ala His Ala

15 (2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Ala Cys Leu Leu Leu Phe Leu Ala Phe Ser Trp Lys Arg Lys
 1 5 10 15

25 Gly Leu Trp Ser Gly Pro Gly
 20

30

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

40 Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
 1 5 10 15

Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
 20 25 30

45 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
 35 40 45

Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
 50 55 60

50

Ala His Thr Val Ala
 65

55

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

60

695

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

5 Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
1 5 10 15

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
20 25 30

10 Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu
35 40 45

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
50 55 60

15 Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys
65 70 75

20

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

30 Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
1 5 10 15

Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
20 25 30

35 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
35 40 45

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
50 55 60

40 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
65 70 75 80

45 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
85 90 95

Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
100 105 110

50 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
115 120 125

Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
130 135 140

55 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
145 150 155

60

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Met Pro Glu Thr Arg Leu Gly His Arg Gln Gln Phe Ala Val Phe His
 1 5 10 15

Leu Xaa Pro Val Pro Pro Cys Gly
 20

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Leu Thr Phe Leu Phe Ser Ala Cys Ala Thr Cys Leu Gly Lys Leu
 1 5 10 15

Ala Ser Pro Leu Ala Pro Val Gly Pro Gln Gln Arg Gly Xaa Pro Pro
 20 25 30

Gly Pro Pro Leu Leu Ser
 35

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Asp Pro Phe His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu
 1 5 10 15

Val Phe Ala Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser
 20 25 30

Arg Arg Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp
 35 40 45

Glu Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
 50 55 60

Gln Lys Ala Glu Asn
 65

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

10 Asn Leu Arg Val Arg Leu Gly Asp Val Ile Ser Ile Gln Pro Cys Pro
 1 5 10 15
 Asp Val Lys Tyr Gly Lys Arg Ile His Val Leu Pro Ile Asp Asp Thr
 20 25 30

15 Val Glu Gly Ile Thr Gly Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr
 35 40 45
 Phe Leu Glu Ala Tyr Arg Pro Ile Arg Lys Gly Asp Ile Phe Leu Val
 50 55 60

20 Arg Gly Gly Met Arg Ala Val Glu Phe Lys Val Val Glu Thr Asp Pro
 65 70 75 80
 Ser Pro Tyr Cys Ile Val Ala Pro Asp Thr Val Ile His Cys Glu Gly
 85 90 95

25 Glu Pro Ile Lys Arg Glu Asp Glu Glu Glu Ser Leu Asn Glu Val Gly
 100 105 110
 Tyr Asp Asp Ile Gly Gly Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu
 115 120 125

30 Met Val Glu Leu Pro Leu Arg His Pro Ala Leu Phe Lys Ala Ile Gly
 130 135 140
 Val Lys Pro Pro Arg Gly Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly
 145 150 155 160

35 Lys Thr Leu Ile Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe Phe
 165 170 175
 Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser
 180 185 190

40 Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro
 195 200 205
 Ala Ile Ile Phe Ile Asp Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu
 210 215 220

45 Lys Thr His Gly Glu Val Glu Arg Arg Ile Val Ser Gln Leu Leu Thr
 225 230 235 240
 Leu Met Asp Gly Leu Lys Gln Arg Ala His Val Ile Val Met Ala Ala
 245 250 255

50 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg
 260 265 270
 Phe Asp Arg Glu Val Asp Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu

275

280

285

Glu Ile Leu Gln Ile His Thr Lys Asn Met Lys Leu Ala Asp Asp Val.
290 295 300

Asp Leu Glu Gln
305

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

Met Gln Ile Lys Leu Leu Lys Ser Val Lys Thr Val Phe Ala Ile Thr
1 5 10 15

Leu Leu Val Leu Phe Leu
20

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

Met Phe Pro Lys Phe Cys Pro Ile Leu Ser Leu Val Asp Phe Ile Ser
1 5 10 15

His Arg Asp Lys Pro Glu Thr Glu
20

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

Met Leu Ile Glu Cys Ala Trp Gln Leu Met Phe Leu Leu Leu Lys Val
1 5 10 15

Glu Gln Leu Gly Ile Leu Asp Lys
20

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

Met

1

10

(2) INFORMATION FOR SEQ ID NO: 598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

20 Met Cys Ile Met Ser Ala Leu Val

1

5

25 (2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

Met Phe Leu Val Trp Phe Phe Trp Gly Leu Ile Ser Ala Leu Ser Asn

1

5

10

15

35

Val His Thr Pro Ser Arg Leu Pro Ala

20

25

40

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

50 Met Xaa Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser

1

5

10

15

Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly

20

25

55

(2) INFORMATION FOR SEQ ID NO: 601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

60

700

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

5 Met Trp Thr Arg Ser Ser Arg Cys Leu Leu Leu Cys Ile Pro Gly Xaa
 1 5 10 15

Ser Arg Arg Arg Arg Ala Gly Ser Gly Met Lys Pro Arg Ser Trp Ser
 20 25 30

10 Ala Trp Arg Pro Ser Gly Gly Thr Gly Thr Ser Ser Ser Gln Ser Ser
 35 40 45

15 Thr Gln Ser Arg Thr Leu Ser Ala Thr Ala Ser Pro Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

20 Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
 1 5 10 15

30 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr
 20 25

(2) INFORMATION FOR SEQ ID NO: 603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

40 Met Pro Pro Lys Gln Glu Leu Gly Ser Gly Val Gly Glu Leu Ala Lys
 1 5 10 15

45 Asn Ser Lys Arg Gln His Trp Asn His Arg Trp Lys Lys Tyr Leu Lys
 20 25 30

50 Leu Ile Arg Trp Glu Asp Gly Leu Leu Leu Glu Gly Leu Leu Leu Val
 35 40 45

Leu Glu His Cys Ala Thr Met Ala Trp Asp Cys Leu Met Arg Leu Glu
 50 55 60

55 Leu Leu Lys Arg Leu
 65

(2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

Lys Ile Val Tyr Ile Leu Gly Asn Pro Leu Lys Phe Asn Ser Arg Val
 1 5 10 15
 Ile His His Leu Val Leu Leu Gln
 20

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Met Asn Leu His Gln Arg Arg Leu Leu Leu Ile Gly His Leu Met Thr
 1 5 10 15
 Leu Val Lys Ala Ser Lys Ser Phe Ser Phe Thr Glu Ile Thr Ser Ser
 20 25 30
 Arg Lys Lys
 35

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr
 1 5 10 15
 Tyr Asn Ile His Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val
 20 25 30
 Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr
 35 40 45
 Val Gly Pro Thr Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu
 50 55 60
 His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Xaa
 65 70 75 80
 Glu Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln
 85 90 95

Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro
 100 105 110

5 - Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln
 115 120 125

Ser His
 130

10

(2) INFORMATION FOR SEQ ID NO: 607:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

20 Met Leu Val Ile Phe Leu Phe Thr Ser Leu Leu Lys Ile Pro Ser Ser
 1 5 10 15

Val Pro Gly Leu Ile Asn Val
 20

25

(2) INFORMATION FOR SEQ ID NO: 608:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

35

Glu Leu Asp Tyr Ile Leu
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 609:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

50 Met Ala Pro Pro Gly Trp Gln Xaa Xaa Xaa Xaa Xaa Trp Leu Ala Cys
 1 5 10 15

Pro Asp Arg Gly Glu Leu Ser Ser Arg Ser Pro Pro Cys Arg Leu Ala
 20 25 30

55 Arg Trp Ala Glu Gly Asp Arg Glu Thr Arg Thr Cys Leu Leu Glu Leu
 35 40 45

Ser Ala Gln Ser Trp Gly Gly Arg Phe Arg Arg Ser Ser Ala Val Ser
 50 55 60

60

703

Ala Gly Ser Pro Ser Arg Leu His Phe Leu Pro Gln Pro Leu Leu Leu
65 70 75 80

5 - Arg Ser Ser Gly Ile Pro Ala Ala Ala Thr Pro Trp Pro Gln Pro Ala
85 90 95

Gly Leu Pro Val Arg Pro Thr Pro Thr Arg Thr Gly Glu Glu Asp Arg
100 105 110

10 Thr Leu Asp Ile Ser Ile Cys Thr Glu Val Leu Ala Gly Thr Glu Gln
115 120 125

Pro Pro Pro Pro Arg Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg
130 135 140

15 Leu Glu Thr Leu Asp Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg
145 150 155 160

20 Gly Lys Leu Asp Phe Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe
165 170 175

Gln Gly Glu Asp Arg Lys Phe Ala Pro Ser Asp Lys Ser Gln Pro Pro
180 185 190

25 Thr Thr Glu Arg Glu Gln Val Pro Val Ser Arg Ile Gln Thr Asp Leu
195 200 205

Thr Glu Ile Gly Ser Ser Met Arg Ser Pro Gly Val Ser Pro Arg Ile
210 215 220

30 Trp Leu Asp Phe Gln Ser Thr Xaa
225 230

35

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

45

Met Val Leu Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu
1 5 10 15

Leu Leu Asn Met Leu Ile Ala Leu Met Xaa Arg Asp Arg Gln Gln Cys
20 25 30

50

Arg His

55

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Met Val Phe Glu Gly Phe Ser Ser Ala Phe Cys Leu Ser Ser Thr Ala
1 5 10 15
Pro Thr Ser His Pro
20

10

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

Gly Lys Lys Asn Gln Leu Leu Val Ile
1 5

25

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
1 5 10 15

35

Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys
20 25

40

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

Met Ala Lys Arg Ser Pro Gly Gly Cys Gly Ser Gly Leu Ile Leu Leu
1 5 10 15

50

Cys Cys Gln Pro Cys Arg Pro Thr Ser Ser Ala Pro Met Arg
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

[illegible]

30 (2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

40 Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu
1 5 10 15
Asn Thr

45

(2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

55 Pro Arg Val Arg Asn Ser Pro Glu Asp Leu Gly Leu Ser Leu Thr Gly
 1 5 10 15

Asp Ser Cys Lys Leu
 20

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

5 Gln Ala Asp Asp Leu Gln Ala Thr Val Ala Ala Leu Cys Val Leu Arg
 1 5 10 15
 Gly Gly Gly Pro Trp Ala Gly Ser Trp Leu Ser Pro Lys Thr Pro Gly
 20 25 30
 15 Ala Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg
 35 40 45
 20 Lys Arg Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

25 Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu Ala Xaa Xaa
 1 5 10 15
 35 Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp Phe Gly Gly
 20 25 30
 Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr Leu Trp Leu
 35 40 45
 40 Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val Val Pro Gly
 50 55 60
 Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val Met Gly Val
 45 65 70 75 80
 Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys Leu Glu Phe
 85 90 95
 50 Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Ile Gln Tyr
 100 105 110
 Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln Glu Ala Trp
 115 120 125
 55 Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala Ala Arg Xaa
 130 135 140
 60 His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg Gln Val Arg
 145 150 155 160

Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met Val Asp Ile
 165 170 175

5 Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn Leu Ser Ser
 180 185 190

Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala Gly Lys Leu
 195 200 205

10 Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro Arg Gln Leu
 210 215 220

15 Pro Glu Pro Ser Gln Gln Ser Lys
 225 230

(2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly
 1 5 10 15

30 Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser
 20 25 30

Gly Ala Gly Lys
 35

(2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
 1 5 10 15

50 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
 20 25 30

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45

55 His Lys Ala Lys Ser His Pro Glu Val
 50 55

(2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln
1 5 10 15
Pro Ser Asp

(2) INFORMATION FOR SEQ ID NO: 623:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

Asn Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser
1 5 10 15
Lys Ser Tyr

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys Ile Phe
1 5 10 15
Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met Asn Ser
20 25 30
Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser Asp Ser
35 40 45
Ala Gly Pro
50

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Ile Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala
1 5 10 15

5 His Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys
20 25 30

Lys Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu
35 40 45

10 Gln Lys Gln Leu Leu Arg His Ala Lys His His Thr
50 55 60

15 (2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

25 Asp Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser
1 5 10 15

Ser His Asn Leu Ala Val His Arg Met Ile His Thr Gly Glu Lys
20 25 30

30 (2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

40 Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile Cys Lys Ser
1 5 10 15

Glu Pro Asn Thr Asp Gln Leu Asp Tyr
20 25

45 (2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

55 Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
1 5 10 15

60 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
20 25 30

710

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45
 5 - His Lys Ala Lys Ser His Pro Glu Val Xaa Ile Thr Ser Thr Asp Ile
 50 55 60
 Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln Pro Ser Asp Xaa Asn Ser
 65 70 75 80
 10 Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys Ser
 85 90 95
 Tyr Xaa Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys
 15 100 105 110
 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met
 115 120 125
 20 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser
 130 135 140
 Asp Ser Ala Gly Pro Xaa Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala
 145 150 155 160
 25 Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met Ile His
 165 170 175
 Thr Gly Glu Lys His Tyr Xaa
 30 180

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His
 1 5 10 15
 45 Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys
 20 25 30
 Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln
 35 40 45
 50 Lys Gln Leu Leu Arg His Ala Lys His His Thr Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

711

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

5 - Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu
 1 5 10 15
 Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

20 Glu Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu
 1 5 10 15
 Met Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val
 20 25 30
 25 Leu Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu
 35 40 45
 30 Trp Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg
 50 55 60
 Met Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val
 65 70 75 80
 35 Gln Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu
 85 90 95
 Asn Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met
 100 105 110

40

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

50

Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg Pro Thr Gly Gln Gln
 1 5 10 15

55 Leu Glu Ser Leu Gly Leu Leu Ala
 20

60

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

Val His Arg Glu Glu Ala Ser Cys Tyr Cys Gln Ala Glu Pro Ser Gly
1 5 10 15

10 Asp Leu

15 (2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Arg Pro Ala Leu Arg Gln Ala Gly Gly Gly Thr Arg Glu Pro Arg Gln
1 5 10 15

25 Lys Arg Trp Ala Gly Leu
20

30

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

40 Ala Val Asn Phe Arg Pro Gln Arg Ser Gln Ser Met
1 5 10

45 (2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val
1 5 10 15

55 Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val Ala Val Asn Asn
20 25 30

Pro Lys Lys Gln Glu
35

60

(2) INFORMATION FOR SEQ ID NO: 637:

5 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

10

Glu Glu Met Ala Asp Ser Val Lys Thr Phe Leu Gln Asp Leu Ala Arg
 1 5 10 15

15

Gly Ile Lys Asp Ser Ile Trp Gly Ile Cys Thr Ile Ser Lys Leu Asp
 20 25 30

Ala Arg Ile Gln Gln Lys Arg Glu Glu Gln Arg Arg Arg Arg Ala Ser
 35 40 45

20

Ser Val Leu Ala Gln Arg Arg Ala Gln Ser Ile Glu Arg Lys Gln Glu
 50 55 60

Ser Glu Pro Arg Ile Val Ser Arg Ile Phe Gln Cys Cys Ala Trp Asn
 65 70 75 80

25

Gly Gly Val Phe Trp Phe Ser Leu Leu Leu Phe Tyr Arg Val Phe Ile
 85 90 95

30

Pro Val Leu Gln Ser Val Thr Ala Arg Ile Ile Gly Asp Pro Ser Leu
 100 105 110

His Gly Asp Val Trp Ser Trp Leu Glu Phe Phe Leu Thr Ser Ile Phe
 115 120 125

35

Ser Ala Leu Trp Val Leu Pro Leu Phe Val Leu Ser Lys Val Val Asn
 130 135 140

Ala Ile Trp Phe Gln Asp Ile Ala Asp Leu Ala Phe Glu Val Ser Gly
 145 150 155 160

40

Arg Lys Pro His Pro Phe Pro Ser Val Ser Lys Ile Ile Ala Asp Met
 165 170 175

45

Leu Phe Asn Leu Leu Leu Gln Ala Leu Phe Leu Ile Gln Gly Met Phe
 180 185 190

Val Ser Leu Phe Pro Ile His Leu Val Gly Gln Leu Val Ser Leu Leu
 195 200 205

50

His Met Ser Leu Leu Tyr Ser Leu Tyr Cys Phe Glu Tyr Arg Trp Phe
 210 215 220

Asn Lys Gly Ile Glu Met His Gln Arg Leu Ser Asn Ile Glu Arg Asn
 225 230 235 240

55

Trp Pro Tyr Tyr Phe Gly Phe Gly Leu Pro Leu Ala Phe Leu Thr Ala
 245 250 255

60

Met Gln Ser Ser Tyr Ile Ile Ser Gly Cys Leu Phe Ser Ile Leu Phe
 260 265 270

Pro Leu Phe Ile Ile Ser Ala Asn Glu Ala Lys Thr Pro Gly Lys Ala
 275 280 285

5 - Tyr Leu Phe Gln Leu Arg Leu Phe Ser Leu Val Val Phe Leu Ser Asn
 290 295 300

Arg Leu Phe His Lys Thr Val Tyr Leu Gln Ser Ala Leu Ser Ser Ser
 305 310 315 320

10 Thr Ser Ala Glu Lys Phe Pro Ser Pro His Pro Ser Pro Ala Lys Leu
 325 330 335

Lys Ala Thr Ala Gly His
 15 340

(2) INFORMATION FOR SEQ ID NO: 638:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Met Ala Lys Phe Met Thr Pro Val Ile Gln Asp Asn Pro Ser Gly Trp
 1 5 10 15

30 Gly Pro Cys Ala Val Pro Glu Gln Phe Arg Asp Met Pro Tyr Gln Pro
 20 25 30

Phe Ser Lys Gly Asp Arg Leu Gly Lys Val Ala Asp Trp Thr Gly Ala
 35 35 40 45

Thr Tyr Gln Asp Lys Arg Tyr Thr Asn Lys Tyr Ser Ser Gln Phe Gly
 50 55 60

40 Gly Gly Ser Gln Tyr Ala Tyr Phe His Glu Glu Asp Glu Ser Ser Phe
 65 70 75 80

Gln Leu Val Asp Thr Ala Arg Thr Gln Lys Thr Ala Tyr Gln Arg Asn
 85 90 95

45 Arg Met Arg Phe Ala Gln Arg Asn Leu Arg Arg Asp Lys Asp Arg Arg
 100 105 110

Asn Met Leu Gln Phe Asn Leu Gln Ile Leu Pro Lys Ser Ala Lys Gln
 115 120 125

50 Lys Glu Arg Glu Arg Ile Arg Leu Gln Lys Lys Phe Gln Lys Gln Phe
 130 135 140

Gly Val Arg Gln Lys Trp Asp Gln Lys Ser Gln Lys Pro Arg Asp Ser
 55 145 150 155 160

Ser Val Glu Val Arg Ser Asp Trp Glu Val Lys Glu Glu Met Asp Phe
 165 170 175

60 Pro Gln Leu Met Lys Met Arg Tyr Leu Glu Val Ser Glu Pro Gln Asp

	180	185	190
	Ile Glu Cys Cys Gly Ala Leu Glu Tyr Tyr Asp Lys Ala Phe Asp Arg		
	195	200	205
5	Ile Thr Thr Arg Ser Glu Lys Pro Leu Arg Xaa Xaa Lys Arg Ile Phe		
	210	215	220
10	His Thr Val Thr Thr Thr Asp Asp Pro Val Ile Arg Lys Leu Ala Lys		
	225	230	235 240
	Thr Gln Gly Asn Val Phe Ala Thr Asp Ala Ile Leu Ala Thr Leu Met		
	245	250	255
15	Ser Cys Thr Arg Ser Val Tyr Ser Trp Asp Ile Val Val Gln Arg Val		
	260	265	270
	Gly Ser Lys Leu Phe Phe Asp Lys Arg Asp Asn Ser Asp Phe Asp Leu		
	275	280	285
20	Leu Thr Val Ser Glu Thr Ala Asn Glu Pro Pro Gln Asp Glu Gly Asn		
	290	295	300
25	Ser Phe Asn Ser Pro Arg Asn Leu Ala Met Glu Ala Thr Tyr Ile Asn		
	305	310	315 320
	His Asn Phe Ser Gln Gln Cys Leu Arg Met Gly Lys Glu Arg Tyr Asn		
	325	330	335
30	Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met Asp Lys Asn Glu		
	340	345	350
	Ile Ala Ser Val Ala Tyr Arg Tyr Arg Ser Gly Lys Leu Gly Asp Asp		
	355	360	365
35	Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val Met Thr Gly Ala		
	370	375	380
40	Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu Asn Glu Trp Asp		
	385	390	395 400
	Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys Leu Asp Ser Gln		
	405	410	415
45	Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn Ser Tyr Lys Leu		
	420	425	430
	Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser Glu Tyr Leu Lys		
	435	440	445
50	Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser Ser Arg His Val		
	450	455	460
55	Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe Ala Ser Gln Ile		
	465	470	475 480
	Asn Leu Ser Val Glu Asn Ala Trp Gly Ile Leu Arg Cys Val Ile Asp		
	485	490	495
60	Ile Cys Met Lys Leu Glu Glu Gly Lys Tyr Leu Ile Leu Lys Asp Pro		

500

505

510

Asn Lys Gln Val Ile Arg Val Tyr Ser Leu Pro Asp Gly Thr Phe Ser
 515 520 525

5 -

Ser

10

(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

20

Lys Lys Arg His Thr Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile
 1 5 10 15

Thr Thr Asp Leu Gly Lys His Gln His Met His Asp Arg Asp Asp Leu
 20 25 30

25

Tyr Ala Glu Gln Met Glu Arg Glu Met Arg His Lys Leu Lys Thr Ala
 35 40 45

Phe Lys Asn Phe Ile Glu Lys Val Glu Ala Leu Thr Lys Glu Glu Leu
 50 55 60

30

Glu Phe Glu Val Pro Phe Arg Asp Leu Gly Phe Asn Gly Ala Pro Tyr
 65 70 75 80

35

Arg Ser Thr Cys Leu Leu Gln Pro Thr Ser Ser Ala Leu Val Asn Ala
 85 90 95

Thr Glu Trp Pro Pro Phe Val Val Thr Leu Asp Glu Val Glu Leu Ile
 100 105 110

40

His Phe Xaa Arg Val Gln Phe His Leu Lys Asn Phe Asp Met Val Ile
 115 120 125

Val Tyr Lys Asp Tyr Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro
 130 135 140

45

Val Ala Ser Leu Asp Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu
 145 150 155 160

50

Lys Tyr Thr Glu Gly Val Gln Ser Leu Asn Trp Thr Lys Ile Met Lys
 165 170 175

Thr Ile Val Asp Asp Pro Glu Gly Phe Phe Glu Gln Gly Gly Trp Ser
 180 185 190

55

Phe Leu

60

(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

Arg Ser Gly Leu Gly Leu Gly Ile Thr Ile Ala Phe Leu Ala Thr Leu
 1 5 10 15
 Ile Thr Gln Phe Leu Val Tyr Asn Gly Val Tyr Gln Tyr Thr Ser Pro
 20 25 30
 Asp Phe Leu Tyr Ile Arg Ser Trp Leu Pro Cys Ile Phe Phe Ser Gly
 35 40 45
 Gly Val Thr Val Gly Asn Ile Gly Arg Gln Leu Ala Met Gly Val Pro
 50 55 60
 Glu Lys Pro His Ser Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser Val Glu
 1 5 10 15
 Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Xaa Xaa Pro Xaa
 20 25 30
 Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr
 35 40 45
 Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe
 50 55 60
 Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile Ser Asn
 65 70 75 80
 Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp
 85 90 95
 Thr Arg Arg Ser Gly
 100

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

718

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

5 Met Glu Ala Gln Gln Val Asn Glu Ala Glu Ser Ala Arg Glu Gln Leu
 1 5 10 15
 Gln Xaa Leu His Asp Gln Ile Ala Gly Gln Lys Ala Ser Lys Gln Glu
 20 25 30
 10 Leu Glu Thr Glu Leu Glu Arg Leu Lys Gln Glu Phe His Tyr Ile Glu
 35 40 45
 Glu Asp Leu Tyr Arg Thr Lys Asn Thr Leu Gln Ser Arg Ile Lys Asp
 50 55 60
 15 Arg Asp Glu Glu Ile Gln Lys Leu Arg Asn Gln Leu Thr Asn Lys Thr
 65 70 75 80
 Leu Ser Asn Ser Ser Gln Ser Glu Leu Glu Asn Arg Leu His Gln Leu
 85 90 95
 Thr Glu Thr Leu Ile Gln Lys Gln Thr Met Leu Glu Ser Leu Ser Thr
 100 105 110
 25 Glu Lys Asn Ser Leu Val Phe Gln Leu Glu Arg Leu Glu Gln Gln Met
 115 120 125
 Asn Ser Ala Ser Gly Ser Ser Ser Asn Gly Ser Ser Ile Asn Met Ser
 130 135 140
 30 Gly Ile Asp Asn Gly Glu Gly Thr Arg Leu Arg Asn Val Pro Val Leu
 145 150 155 160
 Phe Asn Asp Thr Glu Thr Asn Leu Ala Gly Met Tyr Gly Lys Val Arg
 165 170 175
 Lys Ala Ala Ser Ser Ile Asp Gln Phe Ser Ile Arg Leu Gly Ile Phe
 180 185 190
 40 Leu Arg Arg Tyr Pro Ile Ala Arg Val Phe Val Ile Ile Tyr Met Ala
 195 200 205
 Leu Leu His Leu Trp Val Met Ile Val Leu Leu Thr Tyr Thr Pro Glu
 210 215 220
 45 Met His His Asp Gln Pro Tyr Gly Lys
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

60 Ile Arg His Glu Gln His Pro Asn Phe Ser Leu Glu Met His Ser Lys
 1 5 10 15

Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile Leu Ile Leu Pro
20 25 30

5 - Val Cys Ala His Leu His Glu Glu Leu Asn Cys
35 40

10 (2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

Ser Phe Phe Ile Ser Glu Glu Lys Gly His Leu Leu Leu Gln Ala Glu
1 5 10 15

20 Arg His Pro Trp Val Ala Gly Ala Leu Val Gly Val Ser Gly Gly Leu
20 25 30

25 Thr Leu Thr Thr Cys Ser Gly Pro Thr Glu Lys Pro Ala Thr Lys Asn
35 40 45

Tyr Phe Leu Lys Arg Leu Leu Gln Glu Met His Ile Arg Ala Asn
50 55 60

30

35

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97897
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209043
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer <div style="text-align: center; margin-top: 10px;">Susan White PCT International Division</div>	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>119</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97898</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209044
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97899
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209045
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <div style="text-align: center;">Susan White POT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>130</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit April 28, 1997	Accession Number 209011
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97900
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97901
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209046
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209047</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

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A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 22, 1997	Accession Number 209076
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>140</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 .. United States of America	
Date of deposit August 21, 1997	Accession Number 209215
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97904
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>154</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit July 3, 1997	Accession Number 209139
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209049
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97903
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit June 12, 1997	Accession Number 209119
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97902
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209048
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209050
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 12, 1998</u>	Accession Number <u>209627</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
 - (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;
 - (f) a polynucleotide which is a variant of SEQ ID NO:X;
 - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
 - (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
 - (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.
2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.
3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

5 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

10 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15 15. A method of making an isolated polypeptide comprising:
(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
(b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
(b) diagnosing a pathological condition or a susceptibility to a pathological
30 condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
(a) determining the presence or amount of expression of the polypeptide of
35 claim 11 in a biological sample; and
(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
(b) isolating the supernatant;
(c) detecting an activity in a biological assay; and
15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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16/18, C12Q 1/68, G01N 33/50, 33/53,
33/68, A61K 38/17

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(57) Abstract

The present invention relates to 186 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.

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